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All the aims of the present invention have been met by the embodiments as set out below.

The present inventors identified a range of specific nucleotide sequences which are involved in the molecular pathways eventually leading to programmed cell death. The present inventors were able to identify via macro array screening a range of genes involved in a pathway eventually leading to programmed cell death in the yeast *Saccharomyces cerevisiae*. As explained in Example 2, genes showing a difference of a factor 5 or more in expression as a result of *Bax*-induced cell death, were identified as differentially expressed candidate genes. Some of these genes are clearly down-regulated in a *Bax*-expressing strain, while other genes show an upregulated expression (Table 1). Example 3 describes a further experiment wherein the results of differential expression were analysed using the Pathways™ software and differentially expressed nucleic acid sequence were identified.

According to a first embodiment, the invention relates to the use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid sequence is selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more

preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

(c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 75 or 80% identical, more preferably more than 85%, or 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455;
- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e); and
- (g) the complement of any of the nucleic acid sequences as specified in a) to f),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

Sequence similarity searches were performed using the BLAST software package version 2. Identity and similarity percentages were calculated using
5 BLOSUM62 as a scoring matrix.

As known in the art, "similarity" between two polypeptides is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one polypeptide to the sequence of a second polypeptide. Moreover, also known in the art is "identity" which means the degree of sequence relatedness between two polypeptide
10 or two polynucleotide sequences as determined by the identity of the match between two strings of such sequences. Both identity and similarity can be readily calculated. While there exist a number of methods to measure identity and similarity between two polynucleotide or polypeptide sequences, the terms "identity" and "similarity" are well known to skilled artisans (Carillo and Lipton, 1988). Methods commonly employed to
15 determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Huge Computers (Bishop, 1994) and Carillo and Lipton (1988). Preferred methods to determine identity are designed to give the largest match between the two sequences tested. Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine
20 identity and similarity between two sequences include, but are not limited to, GCG program package (Devereux *et al.*, 1984), BLASTP, BLASTN and FASTA (Altschul *et al.*, 1990).

The nucleic acid sequences to be used according to this aspect of the invention from *Saccharomyces cerevisiae* are defined in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15,
25 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207,
30 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 457, 459, 461, 463, 465, 467, 469, 471 and 473.

The invention also relates to nucleic acid sequences from *Candida albicans*, as represented by the SEQ ID NOs 285, 287, 289, 291, 293, 295, 297, 299, 301, 303,
35 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371,

373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481, and 483.

The expression "a pathway eventually leading to programmed cell death" refers to a sequence of steps ultimately leading to cell death and which can be triggered at various steps in this pathway by various agents, such as Bax, Bak, CED4, hydrogen peroxide, diamide and farnesol.

The yeast or fungi according to the invention may be, but are not restricted to, pathogenic yeast or fungi. As such, yeast or fungi may cause infections in healthy individuals as well as in immunocompromised patients.

The expression "treating diseases associated with yeast and fungi", not only refers to diseases or infections caused by said organisms but also refers to allergic reactions caused by said organisms, such as the so-called "professional diseases" in, for instance, bakery and brewery and that are caused by yeast or fungi which are commonly known as "non-pathogenic".

The invention further relates to the use of nucleic acid sequence homologues of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483 but isolated from other yeast and fungi strains which are also involved in a pathway eventually leading to programmed cell death.

According to the invention, these sequences and their homologues in other yeast and fungi as well as the polypeptides which they encode represent novel molecular targets which can be incorporated into an assay to selectively identify compounds capable of inhibiting or activating expression of such polypeptides.

Furthermore, the invention also relates to the potential use of said sequences in alleviating diseases or conditions associated with yeast or fungi infections, such as diseases caused by *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*,
5 *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

According to another embodiment, the invention also relates to a nucleic acid sequence encoding a polypeptide which is involved in a pathway eventually leading to
10 programmed cell death of yeast or fungi selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386,
15 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which
20 is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366,
25 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which
30 is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402,
35 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;

- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NO 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481 or 483;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NO 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481 or 483; and,
- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e), and
- (g) the complement of any of the nucleic acid sequences as specified in a) to f).
- According to a more specific embodiment, these nucleic acid sequences are derived from *Saccharomyces cerevisiae*, *Candida albicans* or *Aspergillus fumigatus*.

A nucleic acid sequence according to the invention may comprise an mRNA sequence or alternatively a DNA sequence and preferably a cDNA sequence. A nucleic acid sequence according to the invention may also comprise any modified nucleotide known in the art.

The present invention further relates to a nucleic acid molecule capable of selectively hybridising to at least one of the nucleic acid molecules according to the invention, or the complement thereof.

The term "selectively hybridising" or "specifically hybridising" means hybridising under conditions wherein sequences can be detected which are homologues of the sequences of the invention, but which are for instance derived from heterologous cells or organisms, and wherein said sequences do not hybridize with known sequences. In a preferred embodiment, mammalian homologues can be detected. It is well known to the person skilled in the art which methods for hybridisation can be used and which conditions are necessary for selectively or specifically hybridising. Preferably, hybridization under high stringency conditions can be applied (Sambrook et al., 1989).

As such, the present invention also relates to the use of the nucleic acid sequences of the invention for detecting homologues in heterologous organisms including but not limited to mammalian organisms.

The term "nucleic acid sequence" also includes the complementary sequence
5 to any single stranded sequence given, or the antisense version thereof.

The invention also relates to mRNA, DNA or cDNA versions of the nucleic acid molecules of the invention.

The present invention more particularly relates to an antisense molecule comprising a nucleic acid sequence capable of hybridizing to any of the above defined
10 nucleic acid sequences.

Polynucleotides according to the invention may be inserted into vectors in an antisense orientation in order to provide for the production of antisense RNA. Antisense RNA or other antisense nucleic acids may also be produced by synthetic means.

The present invention also advantageously provides nucleic acid sequences of
15 at least approximately 10 contiguous nucleotides of a nucleic acid according to the invention and preferably from 10 to 50 nucleotides. These sequences may, advantageously be used as probes or primers to initiate replication, or the like. Such nucleic acid sequences may be produced according to techniques well known in the art, such as by recombinant or synthetic means. The probes will hybridise specifically
20 with any of the nucleic acid molecules of the invention. The primers will specifically amplify any of the nucleic acid molecules of the invention.

The probes or primers according to the invention may also be used in diagnostic kits or the like for detecting the presence of a nucleic acid according to the invention. These tests generally comprise contacting the probe with the sample under
25 hybridising conditions and detecting the presence of any duplex or triplex formation between the probe and any nucleic acid in the sample.

According to the present invention these probes may be anchored to a solid support. Preferably, they are present on an array so that multiple probes can simultaneously hybridize to a single biological sample. The probes can be spotted onto
30 the array or synthesized *in situ* on the array. (Lockhart *et al.*, 1996). A single array can contain more than 100, 500 or even 1,000 different probes in discrete locations. Such arrays can be used to screen for compounds interacting with said probes.

Advantageously, the nucleic acid sequences, according to the invention may be produced using recombinant or synthetic means, such as for example using PCR
35 cloning mechanisms which generally involve making a pair of primers, which may be from approximately 10 to 50 nucleotides to a region of the gene which is desired to be

cloned, bringing the primers into contact with mRNA, cDNA, or genomic DNA from the yeast or fungal cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified region or fragment and recovering the amplified DNA. Generally, such techniques as defined
5 herein are well known in the art, such as described in Sambrook *et al.* (1989). These techniques can be used to clone homologues of the nucleic acid sequences of the invention in other organisms.

The nucleic acids or oligonucleotides according to the invention may carry a revealing label. Suitable labels include radioisotopes such as ^{32}P , ^{33}P or ^{35}S , enzyme
10 labels or other protein labels such as biotin or fluorescent markers. Such labels may be added to the nucleic acids or oligonucleotides of the invention and may be detected using techniques known in the art.

According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a
15 suitable expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to a control sequence, such as a suitable inducible promotor, or the like, to ensure expression of the proteins according to the invention in a suitable host cell. The expression vector may also comprise a reporter molecule. The expression vector may advantageously be
20 a plasmid, cosmid, virus or other suitable vector which is known to those skilled in the art. The expression vector and the host cell defined herein also form part of the present invention. Preferably the host cell is a lower eukaryotic cell such as a yeast cell or a fungal cell. Yeast and fungal cells are particularly advantageous because they provide the necessary post-translational modifications to the expressed proteins of the
25 invention, similar to those of the natural proteins from which they are derived. These modifications confer optimal conformation of said proteins, which when isolated may advantageously be used in kits, methods or the like.

The invention further relates to any nucleic acid as defined above for use as a medicament.

30 Nucleotide sequences according to the invention are particularly advantageous for providing selective therapeutic targets for treating yeast or fungi-associated infections. For example, an antisense nucleic acid capable of binding to the nucleic acid sequences according to the invention may be used to selectively inhibit expression of the corresponding polypeptides, leading to impaired growth or death of yeast and
35 fungi with reductions of associated illnesses or diseases.

According to another embodiment, the invention also relates to the use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from :

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2,
5 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48,
50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92,
94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126,
128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158,
160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190,
10 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222,
224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254,
256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286,
288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318,
320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350,
15 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382,
384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414,
416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446,
448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478,
480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of
20 said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar,
preferably more than 75% or 80% similar, more preferably more than 85%, 90% or
95% similar and most preferably more than 97% similar to any of the amino acid
sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28,
25 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72,
74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112,
114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144,
146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176,
178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208,
30 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240,
242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272,
274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304,
306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336,
338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368,
35 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400,
402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,

434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484; and,

(d) a functional fragment of any of said proteins as defined in a) to c), for the preparation of a medicament for treating diseases associated with yeast or fungi.

The term "functional fragment" of a protein means a truncated version of the original protein or polypeptide referred to. The truncated protein sequence can vary widely in length; the minimum size being a sequence of sufficient size to provide a sequence with at least a comparable function and/or activity of the original sequence referred to, while the maximum size is not critical. In some applications, the maximum size usually is not substantially greater than that required to provide the desired activity and/or function(s) of the original sequence. A functional fragment can also relate to a subunit with similar function as said protein. Typically, the truncated amino acid sequence will range from about 5 to about 60 amino acids in length. More typically, however, the sequence will be a maximum of about 50 amino acids in length, preferably a maximum of about 60 amino acids. It is usually desirable to select sequences of at least about 10, 12 or 15 amino acids.

Functional fragments include those comprising an epitope which is specific or unique for the proteins according to the invention. Epitopes may be determined using, for example, peptide scanning techniques as described in Geysen *et al.* (1996). Preferred functional fragments have a length of at least, for example, 5, 10, 25, 50, 75,
5 100, 125, 150, 175 or 200 amino acids.

The polypeptides to be used according to this aspect of the invention from *Saccharomyces cerevisiae*, are represented by SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106,
10 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276,
15 278, 280, 282, 284, 458, 460, 462, 464, 466, 468, 470, 472 and 474. Also according to the invention is the use of the polypeptides from *Candida albicans* as represented by the SEQ ID NOs 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378,
20 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 476, 478, 480, 482 and 484.

The polypeptide or protein according to the invention may also include variants of any of the polypeptides of the invention as specified above having conservative
25 amino acid changes.

The nucleic acid molecules or the polypeptides of the invention may be provided in a pharmaceutically acceptable carrier, diluent or excipient therefor.

The present invention also relates to a vaccine for immunizing a mammal against infections caused by yeast and fungi comprising at least one (recombinant)
30 nucleic acid molecule or at least one (recombinant) polypeptide of the invention in a pharmaceutically acceptable carrier.

Pharmaceutically acceptable carriers include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolizing macromolecules such as
35 proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids,

amino acid copolymers; and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

A "vaccine" is an immunogenic composition capable of eliciting protection against infections caused by yeast or fungi, whether partial or complete. A vaccine may also be useful for treatment of an individual, in which case it is called a therapeutic vaccine.

Said vaccine compositions may include prophylactic as well as therapeutic vaccine compositions.

The term "therapeutic" refers to a composition capable of treating infections caused by yeast or fungi.

Some of the pathways leading to apoptosis are conserved between mammalian cells and yeast or fungi. Therefore, targets which are part of such a conserved pathway may be used to stimulate or inhibit the apoptosis in mammalian cells. E.g. stimulation of apoptosis is desirable in the treatment of tumor cells/tissues.

According to another embodiment, the present invention provides a method of identifying compounds which selectively inhibit, induce or interfere with the expression/production of the polypeptides encoded by the nucleotide sequences of the invention, or compounds which selectively inhibit, activate or interfere with the functionality of polypeptides expressed from the nucleotide sequences according to the invention, or which selectively inhibit, induce or interfere with the metabolic pathways in which these polypeptides are involved. Compounds may carry agonistic or antagonistic properties. The compounds to be screened may be of extracellular, intracellular, biologic or chemical origin.

Such a screening method may comprise the following steps (a) contacting a compound to be tested with cells having a mutation which results in overexpression or underexpression of at least one of the polypeptides as defined in claim 2, in addition to contacting wild type cells with said compound, (b) monitoring the growth, death rate or activity of said mutated cells compared to said wild type cells; wherein differential growth or activity of said mutated cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth, death rate or activity of said mutated cells compared to mutated cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said mutated cells caused by the addition of the compound to be tested.

The term "cells" as used above relates to any type of cells such as, but not limited to bacterial, yeast, fungal, plant or human cells:

Compounds found using this approach may additionally be tested on their efficiency in killing or inhibiting the growth of wild type cells in order to confirm their utility as medicament for treating wild type pathogenic strains/tumor cells.

According to the invention, the term "mutation" includes point mutations, deletions, insertions, duplications or any modification in the nucleic acid encoding said polypeptide, or at a different location in the genome of said cells, influencing the expression of said nucleic acid or polypeptide. In case point mutations occur, the number of nucleotides will be identical compared to the original sequence; only a change in nucleotide sequence can be observed. This stands in contrast with the other listed mutations where the number of the nucleotides will be different from the number observed in the wild type sequence and consequently will also reflect in a change of the nucleotide sequence.

Changes in morphologic and/or functional properties of cell components which can be monitored include for example morphological and molecular changes such as abnormal cell morphology, nuclear fragmentation, DNA breakage or changes in the expression of certain enzymes such as caspases, as well as monitoring changes in membrane potential or activity of mitochondria and release of cytochrome c from mitochondria. All these changes can be monitored on the whole cell which is contacted to the compound to be tested.

The invention also relates to a method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid sequences as defined in claim 1, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound, (b) monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein

differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested.

Alternative methods for identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said compounds are involved, may comprise the use of any other method known in the art resulting in gene activation, gene inactivation, gene modulation or gene silencing.

The invention also relates to a method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule as defined in claim 1 joined in frame with a reporter gene and (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested. This enables to analyse the influence of the compound onto all/most aspects of transcriptional activation. Alternatively additional tests can routinely be performed to test the influence of the compound onto mRNA stability, translation and protein stability. All these aspects influence the concentration of corresponding proteins and consequently influence the effect of these on the metabolism of the cell.

The invention further relates to a method of identifying compounds which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises (a) contacting a compound to be tested with at least one of the polypeptides as defined in claim 2, (b) detecting the complex formed between the compound to be tested and said polypeptide, (c) alternatively, examining the diminution/increase of complex formation between said polypeptide and a receptor/binding partner, caused by the addition of the compound being tested, (c) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound being tested.

Detection of the complex formation can be performed using several approaches. First, binding of a compound onto a polypeptide can be studied using classical binding tests: one of the binding partners, compound or polypeptide is labeled and interaction of both is measured. Most of these tests comprise following steps:

incubating both binding partners in conditions where binding is allowed, separation of free label from bound label present in the complex formed between both partners, and measuring the number of labeled complexes formed. Separation of free and bound label can be performed via filtration, centrifugation or other means as known by the person skilled in the art. Other techniques allow visualisation of complex formation without the need of such a separating step. For example, test systems using SPA (scintillation proximity assay) beads are based on the principle that radioactive ^3H can only be measured when present in scintillation fluid. SPA beads contain scintillation fluid and can be coated with one of the binding partners. When this bead is approached and binds the other binding partner which is radioactively labeled, a signal will be detected allowing the complex to be visualised. Binding of the radioactive compound onto the scintillation bead is needed in order to result in a detectable signal; non-bound radioactive partners that stay free into the solution will not result in a detectable signal.

The protein or peptide fragments according to the invention employed in such a method may be for example in solution or coated on suspended beads as described above. Alternatively, these can be affixed to a solid support, borne on a cell or phage surface or located intracellularly.

When protein or peptide fragments are coated on solid supports, they can be tested for their binding affinity for large numbers of compounds. These can be used in different kinds of high throughput screenings in order to identify compounds having suitable binding affinity to the polypeptides according to the invention. Platform technologies or technologies based on SPR (see below) can be applied.

One may measure for example, the formation of complexes between the proteins of the invention and the compound being tested. Alternatively, one may examine the diminution or increase of complex formation between the protein according to the invention and a receptor/binding partner caused by the compound being tested.

Proteins which interact with the polypeptide of the invention may be identified by investigating protein-protein interactions using the two-hybrid vector system first proposed by Chien *et al.* (1991).

This technique is based on functional reconstitution *in vivo* of a transcription factor which activates a reporter gene. More particularly the technique comprises providing an appropriate host cell with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA binding domain and an activating domain, expressing in the host cell a first hybrid DNA sequence encoding a first fusion of a fragment or all of a nucleic acid sequence

according to the invention and either said DNA binding domain or said activating domain of the transcription factor, expressing in the host at least one second hybrid DNA sequence, such as a library or the like, encoding putative binding proteins to be investigated together with the DNA binding or activating domain of the transcription factor which is not incorporated in the first fusion; detecting any binding of the proteins to be investigated with a protein according to the invention by detecting for the presence of any reporter gene product in the host cell; optionally isolating second hybrid DNA sequences encoding the binding protein.

An example of such a technique utilizes the GAL4 protein in yeast. GAL4 is a transcriptional activator of galactose metabolism in yeast and has a separate domain for binding to activators upstream of the galactose metabolising genes as well as a protein-binding domain. Nucleotide vectors may be constructed, one of which comprises the nucleotide residues encoding the DNA binding domain of GAL4. These binding domain residues may be fused to a known protein encoding sequence, such as for example the nucleic acids according to the invention. The other vector comprises the residues encoding the protein-binding domain of GAL4. These residues are fused to residues encoding a test protein. Any interaction between polypeptides encoded by the nucleic acid according to the invention and the protein to be tested leads to transcriptional activation of a reporter molecule in a GAL-4 transcription deficient yeast cell into which the vectors have been transformed. Preferably, a reporter molecule such as β -galactosidase is activated upon restoration of transcription of the yeast galactose metabolism genes. Alternatively, other reporter proteins can be used such as EGFP (enhanced green fluorescent protein), or hEGFP. This latter has a decreased lifetime enabling the system to screen for compounds improving the interaction of studied binding partners.

The two-hybrid approach was first developed for yeast, and is an ideal screening system when looking for compounds active in killing yeast or fungi. Indeed, proteins expressed in this system will most probably carry the correct modifications as found in the pathogenic yeast strains. In addition, compounds active in this test system allow to screen and select compounds which are able to enter the cell, this selection is not possible when using *in vitro* test systems. When compounds are needed to target mammalian cells, modification of the studied proteins can be different, changing the structure of corresponding proteins. Moreover working with yeast might block certain compounds to enter the cell, which are normally able to traverse the mammalian cell membrane. Consequently, working with mammalian two-hybrid system for this purpose

will give already an immediate selection of the compounds that may enter mammalian cells.

Alternative *in vitro* methods can be used to investigate protein - protein interactions. Protein interaction analysis *in vitro* can shed light on their role in the intact cell by providing valuable information on specificity, affinity, and structure-function relation ship. Significant process in this respect has become with the advent, in the last few years, of commercially available biosensor technology. This allows to study macromolecular interactions in real-time, providing a wealth of high-quality data that can be used for kinetic analysis, affinity measurements, competition studies, etc. A major advantage of biosensor analysis is that there is no requirement for labeling one of the interacting components and then separating bound from free molecules- a fact that simplifies experimental procedures and provides more accurate measurements. The principle of surface plasmon resonance (SPR) is based on the detection of a change of the refractive index of the medium when a compound or protein binds to an immobilised partner molecule. For the SPR technology, one needs to load one of the interacting partners to the chip surface, followed by the superfusion of the second binding partner or more molecules. The second partner can be available as purified product, but alternatively a complex suspension containing this partner can also be used. Interaction of two or more compounds can be analysed, alternatively, compounds can be identified interfering or increasing this binding affinity towards each other.

SPR is not restricted to protein-protein interactions; any macromolecule with a suitable size will change the refractive index of the medium in contact with the biosensor surface and therefore give a signal. Studies have been done with protein-DNA interactions, as well as protein-lipid interactions. Moreover intact viruses, abd even cells, can also be injected over the biosensor surface, in order to analyse their binding to receptors, lectins, and so on.

Alternatively, NMR is also an excellent tool for a detailed study of protein-protein or DNA-protein interactions. Isotope edited or isotope filtered experiments whereby one compound is isotopically labeled with ¹⁵N or ¹³C are an ideal way to study these complexes. This method does not allow high throughput analysis of compounds interfering or enhancing molecular interactions. Nevertheless, medium or low throughput systems can be used to confirm results obtained by the high throughout assays or in cases where none of the binding partners are labeled. Other techniques which can be used to study interactions are: overlay, ligand blotting, band-shift, co-

immuno-precipitation, size exclusion chromatography and microcalorimetry (In. "Protein targeting Protocols" Ed. Clegg R.A. Humana Press, Totowa, New Jersey).

Compounds modulating pathways leading to apoptosis may change the activity of the polypeptide of the invention. Therefore screening tests may be setup looking for
5 altered protein activity of the polypeptide of the invention. Based on the amino acid sequence a possible function of the polypeptide might be envisaged; activities can be confirmed and corresponding activity test can be started.

Alternatively additional tests can be performed to test the influence of the compound onto protein stability, post-translational modification, precursor processing
10 and protein translocation. All these aspects influence the concentration and/or activity of corresponding proteins and consequently influence the effect of these onto the metabolism of the cell. Also here, medium or low throughput systems can be used to confirm results obtained by the high throughput assays.

In cases compounds need to be found to target tumor cells, screening assays
15 will have to be used focused on the stimulation of the apoptotic pathway. This invention therefore also relates to in vitro and in vivo model systems comprising tumor tissue or cells expressing the polypeptides according to the invention which can be used to screen for therapeutic agents. In vivo modelsystems allow to test for compound efficacy but also the toxicity of these compounds can be tested. The compounds
20 identified using any of the methods described in the invention not only include compounds which exert their effect in promoting cell death of yeast and fungi, but also include compounds which prevent or delay cell death. The latter compounds can be used to prevent or delay apoptosis of endogenic yeast or fungi in humans and other mammals which may be caused by pathogens or toxic environmental components.

25 According to a preferred aspect of the invention, the yeast or fungi according to any of the methods described, are chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.

The invention also relates to a compound identified using any of the methods of the invention.

30 Compounds identifiable or identified using a method according to the invention, may advantageously be used as a medicament. The invention also relates to a method for treating diseases associated with yeast or fungi comprising admixing a compound obtainable by a method of the invention with a suitable pharmaceutically acceptable carrier.

35 The compounds of the invention can be used for the preparation of a medicament to treat diseases or conditions associated with yeast and fungi infections,

for instance *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp.,
Fusarium spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp.,
5 *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*,
Histoplasma capsulatum, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*,
and *Sporothrix schenckii* infections.

These compounds may also advantageously be included in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

10 A medicament according to the invention not only relates to fungistatic compounds for treating humans or mammals but also relates to fungicides for treating plants.

The invention also relates to genetically modified yeast or fungi in which modification results in the overexpression or underexpression of at least one of the nucleic acids or polypeptides of the invention, which overexpression or
15 underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified yeast or fungi. These genetically modified organisms may have a positive effect on the endogenic flora of humans and other mammals. The genetically modified yeast or fungi can be included in a pharmaceutical composition or can be used for the preparation of a medicament for prophylactic or therapeutic use.

20 Also according to the invention is the use of a compound obtainable by a method of the invention for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.

According to another embodiment, the invention also relates to an isolated protein which is involved in a pathway for programmed cell death of yeast or fungi
25 selected from:

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394,
30 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482, or 484 or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90 or
35 95% similar and most preferably more than 90% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304,

306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344,
346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380,
382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418,
422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452
5 454, 476, 478, 480, 482, or 484;

(c) a protein having an amino acid sequence which is more than 70% identical,
preferably more than 75% or 80% identical, more preferably more than 85%, 90%
or 95% identical and most preferably more than 97% identical to any of the amino
acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302,
10 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342,
344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376,
380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416,
418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450,
452, 454, 476, 478, 480, 482, or 484; and,

15 (d) a functional fragment of any of said proteins as defined in a) to c).

According to the invention, the polypeptides as defined above may be used as
a medicament.

Also encompassed within the present invention are antibodies, monoclonal or
polyclonal, capable of specifically binding to one or more epitopes of the proteins of the
20 invention. The term "specific binding" implies that there is substantially no cross-
reaction of the antibody with other proteins.

The antibodies according to the invention may be produced according to
techniques which are known to those skilled in the art. Monoclonal antibodies may be
prepared using conventional hybridoma technology as described by Kohler and
25 Milstein (1979). Polyclonal antibodies may also be prepared using conventional
technology well known to those skilled in the art, and which comprises inoculating a
host animal, such as a mouse, with a protein or epitope according to the invention and
recovering the immune serum. The present invention also includes fragments of whole
antibodies which maintain their binding activity, such as for example, Fv, F(ab') and
30 F(ab')₂ fragments as well as single chain antibodies.

Antibodies according to the invention may also be used in a method of
detecting the presence of a polypeptide according to the invention, which method
comprises reacting the antibody with a sample and identifying any protein bound to
said antibody. A kit may also be provided for performing said method which comprises
35 an antibody according to the invention and means for reacting the antibody with said
sample.

The antibodies according to the invention may be used as a medicament or may be comprised in a pharmaceutical composition. According to a more specific embodiment, the antibodies may be used in the preparation of a medicament for treating diseases associated with yeast and fungi such as, but not restricted to,
5 *Candida albicans*, *Aspergillus* spp., *Fusarium* spp., *Botritis*, spp., *Cladosporium* spp.

The invention also relates to a method of preventing infection with yeast or fungi, comprising administering a composition containing at least one polypeptide of the invention to a mammal in effective amount to stimulate the production of protective antibody or protective T-cell response.

10 According to another embodiment, the invention relates to a genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids of the invention or a human homologue thereof or at least one of the polypeptides of the invention or a human homologue thereof, which overexpression or underexpression of said nucleic
15 acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

Human homologues according to the invention can be obtained by selective hybridisation of the yeast and candida nucleic acid molecules of the invention against human genome or cDNA libraries according to methods well known in the art
20 (Sambrook et al., 1989). Human polypeptide homologues are obtained from the corresponding human nucleic acid homologous nucleotide sequences.

The invention also relates to a method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences of the invention or a human homologue thereof and/or at least one of the polypeptides
25 of the invention or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism as described in the invention.

The invention further relates to the compounds identifiable according to the above-described method and its use as a medicament.

The invention further relates to a method for preparing a pharmaceutical
30 composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound according to claim 40 or 41 with a suitable pharmaceutically acceptable carrier.

The expression "proliferative disorders" or "proliferative diseases" refers to an abnormality within a patient or animal such as cancer. Normal cells start to proliferate
35 due to a change in the coding or non-coding sequence of the DNA resulting in a swollen or distended tissue. Mutation may arise without obvious cause. An abnormal

benign or malignant mass of tissue is formed that is not inflammatory. Cells of pre-existent tissue start to divide unexpectedly and resulting cell mass possesses no physiologic function.

5 The expression "apoptosis" or "apoptosis-related diseases" includes diseases such as autoimmunity diseases, ischemia, diseases related with viral infections or neurodegenerations.

The invention also relates to the use of compounds obtainable by the above described methods for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.

10 According to another embodiment, the invention relates to the use of a nucleic acid molecule or a polypeptide described in the invention or human homologues thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

15 The invention also relates to a pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule of the invention or a human homologue thereof or a polypeptide of the invention or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient therefor.

20 The invention also relates to a vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid molecule of the invention or a human homologue thereof or at least one polypeptide of the invention or a human analogue thereof in a pharmaceutically acceptable carrier.

25 The invention also relates to the use of an antibody of the invention capable of binding to at least one of the polypeptides of the invention or a human homologue thereof for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

30 According to yet another embodiment, the invention relates to an expression vector comprising a human homologue of a nucleic acid sequence of the invention. Said expression vector may comprise an inducible promoter and may further comprise a sequence encoding a reporter molecule.

The invention also relates to a host cell transformed, transfected or infected with any of the above described vectors.

35 According to another embodiment the invention relates to a nucleic acid molecule comprising a human homologue of at least one of the nucleic acid sequences described in the invention.

The invention also relates to an antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to a nucleic acid molecule which is a human analogue of the invention.

- 5 The invention also relates to a polypeptide encoded by the nucleic acid molecule comprising said human homologues of the nucleic acids described in the invention.

- 10 The invention, now being generally described, may be more clearly understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present invention and are not intended to limit the invention. The contents of all references referred to in this text are hereby incorporated by reference.

FIGURE AND TABLE LEGENDS

- Figure 1.** *Saccharomyces cerevisiae* sequences based on information obtained from the Saccharomyces Genome Database (SGD) (SEQ ID Nos 1 to 284)
- Figure 2.** *Candida albicans* sequences (SEQ ID Nos 285 to 456).
- 5 **Figure 3.** Yeast genome macroarray containing a total of 6144 gene ORFs spotted on 2 nylon membrane filters. The filters are cut in the upper right corner for orientation and the DNA is on the labelled side of the filter. Each filter contains 2 fields and each field is divided into 8 grids, organised in 24 rows and 8 columns.
- 10 The spots represent the genome wide expression profile without (A) and with (B) *Bax* modulated expression (Example 2).
- Figure 4.** Results from a second experiment analogous and analysed as described in the examples section (Example 3).
- 15 **Table 1.** Genes modulated by *Bax* expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed more than fivefold in a first experiment (see Example 2). The factor by which the transcript level was affected, is expressed as the Qt value. A Qt value higher than 1 indicates upregulation while a Qt value lower than 1 indicates a downregulation. For instance, a Qt of 0.5 indicates a two-fold lower transcript level of a particular mRNA due to *Bax* expression in *S. cerevisiae*. Upregulation or downregulation of a specific mRNA is stated when Qt had a value of at least five or at most 0,21, respectively.
- 20
- 25 **Table 2.** Genes modulated by *Bax* expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed significantly in a second experiment (see Example 3). In this experiment, the Qt values were calculated using the Pathways Software (Research Genetics).

EXAMPLES

Example 1. Differential gene expression analysis upon Bax-induced cell death

Materials and media

Bacterial strain *Escherichia coli* MC1061 (Casadaban and Cohen, 1980) was
5 used for the construction and the amplification of plasmids. Yeast strains were grown
under normal conditions on standard media (Sherman *et al.*, 1979). The
Saccharomyces cerevisiae strain INVSc1 (Invitrogen®) was transformed by means of
the lithium acetate method (Schiestl and Gietz, 1989) with YIpUTyL or YIpUTyLMuBax,
after linearisation in the Ty δ element (Zhu, 1986).

10

Cloning of mouse BAX cDNA

Mouse *Bax* cDNA, encoding the mouse Bax- α protein, was cloned by Pfu DNA
polymerase (Stratagene®) chain reaction amplification (PCR) from an EL4/13.18
thymoma cDNA library (BCCM™/LMBP-LIB15) by making use of the primers:

15

5'-ATGGACGGGTCCGGGAGCAG-3' and

5'-TCAGCCCATCTTCTTCCAGATGGTGAG-3'.

The resulting PCR product was cloned in a *HincII*-openend pUC19 according to
standard procedures (Sambrook J. *et al.*, 1989).

20 Plasmid constructions

The 2 μ ori and the *URA3* marker gene were removed from pUT332 (Gatignol *et al.*, 1990) by successive digestions with *ClaI* and *BglII*. A *BamHI-HindIII* GAL1
promoter fragment was ligated into the *BglII-HindIII*-opened plasmid. A *XbaI-FspI* FLP
terminator fragment was inserted into this *XbaI-HindIII*(blunted)-opened plasmid so that
25 the plasmid YIpUT was obtained. Insertion of a blunted *EcoRI-BsaAI* Ty δ element in
the *KpnI-AatII*-opened and blunted YIpUT resulted in the plasmid YIpUTy. Subsequent
insertion of the *LEU2* marker gene, as a blunted *BsaAI-BsrGI* fragment, in the *BamHI*-
openend and blunted YIpUTy resulted in the plasmid YIpUTyL.

30 Mouse *Bax* cDNA was excised from pUC19 by digestion with *XbaI* and *HindIII*
and subcloned into the *XbaI-HindIII*-opened plasmid YIpUTyL, obtaining the final
expression plasmid YIpUTyLMuBax.

The plasmid YIpUTyLMuBax has been deposited in the BCCM™/LMBP culture
collection as p5CTyGALmBax with accession number 3871 under restricted use.

GeneFilters

The Yeast GeneFilters™ were purchased from Research Genetics Inc. (Huntsville, AL, USA).

5 The Yeast GeneFilters™ are hybridization ready nylon membranes containing a total of 6144 gene ORFs (Open Reading Frames) individually amplified by PCR and spotted on 2 nylon membrane filters (Filter I and II). The filters are cut in the upper right corner and the DNA is on the labeled side of the filter.

10 Filter I contains 3072 ORFs organized into two fields (fields 1 and 2). Each field contains 1536 ORFs divided into 8 grids (A, B, C, D, E, F, G and H). The grids are organized in 24 rows and 8 columns.

Filter II contains 3072 ORFs organized in two fields (field 3 and 4). Fields 3 and 4 are organized in the same way as fields 1 and 2.

The Yeast ORF target

15 The yeast filters consist of over 6000 PCR products corresponding to 6144 yeast ORFs derived from the SGD. The PCR reactions used ORF specific primer pairs designed to amplify the entire open reading frame. The primers were generated from unique sequences containing the start codon ATG and termination codon (kindly provided by M. Cherry at Stanford Genome Center). Thus the PCR product contains
20 the complete open reading frame including the start and stop codons. These products were purified and resuspended at 50 nanograms per microliter in a colored solution to allow the printing to be monitored. A robotic device was used to spot approximately 1/10 of a microliter of the denatured PCR product solution on a positively charged nylon membrane. The DNA was then UV cross-linked to the membrane.

25

Results**Induction of Bax-expression in yeast cells**

30 *S. cerevisiae* cells (strain INVSc1) were transformed with the expression plasmid YlpUTyLMuBax or the parental plasmid YlpUTyL as a negative control. Alternative yeast strains (such as W303-1A (Thomas and Rothstein, 1989)) with equivalent properties are known in the art and can also be used.

The Ty δ element of both plasmids allowed a stable multi-copy integration in the genome of the yeast cell. Southern analysis of the cells containing YlpUTyLMuBax
35 revealed the integration of 5 GAL1-controlled Bax-cassettes near Ty elements.

The yeast cells containing YlpUTyLMuBax and the yeast cells containing YlpUTyL were grown overnight in 10 ml minimal glucose-containing medium. The precultures were then further diluted to an OD₆₀₀ of 0,2 in 100 ml minimal glucose-containing medium and grown until an OD₆₀₀ of 1 was reached. Subsequently, the yeast cells containing YlpUTyL were washed and a dilution thereof was transferred into 100 ml galactose-containing medium and incubated for 15 hours. After this additional period the cultures reached an OD₆₀₀ of 1. The yeast cells containing YlpUTyLMuBax were also washed and transferred into 100 ml galactose-containing medium and incubated for 15 hours.

RNA isolation

Total RNA was isolated using RNAPure™ Reagent (GenHunter Corporation Nashville, TN, USA) according to the GenHunter protocol. 1.5 10⁹ cells were concentrated in a microcentrifuge tube and 1ml RNAPure™ Reagent was added together with 1 g of glass pearls. The yeast cells were broken by thorough mixing during five 2-minutes periods, and placed on ice in-between to avoid RNA digestion. Chloroform (150 µl) was added to the lysate and centrifuged for 10 min at 4°C and at 15000 rpm. The supernatant was transferred to a new tube and the RNA was precipitated with an equal volume of isopropanol. After 10 min incubation on ice, the RNA was pelleted by centrifugation and the pellet was washed with 70% ice-cold ethanol. The dried RNA pellet was resuspended in 50 µl RNase free dH₂O.

First strand cDNA synthesis in the presence of α-³³P dCTP

Probes with high specific activity were prepared by first strand cDNA synthesis using total RNA isolated from INVSc1 YlpUTyLMuBax or INVSc1 YlpUTyL yeast cells and incorporation of α-³³P dCTP as follows: 2 µl (1 µg/ml) of Oligo dT was added to 20 µg of total RNA in a maximal volume of 8 µl RNase-free dH₂O and incubated at 70°C for 10 min. After cooling down on ice for 1 min, the following components were added:

- 6 µl 5x concentrated First Strand Buffer (GIBCO-BRL)
- 1 µl 0,1 M DTT
- 1 µl RNase Block (40 units/µl) (Stratagene)
- 1,5 µl 20 mM dXTP-solution (X = A, G and T) (Pharmacia)
- 1,5 µl SuperScript™ Reverse Transcriptase (200 units/µl) (GIBCO-BRL)
- 10 µl α-³³P dCTP (10mCi/ml, 3000 Ci/mmol) (Amersham)

and incubated for 2 h at 37°C during which first strand cDNA synthesis took place.

Unincorporated label was separated from the probe on a Sephadex G-50 column (Pharmacia). The radioactivity incorporated in the probe was measured by liquid scintillation. The specific activity of the probes was 3 or 5 10^8 cpm/ μ g for both the INVSc1YlpUTyL and the INVSc1YlpUTyLMuBax probe.

Additionally, the length of first strand cDNA probes was controlled on an alkaline 2% agarose gel using standard electrophoresis techniques, and resulted in the detection, via stimulated phosphorescence autoradiography, of the bulk of the fragments around 500 bp.

Hybridisation with the *S. cerevisiae* Yeast GeneFilters™ and signal detection

The Yeast GeneFilters™ were successively hybridised with the α - 32 P dCTP labelled cDNA probes using the MicroHyb™ solution provided by the manufacturer (Research Genetics Inc., Huntsville, AL, USA). This solution was applied as well in the prehybridisation step as during hybridisation. The MicroHyb solution contains formamide to allow hybridisation to occur at lower temperatures.

The hybridisation experiment was performed essentially as follows: during prehybridisation, the Yeast GeneFilters™ were placed in a hybridisation flask (35x250 mm) filled with 5 or 10 ml MicroHyb™ solution (42°C) containing 5 μ l polydA (0,5 or 1 μ g/ml) and incubated for 24 hours at 42°C whilst rotating (10 rpm). After disposal of the prehybridisation solution, the denatured (3 min at 100°C) cDNA was added in 5 ml prewarmed MicroHyb solution and again incubated overnight at 42°C whilst rotating. Following two wash steps of 20 min in wash buffer (2x SSC, 1% SDS) at 50°C, a third wash step was performed in a second wash buffer (0,5x SSC, 1% SDS) for an additional 15 min at room temperature. The Yeast GeneFilters™ were placed in a PhosphorImager™ cassette with storage phosphorscreen. After 4 days of development the screen was developed and scanned using the PhosphorImager™ 455 SI from Molecular Dynamics. The results of these can be seen in Figure 3.

In-between the hybridisation experiments, the filters were stripped off by incubation in 500 ml of a 0,5% SDS solution (prewarmed to near boiling temperature) during at least 1 hour at room temperature.

Example 2. Quantification of Hybridisation Signals

Quantification of the hybridisation signals was done using the ImageQuant™ 4.1 software tool from Molecular Dynamics (Sunnyvale, CA). The quantification was performed per grid of the Yeast GeneFilters™, and by drawing a roster of 24 columns and 8 rows onto each grid of each filter. As such, each rectangle of the roster corresponds to a spot on the Yeast GeneFilters™. Subsequently, from each grid a volume-report (quantification) was drawn up and the data were transferred to a Microsoft™ Excel sheet. Also for each grid a correction factor was calculated. Signals neighboring big and dark spots were separately quantified. For each grid, a background level was calculated.

10

Statistical processing of quantification results

The statistical processing of the results was accomplished in Microsoft™ Excel. For each grid, the following statistical functions were separately defined:

1. The frequency of occurrence of the values in a precisely defined intensity range(data range), established between 1000 and 61000, split up in intervals of 5000.
2. The frequency in terms of percentage.
3. The cumulated frequency in terms of percentage.

These numeric values were used for the graphical display of the cumulated frequency in terms of percentage.

20

Subsequently, the results of the two experiments (hybridization with cDNA from YlpUTyL containing INVSc1 cells and hybridization with cDNA from YlpUTyLMuBax containing INVSc1 cells) were integrated by determination of a second range of statistical functions:

1. The average of the values of the two experiments for each spot on the filter.
2. The standard deviation on this average. This is a measure for the distribution of the values around this average.
3. The standard deviation in terms of percentage.

The quotient of the values of the second experiment (Bax expression) against the values from the first experiment (control) was determined. This immediately gave the factor by which the expression of a specific gene is changed upon Bax induction.

In order to process all these data and to be able to discriminate between differences in gene expression, a gene showing a standard deviation in terms of percentage of at least 90% and a difference of a factor 5 in expression as a result of Bax induction, was identified as a differentially expressed candidate gene. (Table 1).

Requantification of these candidates confirmed their selection.

When the expression pattern of all 6144 genes is compared in the two experiments, it could be concluded that the expression profile of 142 genes (this is 2,3 %) has been changed with at least of factor 5. An overview of these genes as well as the factors with which they are up- or down-regulated is shown in Table 1. The sequences of these genes and the amino acid sequences which they encode are shown in Figure 1.

Example 3 . Quantification of Hybridisation Signals using the Pathways™ software

Quantification of the hybridisation signals was done using the Pathways™ Software (Research Genetics) and these signals were normalised against all data points. Comparison of these normalised data revealed differentially expressed candidate genes. Visual inspection of the hybridisation spots confirmed their selection. An overview of these genes as well as the factors with which they are up- or down-regulated is shown in Table 2.

Surprisingly, using this Software package for analysing the results in this example and when compared to the results of example 2, some additional genes were found which expression are up-or down-regulated upon *Bax* expression in *S. cerevisiae*.

The sequences of up- and down regulated genes and the corresponding amino acid sequences from Examples 2 and 3 are shown in Figure 1.

Example 4 Search for homologues in *Candida albicans*

Sequence similarity searches against public and commercial sequence databases were performed with the BLAST software package (Altschul *et al.*, 1990) version 2. Both the original nucleotide sequence and the six-frame conceptual translations were used as query sequences. The used public databases were the EMBL nucleotide sequence database (Stoesser *et al.*, 1998), the SWISS-PROT protein sequence database and its supplement TrEMBL (Bairoch and Apweiler, 1998), and the ALCES *Candida albicans* sequence database (Stanford University, University of Minesota). The commercial sequence database used was the PathoSeq™ microbial genomic database (Incyte Pharmaceuticals Inc., Palo Alto, CA, USA).

Sequence similarity searches were performed using the BLAST software package version 2. The identity between 2 sequences was calculated as percentage identical residues, the similarity percentage between two sequences was calculated using BLOSUM62 as a scoring matrix.

Example 5 . Screening for compounds modulating expression of polypeptides involved in induction of cell death of *C. albicans*

The method proposed is based on observations (Sandbaken *et al.*, 1990; 5 Hinnebusch and Liebman 1991; Ribogene PCT WO 95/11969, 1995) suggesting that underexpression or overexpression of any component of a process (e.g. translation) could lead to altered sensitivity to an inhibitor of a relevant step in that process. Such an inhibitor should be more potent against a cell limited by a deficiency in the macromolecule catalyzing that step and/or less potent macromolecule, as compared to 10 the wild type (WT) cell.

Mutant yeast strains, for example, have shown that some steps of translation are sensitive to the stoichiometry of macromolecules involved. (Sandbaken *et al.*, 1990). Such strains are more sensitive to compounds which specifically perturb translation (by acting on a component that participates in translation) but are equally 15 sensitive to compounds with other mechanisms of action.

This method thus not only provides a means to identify whether a test compound perturbs a certain process but also an indication of the site at which it exerts its effect. The component which is present in altered form or amount in a cell whose growth is affected by a test compound is potentially the site of action of the test 20 compound.

The assay to be set up involves measurement of growth or death rate of an isogenic strain which has been modified only in a certain specific allele, relative to a wild type (WT) *Candida albicans* strain, in the presence of R-compounds. Strains can be ones in which the expression of a specific protein is impaired upon induction of anti- 25 sense or strains which carry disruptions in an essential gene. An *in silico* approach to find novel genes in *Candida albicans* will be performed. A number of essential genes identified in this way will be disrupted (in one allele) and the resulting strains can be used for comparative growth and/or death rate screening.

30 **Example 6 . Assay for High Throughput screening for drugs**

35 $35\ \mu\text{l}$ minimal medium (S medium + 2% galactose + 2% maltose) is transferred in a transparent flat-bottomed 96 well plate (MW96) using an automated pipetting system (Multidrop, Labsystems). A 96-channel pipettor (Hydra, Robbins Scientific) transfers $2.5\ \mu\text{l}$ of R-compound at 10^{-3} M in DMSO from a stock plate into the assay plate.

- The selected *Candida albicans* strains (mutant and parent (CAI-4) strain) are stored as glycerol stocks (15%) at -70°C . The strains are streaked out on selective plates (SD medium) and incubated for two days at 30°C . For the parent strain, CAI-4, the medium is always supplemented with $20\text{ }\mu\text{g/ml}$ uridine. A single colony is scooped
- 5 up and resuspended in 1 ml minimal medium (S medium + 2% galactose + 2% maltose). Cells are incubated at 30°C for 8 hours while shaking at 250 rpm. A 10 ml culture is inoculated at 250.000 cells/ml. Cultures are incubated at 30°C for 24 hours while shaking at 250 rpm. Cells are counted in Coulter counter and the final culture (S medium + 2% galactose + 2% maltose) is inoculated at 20.000 to 50.000 cells/ml.
- 10 Cultures are grown at 30°C while shaking at 250 rpm until a final OD_{600} of 0.24 (+/- 0.04) is reached.

200 μl of this yeast suspension is added to all wells of MW96 plates containing R-compounds in a 450 μl total volume. MW96 plates are incubated (static) at 30°C for 48 hours.

- 15 Optical densities are measured after 48 hours.

Test growth is expressed as a percentage of positive control growth for both mutant (x) and wild type (y) strains. The ratio (x/y) of these derived variables is calculated.

Table 1.

ORF	Qt	Sequence ID Number
YAR061W	7.80	SEQ ID NO 1
YAR073W	11.19	SEQ ID NO 3
YBL048W	5.07	SEQ ID NO 5
YBL051C	5.22	SEQ ID NO 7
YBL066C	6.04	SEQ ID NO 9
YBL078C	6.94	SEQ ID NO 11
YBR072W	26.56	SEQ ID NO 13
YBR073W	5.46	SEQ ID NO 15
YBR086C	7.14	SEQ ID NO 17
YBR093C	11.05	SEQ ID NO 19
YBR181C	0.15	SEQ ID NO 21
YCL007C	20.99	SEQ ID NO 23
YCL016C	23767.57	SEQ ID NO 25
YCR052W	10.51	SEQ ID NO 27
YCR064C	14.91	SEQ ID NO 29
YCR073WA	5.92	SEQ ID NO 31
YDL010W	5.31	SEQ ID NO 33
YDL036C	5.34	SEQ ID NO 35
YDL083C	0.16	SEQ ID NO 37
YDL125C	6.80	SEQ ID NO 39
YDL133CA	0.21	SEQ ID NO 41
YDL136W	0.20	SEQ ID NO 43
YDL167C	6.37	SEQ ID NO 45
YDL184C	0.21	SEQ ID NO 47
YDL191W	0.17	SEQ ID NO 49
YDR103W	6.26	SEQ ID NO 51
YDR238C	5.75	SEQ ID NO 53
YDR259C	9.68	SEQ ID NO 55
YDR294C	8.38	SEQ ID NO 57
YDR430C	5.66	SEQ ID NO 59
YDR438W	6.47	SEQ ID NO 61
YDR450W	0.16	SEQ ID NO 63
YDR471W	0.11	SEQ ID NO 65
YDR486C	5.27	SEQ ID NO 67
YDR499W	6.14	SEQ ID NO 69
YDR507C	6.34	SEQ ID NO 71
YDR515W	5.42	SEQ ID NO 73
YDR518W	6.15	SEQ ID NO 75
YDR519W	5.57	SEQ ID NO 77
YER102W	0.19	SEQ ID NO 79
YER153C	5.63	SEQ ID NO 83
YFL014W	41.08	SEQ ID NO 85
YFL015C	5.62	SEQ ID NO 87
YFR022W	9.44	SEQ ID NO 89
YGL011C	6.14	SEQ ID NO 91
YGL031C	0.11	SEQ ID NO 93
YGL032C	0.14	SEQ ID NO 95
YGL043W	10.74	SEQ ID NO 97
YGL102C	0.15	SEQ ID NO 99
YGL103W	0.17	SEQ ID NO 101
YGL130W	8.35	SEQ ID NO 103

YGL147C	0.08	SEQ ID NO 105
YGL213C	6.02	SEQ ID NO 107
YGL235W	6.23	SEQ ID NO 109
YGL260W	6.61	SEQ ID NO 111
YGR085C	0.16	SEQ ID NO 113
YGR118W	0.17	SEQ ID NO 115
YGR142W	8.91	SEQ ID NO 117
YGR236C	12.72	SEQ ID NO 119
YGR277C	6.27	SEQ ID NO 121
YGR284C	5.95	SEQ ID NO 123
YGR285C	5.84	SEQ ID NO 125
YHR010W	0.20	SEQ ID NO 127
YHR021C	0.16	SEQ ID NO 129
YHR141C	0.10	SEQ ID NO 131
YHR217C	7.6	SEQ ID NO 133
YIL112W	11.15	SEQ ID NO 135
YIL115C	7.67	SEQ ID NO 137
YIL148W	0.13	SEQ ID NO 139
YIL150C	6.83	SEQ ID NO 141
YIL167W	6.66	SEQ ID NO 143
YJL034W	11.61	SEQ ID NO 145
YJL035C	14.48	SEQ ID NO 147
YJL070C	5.29	SEQ ID NO 149
YJL078C	5.16	SEQ ID NO 151
YJL179W	0.19	SEQ ID NO 153
YJL180C	0.14	SEQ ID NO 155
YJL181W	0.21	SEQ ID NO 157
YJL187C	0.17	SEQ ID NO 159
YJL188C	0.1	SEQ ID NO 161
YJL189W	0.08	SEQ ID NO 163
YJL190C	0.09	SEQ ID NO 165
YJL197W	0.13	SEQ ID NO 167
YJL198W	0.2	SEQ ID NO 169
YJR049C	0.17	SEQ ID NO 171
YKR094C	0.14	SEQ ID NO 173
YLR040C	10.13	SEQ ID NO 175
YLR048W	8.55	SEQ ID NO 177
YLR088W	6.09	SEQ ID NO 179
YLR159W	0.18	SEQ ID NO 181
YLR167W	0.06	SEQ ID NO 183
YLR232W	7.4	SEQ ID NO 185
YLR233C	7.63	SEQ ID NO 187
YLR234W	5.68	SEQ ID NO 189
YLR238W	6.74	SEQ ID NO 191
YLR241W	6.48	SEQ ID NO 193
YLR321C	12.17	SEQ ID NO 195
YLR322W	5.54	SEQ ID NO 197
YLR325C	0.06	SEQ ID NO 199
YLR344W	0.12	SEQ ID NO 201
YLR367W	0.19	SEQ ID NO 203
YLR393W	7.05	SEQ ID NO 205
YLR423C	8.61	SEQ ID NO 207
YML026C	0.11	SEQ ID NO 209
YML063W	0.16	SEQ ID NO 211

YML128C	5.1	SEQ ID NO 213
YML130C	5.41	SEQ ID NO 215
YMR022W	6.45	SEQ ID NO 217
YMR118C	5.13	SEQ ID NO 219
YMR143W	0.08	SEQ ID NO 221
YMR174C	6.75	SEQ ID NO 223
YMR191W	9.56	SEQ ID NO 225
YMR230W	0.13	SEQ ID NO 227
YNL054W	5.19	SEQ ID NO 229
YNL067W	0.12	SEQ ID NO 231
YNL075W	0.16	SEQ ID NO 233
YNL096C	0.14	SEQ ID NO 235
YNL162W	0.07	SEQ ID NO 237
YNL178W	0.11	SEQ ID NO 239
YNL182C	0.18	SEQ ID NO 241
YNL190W	0.07	SEQ ID NO 243
YNL208W	5.87	SEQ ID NO 245
YNL210W	0.02	SEQ ID NO 247
YOL031C	5.32	SEQ ID NO 249
YOL048C	14.34	SEQ ID NO 251
YOR010C	7.27	SEQ ID NO 253
YOR019W	5.19	SEQ ID NO 255
YOR027W	6.03	SEQ ID NO 257
YOR031W	5.35	SEQ ID NO 259
YOR096W	0.12	SEQ ID NO 261
YOR248W	0.18	SEQ ID NO 263
YOR293W	0.11	SEQ ID NO 265
YOR312C	0.12	SEQ ID NO 267
YOR369C	0.21	SEQ ID NO 269
YPL047W	5.09	SEQ ID NO 271
YPL090C	0.1	SEQ ID NO 273
YPL137C	10.41	SEQ ID NO 275
YPL159C	5.61	SEQ ID NO 277
YPL175W	5.95	SEQ ID NO 279
YPL180W	7.68	SEQ ID NO 281
YPL218W	6.26	SEQ ID NO 283
YPR102C	0.17	SEQ ID NO 285

Table 2.

ORF	Qt	Sequence ID Number
YGR236C	7.25	SEQ ID NO 119
YDR442W	0.049	SEQ ID NO 459
YGR182C	0.602	SEQ ID NO 467
YGR106C	0.478	SEQ ID NO 465
YKR040C	2.23	SEQ ID NO 471
YJL188C	0.075	SEQ ID NO 161
YOR096W	0.067	SEQ ID NO 261
YOR293W	0.107	SEQ ID NO 265
YDR450W	0.056	SEQ ID NO 63
YML026C	0.051	SEQ ID NO 209
YHR021C	0.114	SEQ ID NO 129
YLR167W	0.033	SEQ ID NO 183
YGL147C	0.061	SEQ ID NO 105
YGR085C	0.107	SEQ ID NO 463
YOR312C	0.083	SEQ ID NO 267
YOL127W	0.101	SEQ ID NO 473
YHR010W	0.077	SEQ ID NO 127
YDR471W	0.046	SEQ ID NO 65
YDL191W	0.128	SEQ ID NO 49
YDL136W	0.125	SEQ ID NO 43
YLR325C	0.061	SEQ ID NO 199
YJL189W	0.07	SEQ ID NO 163
YIL148W	0.145	SEQ ID NO 139
YHR141C	0.069	SEQ ID NO 131
YBL003C	0.119	SEQ ID NO 457
YDR529C	0.352	SEQ ID NO 461
YGR183C	0.781	SEQ ID NO 469

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CLAIMS

1. Use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which
- 5 nucleic acid sequence is selected from:
- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300,

- 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261,

- 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483; and
- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e),
- (g) the complement of any of the nucleic acid sequences as specified in a) to f), for the preparation of a medicament for treating diseases associated with yeast or fungi.
2. Use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from :

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,

434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

(c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484; and,

(d) a functional fragment of any of said proteins as defined in a) to c),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

25

3. A pharmaceutical or fungicidal composition comprising a nucleic acid molecule as defined in claim 1 or a polypeptide as defined in claim 2 together with a pharmaceutically acceptable carrier diluent or excipient therefor.

30

4. A vaccine for immunizing a mammal against yeast or fungal infections comprising at least one nucleic acid molecule as defined in claim 1 or at least one polypeptide as defined in claim 2 in a pharmaceutically acceptable carrier.

35

5. A genetically modified yeast or fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 1 or the polypeptides as defined in claim 2, which overexpression or

underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified yeast or fungus.

5 6. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

- 10 (a) contacting a compound to be tested with yeast or fungal cells having a mutation which results in overexpression or underexpression of at least one of the polypeptides as defined in claim 2, in addition to contacting wild type cells with said compound,
- 15 (b) monitoring the growth, death rate or activity of said mutated cells compared to said wild type cells; wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- 20 (c) alternatively monitoring the growth, death rate or activity of said mutated cells compared to mutated cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- (d) alternatively monitoring changes in morphologic and/or functional properties of components in said mutated cells caused by the addition of the compound to be tested.

25 7. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

- 30 (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid sequences as defined in claim 1, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound,
- 35 (b) monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is

indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,

- 5 (c) alternatively monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast of fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- 10 (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested.

8. A method of identifying compounds which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises:

15

- (a) contacting a compound to be tested with at least one of the polypeptides as defined in claim 2,
- (b) detecting the complex formed between the compound to be tested and said polypeptide,
- 20 (c) alternatively, examining the diminution of complex formation between said polypeptide and a binding partner, caused by the addition of the compound being tested.
- (d) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound being tested.
- 25

9. A method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises:

- (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule as defined in claim 1 joined in frame with a reporter gene,
- 30 (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested.

10. A method according to any of claims 6 to 9 wherein said yeast or fungus is chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.
- 5 11. A compound identifiable according to the method of any of claims 6 to 9.
12. A compound according to claim 11 for use as a medicament.
- 10 13. A method for preparing a pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a compound according to claim 12 with a suitable pharmaceutically acceptable carrier.
- 15 14. Use of a compound according to claim 11 or 12 for the preparation of a medicament for treating diseases associated with yeast and fungi.
- 15 15. Use of a compound according to claim 11 or 12 or a genetically modified organism as defined in claim 5 for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.
- 20 16. Use of a compound according to claim 12 where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*,
25 and *Sporothrix schenckii*.
17. A nucleic acid sequence encoding a polypeptide which is involved in a pathway for programmed cell death of yeast or fungi selected from:
- 30 (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418,
35 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452,

454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;

- 5 (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 10 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- 15 (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 20 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- 25 (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483;
- 30 (e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 35 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483; and,

- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e),
- (g) the complement of any of the nucleic acid sequences as specified in a) to e).

5 18. A nucleic acid according to claim 16 characterized in that it is derived from *Candida albicans*.

 19. A nucleic acid molecule capable of selectively hybridizing to a nucleic acid sequence as defined in claim 1 or the complement thereof.
10

 20. A nucleic acid sequence according to any of claim 17 to 19 which is mRNA

 21. A nucleic acid sequence according to any of claims 17 to 19 which is
15 DNA.

 22. A nucleic acid sequence according to any of claims 17 to 19 which is cDNA.

20 23. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridizing to the nucleic acid sequences according to any of claims 17 to 22.

 24. An isolated protein which is involved in a pathway for programmed cell
25 death of yeast or fungi selected from:

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or
30 encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and
35 most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308,

310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348,
352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384,
386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424,
426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476,
5 478, 480, 482 or 484;

(c) a protein having an amino acid sequence which is more than 70% identical,
preferably more than 80% identical, more preferably more than 90% identical
and most preferably more than 97% identical to any of the amino acid
sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304,
10 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344,
346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380,
382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418,
422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452,
454, 476, 478, 480, 482 or 484; and,

15 (d) a functional fragment of any of said proteins as defined in a) to c)

25. An expression vector comprising a nucleic acid sequence according to
any of claims 17 to 23 .

20 26. An expression vector according to claim 25 which comprises an
inducible promoter.

27. An expression vector according to claim 25 or 26 which comprises a
sequence encoding a reporter molecule.

25 28. A host cell transformed, transfected or infected with the vector of any of
claims 25 to 27.

29. A nucleic acid molecule according to any of claims 17 to 23 for use as a
30 medicament.

30. A polypeptide according to claim 24 for use as a medicament.

31. An antibody capable of specifically binding to a polypeptide according to
35 claim 24.

32. An antibody according to claim 31 for use as a medicament.

33. A pharmaceutical composition comprising an antibody according to claim 31 or 32.

5

34. Use of an antibody according to claim 31 or 32, or an antibody capable of binding to at least one of the polypeptides as defined in claim 2, for the preparation of a medicament for treating diseases associated with yeast and fungi.

10 35. Use of an antibody according to claim 34 where the fungus is *Candida albicans*.

36. A nucleic acid probe which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 and which
15 selectively hybridises with any of said nucleic acid molecules.

37. A nucleic acid primer which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 and which selectively amplifies any of said nucleic acid molecules.

20

38. A genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 1 or a human homologue thereof or at least one of the polypeptides as defined in claim 2 or a human homologue thereof, which
25 overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

39. A method for identifying compounds for stimulating or inhibiting
30 apoptosis comprising the use of at least one of the nucleic acid sequences as defined in claim 1 or a human homologue thereof and/or at least one of the polypeptides as defined in claim 2 or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism according to claim 38.

35 40. A compound identifiable according to the method of claim 39.

41. A compound according to claim 40 for use as a medicament.

42. A method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising
5 admixing a compound according to claim 40 or 41 with a suitable pharmaceutically acceptable carrier.

43. Use of a compound according to claim 40 or 41 for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain
10 disorders.

44. Use of a nucleic acid molecule selected from any of the nucleic acid molecules as defined in claim 1 or a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.
15

45. Use of a polypeptide selected from any of the polypeptides as defined in claim 2 or a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

46. A pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule as defined in claim 1 or a human homologue thereof or a polypeptide as defined in claim 2 or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient therefor.
20

47. A vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid molecule as defined in claim 1 or a human homologue thereof or at least one polypeptide as defined in claim 2 or a human analogue thereof in a pharmaceutically acceptable carrier.
25

48. Use of an antibody according to claim 31 or 32 or an antibody capable of binding to at least one of the polypeptides as defined in claim 2 or a human homologue thereof for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.
30

35

55

49. An expression vector comprising a human homologue of a nucleic acid sequence as defined in claim 1.

50. An expression vector according to claim 49 which comprises an inducible promoter.

5

51. An expression vector according to claim 49 or 50 which comprises a sequence encoding a reporter molecule.

52. A host cell transformed, transfected or infected with the vector of any of claims 49 to 51.

10

53. A nucleic acid molecule comprising a human homologue of at least one of the nucleic acid sequences as defined in claim 1.

15

54. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to the nucleic acid molecule of claim 53.

55. A polypeptide encoded by a nucleic acid molecule according to claim 53.

20

FIG. 1:

YAR061W, 704 bp, CDS: 501-704 (SEQ ID NO 1)

AAAATTTGGCACTTCAGAGCTTATCGTATCTTCTCCCGGAGTTCCCTCAAGACTTATACTT
CAGCCCGTTTAGGAATGCATAAAAGCAAATAGGATTCGTTACAAC TGCTGCAGGACTCTT
TAGGACTGCATCAAGGTAAGCCTCGCTGCACCTAAACGCAAATGTGGTTGTAACCTTTT
TAATTTTTTTCTTGAACCTGTTGAGTCGTAATAAATCGTTTCTGGGAAGTGGAAGGTAAT
AATGTAATGGAATCGGCGTTACTCGCATGTGCAGATATCAGCGACAAAAGTGTTGTAGG
GACGTTTCGATACCAAAATTTCTAAATACAGCGCAGGAACATCACTACGCTAAACAAAT
CGTAGCGCATACATCTGATCGAAAAAGACAGTTCCCAAAACAATGACATATGAAGAGAC
CAGCATCAAAATTTTCATCATTAACAGCATGGCTAAAAGTTATTGTTTAATATACCCATA
CCTGATTGACGAACCAAGAAATGCCTTATCACTATTTATTTTTTGGCACTCTTCACCTACC
TGGCCACGTCCAATGTTGTTTCAGGAAGTACACAAGCATGCCTGCCAGTGCGGCCGAGGA
AAAATGGGATGAATGTCAACTTTTATAAATACTCATTACTGGATTCAACAACGTATTCCT
ACCCGCAATATATGACTTCTGGATATGCCTCGAATTGGAATTAG

YAR061W, 67 aa (SEQ ID NO 2)

MPYHYLFLALFTYLATSNVVS GSTQACL PVGPRKNGMNVNFYKYSLLDSTTVSY PQYMTS
GYASNWN

YAR073W, 1712 bp, CDS: 501-1712 (SEQ ID NO 3)

AGTGGCTCATGATCTGTAAATGATCGGTTGACCGCAGTATTATATAATAACATCCGTATA
AGTACATATACTACCATGTCTGTTCTCTACATTGCTTTTTTATTCAAGATTATTGGTTTTTC
CTAACCGCCGCGCGCGCAGGTACCCCGCGCATCTCTCTCTCGAAGAAAGCGGAAAAA
ACAAAAAAGTATAAATAGTGGAGTCTTTTCCATTTAACATTTAGAAAAAATTCG
AATGGAAATTTCTTGCCGAACATTTAACCGGAGACCCCTTGGCGGCTTTTTCTCAGTTTCG
TGGGCTAGTACATTTTACCTAGTATGCTGGGAACTTTTTTTCCGTATTCTATTCTATTCC
TTGCCTTACTTTTCTTATCATTTTTTATATAACCAATTTCAAAAATACTTTTTTAACGTGTC
ATAGACGCATTTTGTATTATACAAATTAAGAATCAAATATAATATGTGCAATTAATAA
CTCCACAAGTAGCGAAAGCAATGGCCGCCATTAGAGACTACAAGACCGCACTAGATCTTA
CCAAGAGCCTACCAAGACCGGATGGTTTGTTCAGTGCAGGAAC TGATGGACTCCAAGATCA
GAGGTGGGTGGCTTATAACGATTTTTTAATCTTACCAGGTTTAGTCGATTTTGGCTCCT
CTGAAGTTAGCCTACAGACCAAGCTAACCAGGAATATTACTTTAAACATTCCATTAGTAT
CCTCTCCAATGGACACTGTGACGGAATCTGAAATGGCCACTTTTTATGGCTCTGTTGGATG
GTATCGGTTTCATTACCATTAACGTACTCCAGAGGACCAAGCTGACATGGTCAGAAGAG
TCAAGAACTATGAAAATGGGTTTATTAACAACCTTATAGTGATTCTCCAAC TACGACCG
TTGGTGAAGCTAAGAGCATGAAGGAAAGTATGGATTGTCAGGCTTCCCTGTCCGCGCAG
ATGGAAAGAGAAATGCAAAGTTGGTGGGTGCCATCACCTCTCGTGATATACAATTCGTTG
AGGACAAC TCTTTACTCGTT CAGGATGTCATGACCAAAAACCTGTTACCGGCGCACAAG
GTATCACATTATCAGAAGGTAACGAAATCTAAAGAAAATCAAAAAGGGTAGGCTACTGG
TTGTTGATGAAAAGGGTAACTTAGTTTCTATGCTTTCCCGAACTGATTTAATGAAAAATC
AGAAGTACCCATTAGCGTCCAAATCTGCCAACACCAAGCAACTGTTATGGGGTGCTTCTA
TTGGGACTATGGACGCTGATAAAGAAAGACTAAGATTATTGGTAAAAGCTGGCTTGGATG
TCGTCATATTGGATTCTCTCAAGGTAAC TCTATTTTCCAATTGAACATGATCAAATGGA
TTAAAGAACTTTCCAGATTGGAATCAATTGCTGGTAACGTTGTCACCAAGGAACAAAG
CTGCCAATTTGATTGCTGCCGGTGCGGACGGTTTGAGAAATGGGTATGGGAACTGGCTCTA
TTTGATTATCCCAAAAAGTTATGGCTTGTGGTAGGCCACAAGGTACAGCCGTCTACAACG
TGTGTGAATTTGCTAACCAATTCGGTGTTCCATGTATGGCTGATGGTGGTGTTCAAAAAC
ATTGGTCATATTATTACCAAGCTTTGGCTCTTGGTTCTTCTACTGTTATGATGGGTGGT
ATGTTGGCCGGTACTACCGAATCACCAGGTGA

YAR073W, 403 aa (SEQ ID NO 4)

MAAIRDYKTA LDKSLPRPDGLSVQELMSKIRGGLAYNDFLILPGLVDFASSEVSLQT
KLTRNITLNIPLVSSPMDTVTESEMA TFMALLDGIGFIHNNCTPEDQADMVRRVKNYENG
FINNPVISP TTTVGEAKSMKEYGFAGFPVTADGKRNAKLVGAITSRDIQFVEDNSLLV
QDVMTKNPVTGAQGITLSEGNEILKKIKKGRLLVVDEKGNLVSMLSR TDLMKNQKYPLAS
KSANTKQLLWGASIGTMDADKERLRLLVKAGLDVVILDSSQGSNIFQLNMIKWIKETFPD
LEIIAGNVVTKEQAANLIAAGADGLRIGMTGSICITQKVMACGRPQGTAVYNVCEFANQ
FGVPCMADGGVQKHWYSYYYQSFGSWFFYCYDGWYVGRYYRITR

YBL048W, 812 bp, CDS: 501-812 (SEQ ID NO 5)

GGGAGAAGCTTATCTTACTGTAGAAAGAAAATGGGATTGCGTTACTCCATATATATTGAAA
ATCCGTTATCTTCCCCATCATCATCGTATAAATCAATAAACGACCCGTTATTCCACTCTC
AGCATCGATCGCAAAAAACGTGAGCTTCATCACCTACGGTTGTAGACATTGCAAGACAC
ATCTTTCCAGTTCCTTCCAGATTATTTCTAGAGATTATAGGGGTAGGACCGGAACGTGCTT
ATTTAATGAACAAAGTTGTTAATGTCGTTGAAGGAAAGGTGAGCAACGAAGAATGTTGA
CTGGCGACTACTTAGTCTGTGATATTCTTTGTCATTGGTGCAAGAGGAACGTAGGTTGGA
AATACTTGCAGAGCAGCAATGATGATCAGCAGTATAAGGAAGGAAAGTTTATCTTAGAGC
TGAAAAACATTTGTAAATGTACTTGATGTCTTCTTTGTCTGCTATCTAGCACCTCTCGT
CTTTTAGTGTCTTTTAGCGTATGATTCTTTTAAAGAATCTGGTCTTTCTTCTTCTATTT
TGATTGGGTATATTTCTATTCTGTTTCACTACTGGTCTGGGTAAATTGGGTTTTGGTTT
GGTCCAGTTGTTTTCAAGTAGCCTTTATTTTTCATTGTGGTATTTTATCTTATCGATT
ATACTTTTTTTTATTCAAAGAAAAATTAACAGATAATCTCTTATGAGCCTAGCTTTG
TTTTTCTTACAGGGCCATTGACTTATGCCCTGAACGAGTCTTACTTTACTTTTTTTGTA
TTTTCAATAATGTCGTGTTTCCCATGTTGTAA

YBL048W, 103 aa (SEQ ID NO 6)

MILFKNLVFLPSILIGYISIRVSLVWVNWVWVWSSCFQVAFIFSLWYFILSIYTFYFSK
KIKQIISYEPSYFVFSYRAIDLCPERVLLYFFCIFNNVFPML

YBL051C, 2507 bp, CDS: 501-2507 (SEQ ID NO 7)

GGGAAATATCAATTCCCGTATTTCAATGTTAGTAATTTGCCTTCGTAAATTACGGAATCA
CATAGCTTTTCATTTTGTTCCTTTTGATATATTTCCCTACTACATACTCTTTTCAATAACTC
TACAGGGTCTGACATTTTAACTTTCAGGTTAATGATGGTGTCTTACTATATTCTCGAG
TCGTACAGAAGTTAGTTCAGATAAACTGCTTCGGTGCTGCCCACTTCTTATCATTACTTC
AACTTTTACCTTCCCTATACCTGTGTCTCTTATTAATTCAAGTTAATCCGAGGTAATAGA
TTAGGGTAACCTTCAATGATGTACGAAACACGGATGCTGCAACTTTGCGATTTTTTCT
GGAAAAGAATAACAATTAAGGCAGCCTTTCAGCTGAGATTACCAGCAGGTCTTTGGAGA
TTAGCGCAAGAAAGTGTGATATAGTACTCATAGAGGCAGGCTACAGACTAGGGAAAGC
GTGTTCAACAACAATAAGAAATGGAGACCAGTTCTTTTGAGAATGCTCCTCCTGCAGCCA
TCAATGATGCTCAGGATAATAATATAAATACGGAGACTAATGACCAGGAAACAAATCAGC
AATCTATCGAACTAGAGATGCAATTGACAAAGAAAACGGTGTGCAACCGGAAACTGGTG
AGAATCTGCAAAAAATGCCGAACAAAACGTTTCTTCTACAAATTTGAATAATGCCCCCA
CCAAATGGTGTCTTGGACGATGATGTTATCCCAAATGCTATTGTTATTAAAAACATTCGGT
TTGCTATTAAAAAAGAGCAATTGTTAGACATTATTGAAGAAATGGATCTTCCCTTCTTT
ATGCCTTCAATTACCATTGATAACGGTATTTTCAGAGGACTAGCCTTTGCGAATTTCA
CCACTCCTGAAGAACTACTCAAGTGATAACTTCTTTGAATGGAAAGGAAATCAGCGGGA
GGAAATTGAAAGTGGAATATAAAAAAATGCTTCCCAAGCTGAAAGAGAAAGAATCGAGA
GGGAGAAGAGAGAGAAAAGAGGACAAATTAGAAGAACAACACAGATCGTCATCTAATCTTT
CTTTGGATTCTTTATCTAAAAATGAGTGGAAGCGGAAACAATAATACTTCTAACAATCAAT
TATTCTCGACTCTAATGAACGGCATTAATGCTAATAGCATGATGAACAGTCCAATGAATA
ATACCATTAACAATAACAGTTCTAATAACAACAATAGTGGTAACATCATTCTGAACCAAC
CTTCACTTTCTGCCCAACATACTTCTTCATCGTTGTACCAACAAACGTTAATAATCAAG
CCCAGATGTCCACTGAGAGATTTTATGCGCCTTTACCATCAACTTCCACTTTGCCTCTCC
CACCCCAACAACTGGACTTCAATGACCTTGACACTTTGGAAATTTATTCCCAATTATTGT
TATTTAAGGATAGAGAAAAGTATTATTACGAGTTGGCTTATCCCATGGGTATATCCGCTT
CCCACAAGAGAAATTATCAATGTTTGTGCTCGTACTTAGGGCTAGTAGAAGTATATGATC
CAAGATTTATTTATTCAGAAGAAAGATTCTGGATCATGCTAATTTACAATCTCATTTGC
AACAAACAGGTCAAATGACATCTGCTCATCTTTGCAGCCAAACTCCACTGGCGGCTCCA
TGAATAGGTGCAATCTTATACAAAGTTGTTACAGGCCCATGAGCAGCTGCAGCGAATA
GTATTAGCAATCAGGCCGTTAACAATTTCTTCCAACAGCAATACTATTAAACAGTAATAACG
GTAACGGTAACAATGTCATCATTAATAACAATAGCGCCAGCTCAACACCAAAAAATTTCTT
CACAGGGACAAATCTCCATGCAACCAACACTAACCTCACCTAAAATGAACATACACCATA
GTTCTCAATACAATTCCGCGAGCAACCGCAACAACCTCAACCACAAACACAGCAAAATG
TTCAGTCAGTGGCAACAACAACATCTTTTTAAGACAACAAGCTACTTTAACACCAT
CCTCAAGAAATTCATCCGGTTATTCTGCCAACCATTATCAAAATCAATTCCGTTAATCCCT
TACTGAGAAATTTCTCAAAATTTACCTCCAAATTCACAAATCCCAATCAACAGCCAAACCC

TATCCCAAGCGCAACCACCAGCACAGTCCCAAACTCAACAACGGGTACCAAGTGGCATAACC
AAAATGCTTCATTGTCTTCCCAGCAGTTGTACAACCTTAACGGCCCATCTTCAGCAAACCT
CACAGTCCCAACTGCTTCCACAGCACACAAATGGCTCAGTACATTCTAATTTCTCATATC
AGTCTTATCACGATGAGTCCATGTTGTCCGCACACAATTTGAATAGTGCCGACTTGATCT
ATAAATCTTTGAGTCACTCTGGACTAGATGATGGCTTGGAAACAGGGCTTGAATCGTTCTT
TAAGCGGACTGGATTTACAAAACCAAAACAAGAAGAATCTATGGTAA

YBL051C, 668 aa (SEQ ID NO 8)

METSSFENAPPAAINDAQDNNINTETNDQETNQSSIETRDAIDKENGVOETETGENSAKNA
EQNVSSSTNLNNAPTNGALDDDDVIPNAIVIKNIPFAIKKEQLLDIIIEEMDLPLPYAFNYHF
DNGIFRGLAFANFTTPEETTQVITSLNGKEISGRKLKVEYKKMLPQAEERIEREKREKR
GQLEEQRSSSLSLDSLKMSGSGNNNTSNNQLFSTLMNGINANSMMNSPMNNTINNNS
SNNNNSGNIILNQPSLSAQHTSSSLYQTNVNNQAQMSTERFYAPLPSTSTLPLPPQQLDF
NDPDTLEIYSQLLLFDREKYYYELAYPMGISASHKRIINVLC SYLGLVEVYDPRFIIIR
RKILDHANLQSHLQQQGQMTSAHPLQPNSTGGSMNRSQSYTSLQAHAAAAANSISNQAV
NNSSNSNTINSNNGNGNNVIINNNSASSTPKISSQGQFSMQPTLTSPKMNIIHSSSQYNSA
DQPPQPQPQTQQNVQSAAQQQQSFLRQQATLTSSRIPSGYSANHYQINSVNPLLRNSQI
SPFNSQIPINSQTL SQAQPPAQSQTQQRVPVAYQNASLSSQQLYNLNGPSSANSQSQLLP
QHTNGSVHSNFSYQSYHDESMLS AHNLSADLIYKSLSHSGLDDGLEQGLNRSLSGLDLQ
NQKKKNLW

YBL066C, 3674 bp, CDS: 501-3674 (SEQ ID NO 9)

ATCCCAAGAAGAAGATTAGACTGATTTTACCTACCCCTCCACCGTCGGAAGAAACACTT
CTGAAGTGTTAAGGGTAATCGACGCCCTTGCAATTGACTGACAAGGAGGGCGTAGTAACTC
CAATTAATTGGCAGCCAGCTGACGATGTCATTATTCTCCCTCTGTCTCCAATGATGAGG
CGAAGGCTAAATTTGGTCAATTTAATGAAATTAACCCCTATTTAAGATTACCAAGTCGA
AATAAGCTTTGAAATAAACGACTTTACTATATACAGGTATATGAAGTATCTCTAACTAAA
ACTTTTATCTATCTTTTATTCTTATTATATCTCATCTCGTACGAAGGGCCGCTCATTGGA
TCATTTTCTTTTACATACCGTAAAGGAATGGCGTTAAAAATATATATATGAAATGCATG
TAATAAACTCTCTGCAGAAACCTTAATGTCAAAGGTCCCGTATACAGATTATATTGGCTC
TGCGTATACGCATTCTCGTCAATGGAAGGATAATCGAGATTCTGACCAAGACCAAGATT
TTAGTTCTGCTCACATGAAAAGACAACCGGAGCAGCAACAGTTGCAACAGCACCAGTTCC
CAAGTAAGAAACAACGAATATCTCACCATGATGACAGTCATCAAATCAACCATAGACCAG
TTACCTCATGTACACATTGTAGACAGCACAAAATCAAATGCGATGCTAGTCAAATTTCC
CTCATCCTTGCTCCAGATGCGAAAAAATTTGGTCTCCACTGTGAAATCAATCCTCAATTCA
GGCCTAAGAAGGGCTCACAGTTGCAACTACTGAGACAAGATGTGGATGAAATCAAATCTA
AACTCGATACTCTTCTGGCCAATGACAGCGTTTTCGTTTCTTTTACAACAGATTCCCA
TGGGCAATAGCCTTTTGAATAAGCTCAATCTGCATCCAACCTCCAACCTCCGGGTACTATTA
TCCCTAACCAGATTCTTCTCCTTCTCAGGTTCTCCAACCTTCTTCCGCGGCTCAACGAG
ATTCTAAGGTTTCAAGTTCAAACCTTATTTGTCCAGGGAACCCCAACTCTTACAAGCAAATC
AGGGCAGCAATACGAATAAATTTAAAGCAAATAATGAAGCATCTTCTCACATGACGTTGC
GCGCATCTTCTTTAGCGCAAGATTGGAAGGCTTGGTTGCAACAGAGCCAAATAAGCTGC
CCCCGCTGCTAAATGACTCAGCATTGCCTAATAATTCAAAGAATCTTTACCTCCTGCTT
TGCAAAATGGCTTTTATAAGAACAACCTCTGCAGGTAACACTCCGAACGGCCCCCTTCTCTC
CAATTCAAAAAACATATTTCCCTCATACTACGTCGACCACCGTTACAACGACAACAAATC
AACCACCATTTGCAGCAACAAGCCACGTAGCAACAAATAACAATGCAGATAGGACGAAGA
CGCCGGTAGTAGCCACCACGACTATGCCATTATTGCCTTCCGCGCATGCAATGTAG
ATGAGTTTGTACTGGGCGATATTAGTATTTCCATTGAAAAAGCGAATAGATTACACCATA
TTTTCTGTGACTAGGTATCTGCCGATTTTCTTATTATGTATTCCAATAACGCCACCGAAT
TATACTCCCAATCTCAGTTGCTTTTCTGGACCGTGATGTTGACGGCATGTCTGTCTGATC
CTGAACCGACGATGATTGCAAGCTAAGCTCTTTGATCAAGCAACTTGCCATAGAGACCT
GCTGGATAAGAACAACCTAGATCCACACATATTTGCAAGCTTTGTTAATATTGTGCATTT
GGCTTTGCCTAACCACAAAGTCTTAGATGATTGTTCTTACCGTTTGTAGGATTAGCAA
AGTCACTGTCTTATCAATTAGGTTTGCACAGAGGTGAATTCATTTCTGAATTCACAAGAA
CTCAAACATCAATGCCAAATGCAGAAAAGTGGAGAACTAGGACTTGGCTGGGAATATTTT
TTGCCGAACCTTTGTTGGGCGAGTATCCTTGGTTTGGCCACCAACTTCACAGACAGACTATT
TATTAGAAAAAGCCTTATCCTGTGGTGACGAAGAATCAGAAGAAGATAACAATGACAGTA
TTGAAACATAACAACAATGATAAAAGGAACAAGAAAGACGAGCCGACGTTGAAAGTAAAT
ACAAACTACCGGGCAGTTTGTAGAAGATTGCTCAGCCTGGCGAATTTCCAAGCAAAATGTG
CTCATATCATTGGTTCTTCCACTTCCAGTCCTGATGGTTTATTGGAACCAAGTATCGTG

CTGAGACACTGTCCATCTTGGGAAAAGAGTTAGATTTATTAGCAAAAACCTTTAAATTTCC
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CATTCCTACCCGAAACACCTCCTACCGATCAAATTCATATGTCACAGAGCCCTATCTAA
CAGCTACTAAAAATTGTCACCTCTATTGAATAATCTTTTAGAAAACACACCAATTAATTGAAC
TGCCCTATTTATATTAGACAAGCTGCTACATTTTCTGCACTGATTCTCTTTAAATTGCAGT
TGACTCCTTTACTTCTGACAAATATTTTGATTGAGCAAGGCAATCCGTGGTCACTATCC
ATAGACTTTATAGAAAATCAGTTAACTGCGTGGGCCACTAGTGTGAGAATGATATTTTCGA
GAACTGCAAGTATGTTAGAAAACTGAACCTTCGTACTGATCATGCATCCAGAAGTTTTTG
TGGAAGAAGACGGTATTATTTCTAGGATGAGATCACATTTAACAGGGTCTCTATTCTATG
ATTTGGTTTGGTGTGTTTACGAGGCGAGAAGAAGGAAATGGATCCCGAATATAACAAGC
AAGCCTTAGAGAAAGCCGCTAAGAAAAGAAAATTTTCTCAAATGGTATCTACAATGGCA
CTTCGTCTACGGGTGGCATAACGGACAGAAAACCTATATCCATTGCCACTATATAACCATA
TCTCCAGAGATGACTTTGAAACTGTAAACAAAAACAACACCAAGTGAACCACTGTTACCA
CTTTAGTTCTCTACTAAGAATGCCTTAAAGCAGGCAGAAAAGCTAGCCAAGACAAATAACG
GAGATTTCTGACGGTTCTATAATGGAGATTAACGGGATACCTCTTTCCATGCTCGGGGAAA
CAGGCAGCGTAAAAATTTCAAAGTTTATTTCGCTAATACCTCGAATAGTAACGATTATAATA
ATAATAGGACGTTATTGGATGCGTCTAATGACATATCAATTCCCTCTAATTCAATTTATC
CAGTGGCTTCTGTCCCCGCTTCGAATAACAATCCACAAAGTACTAAGGTAGACTATTATA
GTAACGGACCTAGTGTAATTCCTGATCTCTCCATGAAAAGATCAGTAAGCACTCCCGTTA
ATCATTTTCCGCTCCGTTCCAGGGTTAAGGAACCAACCCCGTTGGCACTTATCTAATA
ATGTTACATTGGGAATAGACCACCTTATTTCCAAGGAGCACAGTAATTTACAAAATGTCA
CCATGAATTATAATAATCAATTCAGCAACGCCAACGCGATTGGAAGATCACAAAGTAGTA
TGTCCTATTCACGTACACCTTTGTTTCCGGTCAATATATGACAGTTGGATTCCGCGTCCGA
CCCCGGTCTCTAA

YBL066C, 1057 aa (SEQ ID NO 10)

MVKDNRDSQDQDFSSAHMKRQPEQQQLQHQFSPKKQRISHHDDSHQINHRPVTSCTHC
RQHKIKCDASQNFPHPCSRCEKIGLHCEINPQFRPKKGSQQLLRQDVDEIKSKLDTLLA
NDSVFVHLLQQIPMGNSLLNKLNLHPTPTPGTIIIPNPDSPPSSGSPTSSAAQRDSKVSQ
TYLSREPQLLQANQGSNTNKFKANNEASSHMTLRASSLAQDSKGLVATEPNKLPPLNDS
ALPNNSKESLPPALQMAFYKNSAGNTPNGPFSPIQKTYSPHTTSTTVTTTTNQPPFAAT
SHVATNMNADRTKTPVVATTTTTPLLPSPHANVDEFVLGDISISIEKANRLHHIFVTRYL
PYFPIMYSNNATELYSQSOLLFWTVMLTACLSDPEPTMYCKLSSLIKQLAIETCWIRTPR
STHISQALLILCIWPLPNQKVLDDCSYRFVGLAKSLSYQLGLHRGEFISEFTRTQTSMPN
AEKWRTTTLWLGIFFAELCWAASILGLPPTSQTDYLLEKALSCGDEESEEDNNDSDNNND
KRKKDEPHVESKYKLPGSFRRLSLANFQAKLSHIIIGSSTSSPDGLLEPKYRAETLSIL
GKELDLLAKTLNFQSDDTVNIYFLYVKLTVCFAFLPETPPTDQIPYVTEAYLTATKIVT
LLNNLLETHQLIELPIYIRQAATFSALILFKLQLTPLLDPKYFDSARQSVVTIHRLYRNO
LTAWATSVENDISRTASMLEKLNFLIMHPEVFVEEDGIIISMRSHLTGSLFYDLVWCVH
EARRREMDPEYNKQALEKAAKKRFSSNGIYNGTSSTGGITDRKLYPLPLYNHISRDDFE
TVTKTTPSGTTVTTLVPTKNALKQAEKLAKTNNGSDSGSIMEINGIPLSMLGETGSVKFQ
SLFANTSNSNDYNNRNLDDASNDISIPSNSIYPVASVPASNNNPQSTKVDYYSNGPSVI
PDLMSKRSVSTPVNHFPASVPGLRNHPVGNLSNNVTLGIDHPIPREHSNLQNVMTMNNNQ
FSNANAIGRSQSSMSHSRTPLFRSIYDSWIPRPTPVL

YBL078C, 854 bp, CDS: 501-854 (SEQ ID NO 11)

TAGTGGAGTACGAATTAGTTAAAGATACTACGACTTTGAAGCCATTGTCAAAGAACATT
TTGATATGTTAAGCAAGACCTGTAGATCCGACATTGCCAAATATGACGGCTCAAAGACAG
ACCCAATTGGTGATGAAGAACAATCTATTAATGACACCATTTTCAAATTTAAAGTGTTCA
AATTATGAAAACAACCTCATATAAATACGTACAAATTTTCTCTACTCGAAGTGATATAGA
TGTATATGTGTAAGTTTACGTTTAAAGTTAGAGTCATGTAATGCTAACTGTCTCCACCGAT
AATGTTGTATAATACCCGTGAAATCATAGCACATGATATATCATCACCCGGAGGCCGGTT
ATTTTCGGCGCGGCAAAAATATTTGGTATAATTATGGAATACAAAAAGGGGAACCAAT
AAAGGTTGAGGAGGGGATTGATAAGAGAATCTAATAATTGTAAAGTTGAGAAAAATCATAA
TAAAAATAATTACTAGAGACATGAAGTCTACATTTAAGTCTGAATATCCATTTGAAAAAA
GGAAGGCGGAGTCGGAGAGGATTGCTGACAGGTTCAAGAATAGGATACCTGTGATTTGCG
AAAAAGCTGAAAAGTCAGATATTCCAGAGATTGATAAGCGTAAATATCTAGTTCCTGCTG
ACCTTACCGTAGGGCAATTTGTTTATGTTATAAGAAAGAGAATTATGCTACCCCTGAGA
AGGCCATCTTCATTTTGTGTAATGATACCTTTGCCACCTACTGCGGCGTTGATGTCTGCCA
TATATCAAAGACACAAGGATAAGGACGGGTTTTTGTATGTCACCTTACTCAGGAGAAAAATA

CATTTGGCAGGTAG

YBL078C, 117 aa (SEQ ID NO 12)

MKSTFKSEYPFEKRKAESERIADRFKNRIPVICEKAEKSDIPEIDKRKYLVPADLTVGQF
VYVIRKRIMLPPEKAIFIFVNDTLPPTAALMSAIYQEHKDKDGLYVTYSGENTFGR

YBR072W, 1145 bp, CDS: 501-1145 (SEQ ID NO 13)

GCAGCAGCAACTCCGTGTGTACCCCTAACTCCGTGTGTACCCCTAAAGAACCCTTGCCCTGT
CAAGGTGCATTGTTGGATCGGAATAGTAACCGTCTTTACATGAACATCCACAACCAACGA
AAGTGCCTTTTCAAGCATTGCTTGATTTCTAGAAAGATCGATGGTTATTCCCTCCCCCTT
ATGCGTCCAAAAATATAGGGTGCTCGTAACAGTAAGGTATTTCGCACTTAGCGTGCTCGCA
ACACAAAATTAAGTAATATGCGAGTTTTAGATGTCCTTGCGGATCTATGCACGTTCTTGA
GTGGTATTTTCATAACAACGGTCTTTTTTACCCTTATTCTTAAACATATAAATAGGACCT
CCATTAGTTAGAGATCTGTTTTTAATCCATTACCTTTTATTCTACTCTCTTATACTAAT
AAAACCAACGATAAAGATATATCAGATCTCTATTAAACAGGTATCCAAAAAGCAAACA
AACAACTAAACAAATTAACATGTCAATTAACAGTCCATTTTTTGATTTCTTTGACAACA
TCAACAACGAAGTTGATGCCTTTAACAGATTGCTGGGTGAAGGCGGCTTAAGAGGCTACG
CACCAAGACGTCAGTTAGCAAAACACACCCGCAAAGGATTCTACTGGCAAGGAAGTTGCTA
GACCAAAATAACTATGCTGGCGCTCTTTATGATCCCAGAGATGAAACCTTAGATGATTGGT
TCGACAATGACTTGTCCCTGTTCCCATCTGGTTTCGGTTTCCCTAGAAGTGTGCGAGTTC
CAGTTGATATTTTGGACCATGACAACAACACAGAGTTGAAAGTCGTGGTTCTCGTGTCA
AAAGCAAGAAGGACATTGATATTGAGTACCATCAAAACAAGAACCAATTTTGGTTTCTG
GTGAAATTCATCTACCTTGAATGAAGAGAGTAAAGACAAGGTCAAGGTCAAGGAGAGCA
GCTCTGGTAAGTTCAAGAGAGTCATCACTTTGCCAGACTACCCAGGTGTGGATGCAGACA
ACATTAAAGCAGACTACGCAATGGTGTTTTGACATTAACAGTTCCAAAATTGAAGCCTC
AGAAGGATGGTAAGAACCACGTCAAGAAGATTGAGGTTTCTTCTCAAGAATCGTGGGGTA
ACTAA

YBR072W, 214 aa (SEQ ID NO 14)

MSFNSPFFDFFDNINNEVDAFNRLLGEGGLRGYAPRRQLANTPAKDSTGKEVARPNNYAG
ALYDPRDETLDWFDNDLSLFPSPGFPRSVAVPVDILDHDNNYELKVVPVGVKSKKDID
IEYHQKNQILVSGEIPSTLNEESKDKVKVKESSSGKFKRVITLPDYPGVDADNIKADYA
NGVLTTLTVPKLPQKDGKNHVKKIEVSSQESWGN

YBR073W, 3377 bp, CDS: 501-3377 (SEQ ID NO 15)

AGAAGGATGGTAAGAACCACGTCAAGAAGATTGAGGTTTCTTCTCAAGAATCGTGGGGTA
ACTAAAGTGAGTGGCTCTATAGTGTGTGTCCTCTCGCGAGGACCATTTGCTTGCATATA
TGGCTTGAAACATATGTCATCACATCTGAGCGATTTTACCTCTTAGAATTAGTTTAGATA
TATATGAGTTGATGAATAAATAGTTATAAAAACTTGCTTTGGCTTCGATATATGACCGTT
ATTTTTGACTAAGTTTTAACGAAGGAATCTAACCTCGTTCTTGTAATTACCAAAATCTTC
AACACGCGCTGTTGGAGGTATCTCTATGGATGTGGCTTGAAATATGGATGTCTTGCCTA
CTTCTACTTCTGGGAAAGGCATTTTTTACTCGATCGCGTTAATATATGCATCAAGAAAATA
AAAAATAAAACGCGAAGAGCTAAAAAAGAAAACCTACTATAAATAACCGATTAG
AATCGAGTTTTTGTATTGAAATGGCGGTAATAAGCGTTAAACCTCGACGAAGAGAGAAGA
TCCTACAGGAGGTAAAAACAGCTCGGTATATCAACCGGTATTTGATTCCGGTACTACTC
AAATGCAGATACCGAAATATGAGAACAAGCCATTCAAGCCTCCAAGAAGGGTTGGATCAA
ATAAGTACACAACTCAAACCAACCGCCACTGCAGTCACAACAGCCCCATATCTAAAG
CCAAAGTTACTGTCAACTTGAAAAGAAGCATTTTCGGCGGGACCTACTTTAAATCTTGCCA
AGAAGCCGAATAATCTGTCTCAAATGAAAACACTAGATATTTTACTATCATGTACAGGA
AGCCTACTACCAAAAAGCACAAGACTTGGAGTGGTGATGGCTACGCTACCTTAAAGCCA
GTAGCGATAAGTTATGCTTTTATAACGAAGCAGGGAAATTTCTTGGGTCAAGTATGCTAC
CAAGTGATTCAGATTCTCTCTTCAAACTCTTTTCAAAGCAGGCTCCAATGAAGTACAAT
TGGATTACGAATTGAAGGAAAATGCAGAAATACGTAGCGCCAAAGAAGCCTTATCAAAA
ACATGGGAAATCCCAGCCCACCGACCACAAGCACAACAGAAACAGTGCCTTCTACGAAGA
ATGACGGTGGCAAAATACCAATGCCTCTGTCTCAGCTGTTTTTCACTAAACACTGTGAAAA
GATTCAAATCAGTAACAAAGCAAACAAATGAACACATGACCACAGTACCTAAAACAGTC
AAAATTCCAAAGCCAAAAAATATTATCCAGTATTTGATGTCAACAAAATCGATAATCCTA
TAGTAATGACCAAAAAATGCAGCCGCTGAAGTTGACGTAATTGTTGATCCATTACTGGGCA
AATTCCTGCGCCCTCATCAGAGGGAAGGGGTGAAGTTCATGTATGATTGCTTAAATGGGCT
TGGCAAGACCAACTATTGAAAATCCGGATATCGATTGTACTACTAAAAGTTTAGTGTAG

AAAATGACTCAGATATTAGTGGATGCCTTTTGGCTGATGATATGGGTTTAGGTAAAAACAC
TAATGAGTATAACTTTGATTTGGACATTAATTAGGCAAAACCTCTTTTGCATCAAAAAGTTT
CATGTTTCGCAATCAGGCATACCATTAAGTGGACTTTGTAAGAAGATTTTAGTCGTTTGTC
CCGTTACTTTAATAGGAAATTGGAAAAGAGAATTTGGAAAATGGTTAAATTTGTCAAGAA
TAGGTGTTTTGACATTAAGCTCAAGGAATTCCTCGATATGGATAAAAATGGCTGTCAGAA
ATTTTTTAAAAGTGCAACGAACCTTATCAAGTCTTGATTATTGGCTACGAAAAACTCTTGA
GTGTTTCTGAAGAATTAGAGAAAAATAAACATTTGATTGACATGCTGGTGTGTGACGAAG
GCCATCGACTAAAAAACGGGGCTTCTAAAATTTTAAATACGCTGAAGAGTTTAGACATAA
GAAGGAAGCTTTTGCTTACGGGAACCTCTATACAAAATGATCTTAATGAGTTTTTCACTA
TTATAGATTTTCATAAACCCAGGAATCCTTGGAAAGCTTCGCTTCTTTCAAAGAGATTCAT
TTATCCCTATAACTAGAGCCAGAGACACTGCAACAGATACAAAGGAATTTGTTGGAAA
AGGGGGAAGAAAGGTCAAAAGAGATGATAGAAATTACGAAAAGATTTATTTTGAGACGAA
CAAATGCGATTTTAGAAAAGTACCTTCTCCAAAGACGGATATAATTTTATTCGTAAAC
CATACAGCCAACAGATATTGGCATTCAAAGATATTTTGCAGGGCGCACGTTTAGATTTTG
GACATATTGACGTTTCAAGTTCTTTCGCTAGGACTAATAACATTACTGAAAAAGGTTTGTAAC
CTCCTGGATTGGTTGGCTCAGATCCCTATTACAAATCACATATAAAGGATACCCCAATCTC
AGGACAGCTATAGTCGTTCTTTGAACTCTGGTAAGTTAAAGGTATTAATGACATTACTAG
AAGGTATTAGGAAGGGTACCAAGGAGAAGGTGCTCGTAGTGTCTAACTACACTCAAACAT
TGGATATAATTGAAAATTTGATGAATATGGCTGGGATGTCACATTGCAGACTCGACGGTT
CCATACCTGCTAAACAAAGGGACTCTATCGTCACATCTTTCAATCGGAATCCAGCCATAT
TTGGATTCTTTGTTGAGTGCAAAATCGGGAGGTGTAGGATTGAATCTAGTCGTTCTCGC
GACTTATTTTATTTGATAATGATTGGAATCCTTCAGTAGATTTGCAAGCGATGTCACGAA
TTCATAGAGATGGTCAAAAAAGCCGTGCTTCATATATAGACTTGTACAACTGGGTGTA
TCGATGAGAAAATATTGCAAAGGCAATTAATGAAGAACAGTTTGAGCCAAAAATTTCTAG
GTGACTCGGAGATGAGAAATAAGAATCTTCTAATGATGATCTTTTCAATAAAGAGGACT
TGAAGGACCTGTTTTCTGTCATACAGATACCAAGAGTAACACACATGACTTAATTTGTT
CTTTCGATGGTTTAGGTGAGGAAATTGAATATCCTGAAACAAATCAACAGCAGAACCCG
TAGAGCTGAGAAAGCGTAGCACTACGACATGGACAAGTGCCTGGATTTACAAAAAGAAA
TGAATGAAGCAGCCACCAACGATGATGCCAAAAAGTCACAATACATTAGGCAATGTCCTCG
TTCATTATAAGCATATCGATCCAGCAAGACAAGATGAATTATTTGATGAGGTTATCACAG
ATTCGTTACCCGAATTGAAAGATAGTATTACCTTTGCGTTTGTAAAGCCCGCGAGATAT
GTCTCAGAGAACAAATGA

YBR073W, 958 aa (SEQ ID NO 16)

MAVISVKPRRREKILQEVKNSSVYQTVFDSGTTQMQUIPKYENKPFKPPRRVGSNKYTQLK
PTATAVTTAPISKAKVTNVLKRSISAGPTLNLAKKPNNLSSNENTRYFTIMYRKPTTKKH
KTWSGDGYATLKASSDKLCFYNEAGKFLGSSMLPSDSLSLFTLFKAGSNEVQLDYELKE
NAEIRSAKEALSQNMGNPSPPTTSTTETVPSTKNDGGKYQMPLSQLFSLNTVKRFKSVTK
QTNEHMTTVPKTSQNSKAKKYPVFDVNKIDNPVIMNKNAAAEVDVIVDPLLKGLRPHQ
REGVKFMYDCLMGLARPTIENPDIDCTTKSLVLENDSDISGCLLADDMGLKTLMSITLI
WTLIRQTPPFASKVSCSQSGIPLTGLCKKILVVCPTVLIGNWKREFGKWLNLNRIGVLTLS
SRNSPDMDKMAVRNFKVQRTYQVLIIGYEKLLSVSEELEKNKHLIDMLVCDEGHRLKNG
ASKILNTLKSLLDIRKLLLTGTPIQNDLNEFFTIIDFINPGILGSFASFRRFIIPITRA
RDTANRYNEELLEKGEERSKEMIEITKRFILRRTNAILEKYLPPKTDIILFCKPYSQQIL
AFKDILQGARLDGQLTFSSSLGLITLLKKVCNSPGLVGSDPYKSHIKDTQSQDSYSRS
LNSGKLKVLMTLLEGIRKGTKEKVVVVSNTQTLDI IENLMNMAGMSHCRLDGSIIPAKQR
DSIVTSFNRNPAIFGFLLSAKSGGVGLNLVGRSRLILFDNDWNPSVDLQAMSRIHRDGQK
KPCFIYRLVTTGCIIDEKILQRLMKNSLSQKFLGDSEMRNKESNDDLNFNKEDLKLFSV
HTDTKSNTHDLICSDGLGEEIEYPETNQOQNTVELRKRSTTTWTSALDLQKMNNEAATN
DDAKKSQYIRQLVHYKHIDPARQDELDFDEVITDSFTELKDSITFAFVKPGEICLREQ

YBR086C, 3341 bp, CDS: 501-3341 (SEQ ID NO 17)

AGATCCTAAAACAGCACGAAGCATATTATTGCGCATAATTTGTTCTTGTAGGATCTTTTC
TTGACATTTTTTTTCACTCTGCGAGAACTTCTCTTTTTTTTTTCTTCTAGGGACGAAAA
CAAACAAGGGCACTTTTTTTTATCTTTTTTTTTTCTCTGTTGTTTTCAAAAACAAAAGAT
TCCACCACTACATCAGTGTGAAAGACTGTAAAAGCTTTCTGATAAATAAGCACTTTCCAT
ATTTTTCAACTGAAAAATAGTTTTCTTTTTTGCAGCTATTATTGACTTCATTAAGAAATAT
CCCTTTTTTCCCGTTGCAATTATTTCTATAAGGGAAGCTGGAAATAGGGGGCTGGAAAA
GATATTTGAACAGTCGCTCCAATAACGTTCTCACCATCATTAACATTTTTGAAGGTGAA
TACTGTTTCGGTCGATTTATGGCTAATTTGTCAAATACATTTGAAAAAGATTAAAAACAAG

CACAAGCGGTTGAGCATACTATGTGCGCAGACAATTACATCTCTAGATCCGAATTGTGTTA
TTGTATTCAATAAACTTCGAGTGCAAACGAGAAGAGTTTGAATGTGCAATTCAAACGTT
TGAATATACATTCTATTATCGAACCTGGCCATGATCTGCAAACAAGCTATGCGTTTATTA
GAATCCATCAGGATAATGCGAAACCGCTTTTTTCATTTTTTGAGAATCTGGACTTCATTG
AATCCATCATACCATATCATGATACTGAATTGTCCGATGATTTCATATAAAGCTGTTCTA
TCAGCAAATCAAAAATACTGGAGGCTCCAAAACAGTATGAGTTGTACAACCTATCGAATT
TGACCAATAATCCCAAACAATCCTTATATTTTGCATTCTTACAGAACTATATAAAATGGT
TGATTCCCTTCTCTTTTGGATTATCAATTAGATTTTATCTAATTTTACGTATGAAT
TCAATTCACATACTCGCTGTTGCGCCATCCTATGGACATTGTCAATTTACAGCCTTTTGGC
TTTATAAATATGAACCATTTTGGTCTGATAGACTGAGTAAATACTCATCATTTTCTACCA
TTGAGTTTCTTCAAGATAAAACAGAAAGCCCCAAAAAAGCTAGTTGCGTTATCATGTTGA
AGAAATGTTGTTTATTCCTGTGGCTTTGTTGTTTGGCGCAATATTACTATCATTTCCAGC
TATATTGTTTTCGCTTGGAAATTTTCTACAAGCAAATTTATAACGGCCCAATGATTTCCA
TCTTGTCTTTTTTGCTACTATACTTATTTGCACGTTTACTCCGGTTTTAACTGTGATTT
ACAACAAATATTTTCGTAGAACCAATGACAAAGTGGGAAAATCATAGCAGTGTGTGAATG
CAAAGAAATCTAAAGAAGCTAAGAAGCTTTGTTATTATTTTTCTATCCAGTTACGTTCCCC
TATTAATTACACTATTTCTTTATCTGCCAATGGGGCATTGTTGACCGCAGAAATAAGAA
CTAAGGTTTTCAATGCCTTTTCAATATTGGCCCGTTTACCTACCCATGATTCAGATTTTA
TTATTGATACAAAGCGCTATGAAGATCAATTTTTCTACTTTATTGTTATCAACCAACTGA
TTCAATTTAGCATGGAAAACCTTTGTTCCAAGCCTTGTAGCATTTGCTCAGCAGAAAATTA
ATGGACCAATCCTTAACCTTTGTCAAAGCTGAGAGTGAATTCGGTAAAGCTCAACTCAGCT
CATCAGATATGAAAATTTGGTCAAAGGTTAAGTCGTACCAAACAGACCCCTGGGGAGCAA
CATTTGATTTGGACGCCAATTTCAAAAAGCTTCTTCTACAATTCGGGTATCTTGTATTGT
TTTCTACAATTTGGCCACTAGCTCCATTTATCTGTTTGATAGTCAATTTGATTGTTTACC
AAGTCGATTTGAGGAAAGCTGTGCTTTATAGTAAACCTGAGTATTTTCCATTTCCAATCT
ACGATAAGCCATCCTCTGTGTCTAATACCCAAAAACTGACGGTTGGTCTATGGAATCTG
TCTTAGTTATGTTCTCCATCTTAGGTTGTGTTATCACTGCTACTTTGACCTATGCTACC
AGAGCTGTAATATACCAGGTGTGCGCGCTCATACTTCCATCCATACGAATAAAGCTTGGT
ACCTAGCAAATCCAATAAACCCTCGTGGATAAATATTGTACTATATGCTGTTTTTATTG
AGCATGTTAGTGTGCTATTTTCTTCTTTCTCTAGTATTTTGAATCTTCCCATGATG
ACGTTGCAAATGGCATTGTGCCAAAGCATGTAGTTAACGTGCAAACCCACCAAAACAG
AAGTCTTTGAAAAAATTCCTTCCCTGAATTTAATTCGAATAACGAAAAAGAACTAGTTC
AAAGAAAAGGGTCTGCGAATGAGAAGTTGCACCAAGAACTCGGTGAGAAACAGCCTGCCT
CTTCTGCCAATGGATATGAGGCACATGCTGCCACTCATGCCAACAATGATCCGCTCTTCTT
TATCCTCAGCCTCCTCGCCTTCATTATCTTCTTCTTCTTAGCAGCAAAACCGGTGTAG
TCAAAGCTGTTGATAACGATACAGCCGGATCTGCTGGTAAAAAGCCATTGGCCACAGAAA
GTACTGAAAAAAGAAATCTTTGGTGAAGGTGCCTACCGTTGGCTCATATGGTGTGTCGG
GCGCCACTTTACCAGAAACAATTCCAACATCTAAAAATTACTACTTAAGGTTTGTAGGAG
ACGGTAAATCCATTAGGGATGCGAAATCCAGTGCAGAATCTTCCAACGCCACCAATAACA
ACACCTTAGGCACGGAAGTAAGCTTTTGCCAGATGGTGACGCCGTTGATGCACATAAGTA
GAAAAATTGATCAAAATACCCAAATTTGCTGTTACTGGTGGCGAAAATAACGAAAATACCC
AGGCCAAAGACGATGCTGCCACTAAGACTCCACTCATTAAAGATGCAAATATTAAGCCTG
TTGTCAACGCAGCTGTTAACGATAACCAATCGAAGGTTTCAGTGGCTACTGAACAAACAA
AAAAGACTGAAGTAAGCACGAAAAATGGCCCATCAAGATCTATTTCCACGAAGGAACTA
AGGATTCTGCGAGACCATCTAATAACAATACTACTACTACTACTACTACAGATGCTACTC
AGCCCCACCATCATCATCACCACCACCGCCATCGTGATGCTGGAGTGAAGAATGTCACGA
ACAATTCTAAGACAACCGAATCCTCTTCTCTTCTCATCGGCGCAAGGAAAAACCAAAAC
ATAAAAAGGGGCTATTGCATAAGCTGAAAAAGAAGCTTTAA

YBR086C, 946 aa (SEQ ID NO 18)

MSQTITSLDPNCVIVFNKTSANESKSLNVEFKRLNIHSIIIEPGHDLQTSYAFIRIHQDNA
KPLFSFLQNLDFIESIIPYHDELSDDLHLKLSISKSKILEAPKQYELYNLSNLTNPKQ
SLYFAFLQNYIKWLIPFSFFGLSIRFLSNFTYEFNSTYSLFAILWTLSTAFWLYKYEPF
WSDRLASQYSSFSTIEFLQDKQKAKASSVIMLKCCFIPVALLFGAILLSFQLYCFAL
IFYKQIYNGPMISILSFLPTILICTFTPVLTVIYNKYFVEPMTKWENHSSVNAKKSKEA
KNFVIIIFLSSYVPLITLFLYLPMDHLLTAEIRTKVFNAFSILARLPTHDSDFIIDTKRY
EDQFFYFIVINQLIQFSMENFVPSLVSIAQQKINGPNPNFVKAESEIGKAQLSSSDMKIW
SKVYSQYDFPWGATFDLDANFKLLQLFGYLVMFSTIWPLAPFICLIVNLIVYQVDLRKA
VLYSKPEYFPPIYDKPSSVSNTQKLTGLWNSVLVMSILGCVITATLTMYQSCNIPG
VGAHTSIHTNKAWYLANPINHSWINIVLYAVFIEHVSVAIFFLSSILKSSHDDVANGIV

PKHVNVQNPQKQEVFEKIPSPPEFNSMNEKELVQRKGSANEKLHQELGEKQPASSANGYE
AHAATHANNPSSSLSSASSPSLSSSSSSSSSKTGVVKAVDNDTAGSAGKKPLATESTEKRNS
LVKVPTVGSYGVAGATLPETIPTSKNYLRFDEDEGKSIRDAKSSAESSNATNNNTLGTES
KLLPDGDAVDALSRKIDQIPKIAVTGGENNENTQAKDDAATKTPLIKDANIKPVVNAAVN
DNQSKVSVATEQTKKTEVSTKNGPSRSISTKETKDSARPSNNNTTTTTTTTDTATQPHHHHH
HHRHRDAGVKNVTNNSKTTESSSSSSAAKEKPKHKKGLLHKLKKL

YBR093C, 1904 bp, CDS: 501-1904 (SEQ ID NO 19)

ACGTATTTGGAAGTCATCTTATGTGCGCTGCTTTAATGTTTTCTCATGTAAGCGGACGTC
GTCTATAAACTTCAAACGAAGGTAAAAGGTTTCATAGCGCTTTTTCTTTGTCTGCACAAAG
AAATATATATTAAATTAGCACGTTTTTCGCATAGAACGCAACTGCACAATGCCAAAAAAG
TAAAAGTGATTAAAAGAGTTAATTGAATAGGCAATCTCTAAATGAATCGATACAACCTTG
GCACTCACACGTGGGACTAGCACAGACTAAATTTATGATTCTGGTCCCTGTTTTTCGAAGA
GATCGCACATGCCAAATTATCAAATTGGTCACCTTACTTGGCAAGGCATATACCCATTTG
GGATAAGGGTAAACATCTTTGAATTGTGCAAAATGAAACGTATATAAGCGCTGATGTTTTG
CTAAGTCGAGGTTAGTATGGCTTCATCTCTCATGAGAATAAGAACAACAACAATAGAGC
AAGCAAATTCGAGATTACCAATGTTTAAATCTGTTGTTTATTCAATTTTAGCCGCTTCTT
TGGCCAAATGCAGGTACCAATTCCTTAGGCCAACTAGCCGATGTCGACAAGATTGGTACCC
AAAAAGATATCTTCCCATTTTTTGGGTGGTGCCGGACCATACTACTCTTTCCTTGGCGACT
ATGGTATTTCTCGTGATTTGCCTGAAGGTTGTGAAATGAAGCAACTGCAAATGGTTGGTA
GACATGGTGAAAGATACCCCTACTGTCACTGTGGCTAAGACTAACAAGAGTACATGGTATA
AGTTGAGCAATTACACTCGTCAATTCAACGGCTCATTGTCTATTCTTGAACGATGATTACG
AGTTTTTTCATCCGTGATGACGATGATTGGAAATGGAACCACTTTTGCCAACTCGGACG
ATGTTTTGAACCCATACACTGGTGAAATGAACGCCAAGAGACATGCTCGTGACTTCTTGG
CTCAATACGGTTACATGGTCAAAAACCAACAGTTTCGCCGTTTTTACCTCTAATTCTA
AGAGATGTCATGACACTGCTCAATATTTCAATTGATGGTTTAGGTGACCAATTCAACATCA
CCTTGACGACTGTCACTGAAGCTGAATCCGCTGGTGCCAACTTTGAGTGCTTGTAACT
CATGTCCTGCTTGGGACTACGATGCCAATGATGACATTGTAAATGAATACGACACAACCT
ACTTGGAATGACATTGCCAAGAGATTGAACAAGGAAAACAAGGGTTTGAACCTTGACCTCAA
CTGACGCTAGTACTTTATTTCTCGTGGTGTGCATTTGAAGTGAACGCTAAAGGTTACAGTG
ATGCTCTGTGATATTTTACCAAGGATGAATTAGTCCATTACTCTACTACCAAGACTTGC
ACACTTATTACCATGAGGGTCCAGGTTACGACATTATCAAGTCTGTCCGTTCCAACCTTGT
TCAATGCCCTCAGTCAAATTATTAAGCAAAGTGAGATTCAAGACCAAAAGGTTTGGTTGA
GTTTTTACCACGATACCGATATCCTAAACTTTTTTGACCACCGCTGGTATAATTGACGACA
AAAACAACTTAACTGCCGAATACGTTCCATTTCATGGGCAACACTTTCCACAGATCCTGGT
ACGTTCCCTCAAGGTGCTCGTGTCTACACCGAAAAATTCCAATGTTCTAACGACACCTACG
TCAGATACGTCATTAACGATGCTGTGTTCCAATTGAAACCTGTTCCACTGGTCCAGGGT
TCTCTTGTGAAATCAATGACTTCTACGACTATGCTGAAAAGAGAGTAGCCGGTACTGACT
TCCTAAAGGTCTGTAACGTCAGCAGCGTCAGTAACTCTACTGAATTGACCTTCTACTGGG
ACTGGAACACTACTCATTACAACGCCAGTCTATTGAGACAATAG

YBR093C, 467 aa (SEQ ID NO 20)

MFKSVVYSILAASLANAGTIPLGKLADVDKIGTQKDIFFFLGGAGPYYSFPGDYGISRDL
PEGCEMKQLQMVGRHGERYPVSLAKTIKSTWYKLSNYTRQFNGLSFLNDDYEFFIRDD
DDLEMETTFANSDDVLNPHYTGEMNAKRHARDFLAQYGYMVENQTSFAVFTSNSKRCHDTA
QYFIDGLGDQFNITLQTVSEAESAGANTLSACNSCPAWDYDANDDIVNEYD'TTYLDDIAK
RLNKENKGLNLTSTDASTLFSWCAFEVNAKGYSVDCDIFTKDELVHYSYQDLHTYYHEG
PGYDIKSVGNSLNFNASVKLLKQSEIQDQKVLWSFTHD'TDILNFLT'TAGI IDDKNNLTAE
YVPFMGNTFHRSWYVPQGARVYTEKFQCSNDTYVRYVINDAVVPIETCSTGPGFSCEIND
FYDYAEKRVTGDFLKVCSNVSSVSNSTELTFYWDWNTTHYNASLLRQ

YBR181C, 1563 bp, exon1: 501-506, intron1: 507-858, exon2:
859-1563 (SEQ ID NO 21)

TAACTTCTCAACATAATTATGTAAAAAATTATCTCATTAAGCCAGATAGCAAATATATCA
CATATTGCATTGATTAATTTGAGAAAAATATACATGTATCTTTTCAGTTAATTTTATTAA
AAATAAATTATTTTCTTACTTTTTTTTCTACAGTTTGCACCATTAACTCTTTTCTTGCA
TCCATACATCTTTGAACTCCATACATCTTATTTTTTTTGCTGTTTTTTTTTTCAGTGTCTCGG
GCATACAGGCGCTTATCTTCATGCCGGCCCATCTCTAGGAACTCTTTCCGGTATGGG
CCAAGGCGAGCGAAAAATCCTATGTGCGTGGAGCTGATAAATCTCGGCTGGCTTGGTTT
GTAGGGCACGGTCAATGAATGCCTGATGGGAGAAAAATTATCTTTTATGAAAAGTGATCT

TAATTTGAATAGTGTGCCCTTCAAAACATTTGGAAGTCATTAATTGAAACTATCCAGTGT
GAATAGACGACTGAGCCATCATGAAGGTATGTAATATCACCCAAATCCTTAGAATTCCTAA
TGAATCAGCACGCGCTAACCGGCTGTTTCTGACTGTTTGATAAACGTATACCCACAAATT
AGTGCACTATAATAAAAAATCTCAAGAACAACGTTGTTTAAACGAGATAATTCCTCTAA
TATACACGTACCGACACTTAGGAAAATATCTCGCTAAGTTCAAATTAAGGAATGAAAAAG
GAATTTACGAAAAGGGTTTAGAAATATCAATGAAAATAAGAAAAACCTGTAACGGAAGAA
AGGACAGCAGGGATTCGTTGGAATTTGTCTGATATTGGCTTCGGACAACCTTTACTAACAAA
TGGTATTATTTATAACAGTTGAACATTTCTTACCCAGTCAACGGGTCTCAAAAGACCTTC
GAAATTGATGATGAACACCGTATTTCGTGTTTCTTCGACAAGAGAATCGGTCAAGAAGTC
GATGGTGAAGCCGTTGGTGATGAATTCAGGGCTACGTCTTCAAGATCTCTGGTGGTAAC
GACAAACAAGGTTTCCCAATGAAGCAAGGTGTTTGTGTTGCCAACTAGAATCAAGTTGTTG
TTGACCAAGAACGTTTCTTGTACAGACCAAGACGTGATGGTGAAAGAAAGAGAAAGTCC
GTCAGAGGTGCCATTGTTGGTCCAGATTTGGCTGTCTTGGCTTTGGTCAATTGTCAAGAAG
GGTGAACAAGAATTGGAAGGTCTAACTGACACTACTGTTCCAAAGAGATTGGGTCCAAAG
AGAGCTAACAAATCAGAAAGTTCTTCGGTTTGTCCAAGGAAGATGACGTTTCGTGATTTT
GTCATCAGAAAGAGAAGTCACCAAGGGTGAAAAGACTTACACCAAGGCTCCAAAGATCCAA
AGATTGGTTACTCTCAAAGATTGCAAAGAAAGAGACACCAAAGAGCTTTGAAGGTCAGA
AACGCTCAAGCTCAAAGAGAAGCTGCTGCCGAATACGCTCAATTGTTGGCTAAGAGATTG
TCTGAAAGAAAGGCTGAAAAGGCCGAAATCAGAAAGAGAAGAGCTTCTTCTTTGAAGGCT
TAA

YBR181C, 236 aa (SEQ ID NO 22)

MKLNI SYPVNGSQKTFEIDDEHRIRVFFDKRIGQEV DGEAVGDEFKGYVFKISGGNDKQG
FPMKQGVLLPTRIKLLLTKNVSCYRPRRDGERKRKSVRGAI VGPDLAVLALVIVKKGEQE
LEGLTDTTPVKRLGPKRANNIRKFFGLSKEDDVRDFVIRREVTKEKTYTKAPKIQRLVT
PQRLQRKRHRQALKVRNAQAQREAAA EYAQLLAKRLSERKA EKA EIRKRRASSLKA

YCL007C, 893 bp, CDS: 501-893 (SEQ ID NO 23)

ATTACTTTAAATTTGTTGTCTATTCCAACATAATCATTAGCAGCACATGTCGAGCAACAG
ATAAACACAGCAGCGGCACGGTGAACCACATAAGTGTATGTGCACACGCGTGTTTTGTGC
AGTGATTACCAACTTGCGCATGCAAGGATATCACACTCCTGTTTCTGCCTCATGTCCTTT
TAAACCGCTTCCACGGGACATGGGTTCTAATTATGGAGAAGATCAAGCTTTGAAATGGCC
CGTTTACACATTTTGATACAACCGTAGACGGCGTCTCGTTTCAAAGACCGTGTGGTTGTC
TATCAGTATATACTCATTGTGTTTTTCAAAAAATCTCTGGGTTGTTTAGATGCCACTATA
TTCTATTCGTATTATTTTATGTATACTTATTTTGCTTATTTTCTTATACTCAGGAA
ACGTCACTTGGCTTGATATACTCGACGCTTTATTCTGCAAATTCAGGTCTCAAATCTGAA
CGCGTGGAGCCACCAAGGGATGGAGCTGGCAAAGGAACGTAATGGGCCACATCAAAAC
ATCATGGCCAATGTCAAATCACTGTACTTCTCCAAACACTGTACGACAAAACAAAACAA
ACAACTCTTGTTAGTAAAAAAGAAAGGGAACTAGTAATATGGAGACACATCGTAAAAA
AAATGTTGCACATACGCTTGGTTGTTCTTTGGAGCCATTATCCAGAACAGCACGGACATG
GCACTAACCACTATGAATACCAACAACAGTATAGCTAAATTGGACGCGCAGAGAGTTA
GTAGAAGAAGAAGGAAGAAAAGGGAAGCGGAGAGAAGAGATTATGACACATACAAACTAC
TCATTACTCTTTGTTCTTTATTATTCTGTTGGACCTTTGTTTCTTAAAGTATAG

YCL007C, 130 aa (SEQ ID NO 24)

MELAKERNGP HQKHGQCQNHCTSPNTV RQNTKNLLLVKKKGKLV IWRHIVKKMLHIRL
VVLWSHYPEQHGHTNHYEYTNNSIAKLDAQRV SRRRRKKREAERRDYDTYKLLITLCSL
LFVGPLFLKV

YCL016C, 1430 bp, CDS: 501-1430 (SEQ ID NO 25)

ACATGACCTAATTTATAGCTTAGGGTTCTTTTTTGTCAATTCATGCGTATGACAAAGA
GCACCACGATGGTGATCGAAATCTCTAGGAGTAGCATACCACAGCGATATTATTTAGTAG
TAGGCGGTTTATTATCTTTGTCCCTTTATACTGTTGTGTTTCTTGCTTATTGCTTCAGTA
GGCAGCGTATAGTATAACCAAGAAAAGTGAAAAATAAACTAAAAAAGCACTATGAGATG
AACGGTAAAAATCCACCAGAGATTTGCTCACTAATAATCCTGTACCATGTCCATCAACCT
ACATTCCGCACCCGAGTATGATCCATCTTATAAGCTGATCCAGTTGACACCAGAGTTACT
GGATATAATACAGGATCCGGTTCAAATCACCAGTTAAGGTTTAAAGTCATTGGACAAAGA
CAAGTCTGAAGTTGTACTGTGTTTCGCACGACAAGACTTGGGTGCTGCAAGCAGCGCAAC
ATTCAAACACAGTTCTACTAATGAGAGAATTTGTTCTGAACAACCTATTACTTTTCGACG
AAACGCTCTTGTTTGGACTGTCCAAGCCGTACATGGACGTCGTGGGATTTCGCAAGACTG

AATCAGAATTTGAGACCAGAGAGACACATGGCGAATTGAACTTGAATTCAGTACCAATAT
ACAACGGAGAACTGGATTTCTCCGACAAAATCATGAAGAGGTCATCTACAAAGGTTATCG
GGACCTTGAAGAACTACTTGAGAACTCACCATGTTCTGCGCTAGAAGGTATATCAAAT
GGCATAAGATTGGTGGATCTGTGAAAGACGGTGTGTTGTGTATTCTTTTACAAGACTTCC
TTTTCAAAGCACTGCATGTACTACTGATGAGCGCAATGGCAGAATCACTCGATCTACAGC
ATCTGAATGTTGAGGATACACATCACGCTGTGGGGAAGGACATTGAGGACGAGTTCAATC
CATACACAAGAGAAATCATTGAAACAGTGCTGAATAAATTTGCTGTTCAAGAGCAAGAGG
CTGAAAAACAATACGTGGCGCTTGAGAATACCGTTTATAGCTCAGTGGTACGGGATTCAAG
CGCTAAGGAAATATGTTTCTGGAATAAGCATGCCAATTGATGAGTTCCTCATCAAGTGGA
AGTCCCTTTTCCCACCTTTCTTCCCATGTGACATTGACATTGACATGCTGCGAGGCTATC
ATTTCAAGCCTACCGATAAGACTGTCCAGTATATAGCGAAAAGCACACTACCAATGGACC
CCAAAGAACGGTTTAAAGTCTGTTTAGGCTACAGTCACAGTGGGACTTGGAGGATATCA
AGCCTCTAATTGAAGAACTAAATTCAAGAGGTATGAAAATAGACAGTTTCATCATGAAGT
ATGCCCCCGGTAAAAGACTGGGCAAAAAGACCGTGGTCACGAGCAGGTAG

YCL016C, 309 aa (SEQ ID NO 26)

MREFVPEQPITFDETLFLGLSKPYMDVVGFakteSEFETRETHGELNLSVPIYNGELDF
SDKIMKRSSTKVIPTLEELLENPCSALEGISKWHKIGGSVKDGVLCILSQDFLFKALHV
LLMSAMAESELLQHLNVEDTHHAVGKDIEDEFNPYTREIIETVLNKFVQEQEAENNTWR
LRIPFIAQWYGIQALRKVYVSGISMPIDEFLIKWKSIFPPFFPCDIDIDMLRGYHFKPTDK
TVQYIAKSTLPMDPKERFKVLFRLQSQWLEDIKPLIEELNSRGMKIDSFIMKYARRKRL
GKKTVVTSR

YCR052W, 1952 bp, CDS: 501-1952 (SEQ ID NO 27)

GTCATCGACAGCAAATTGCTGGAAGAGTTCAAGGACAACGTGAGATACACCTTGGAAAAAT
GACCTTGAGGAAGGAGCCGATGAGGCCACTCTGCAACGCAGGAGGCAGTTGGAACAGATC
ATTCGGGAGAGCAACGCTGAGGAGGAGTTGGAAGGTACATCCGTGCTATGGTCAGAGAG
CAGATGCTGGGCCAGGGCTCCATGGCGGGTTCCGGGGACGAACCAGATTCCAAGAGAAGA
AAATAACGACCCAGCACAAGGCTCTTACAGCTTGCTAAAAGAAATTGAACGCGACGCTA
CATGAACTACTTCTTTCTCTTACATAGTCTTTTCCCTTATGTATCTTTTCTGTACATTAA
TAGACGTTCTTACAAGGTAAAATTTACCGCGTTTTAAATAGAATGAAAAAACGTTGT
AGAGTGAAAGAAAAAGCAAAATATACAGTTTACAAGGCAGCTTCGTATAGTATACAGC
ACGAAAAACAGCTCATAGAAATGGTAACACAGACCAATCCGGTCCCTGTTACATATCCAA
CGGATGCTTATATCCCCACGTATCTGCCCCGATGATAAGGTCTCCAATCTGGCAGATTGTA
AAAAATTGATAGAAATGGAATTCAGACTAGATTTGTATCTGACAAGAAGGAGGCTGGATA
CGTCCATCAATTTACCTACAAACACCAAGACCAAGGACCATCCCCCAATAAAGAGATGC
TGAGGATTTACGCTTACAACACTACGGAAGCAGCCCTCGCAGCGATTCTGGCACCCAG
CGGACTCAGGCAAGACTACATGGACACTGAGAATAGAAGGTAAGCTTCTGCACGAGTCCG
CAAACGGAAAGCACCCATTTAGTGAGTTTTTGAAGGTGTGCGGGTGCAGTTTAAAAGAC
TGAAACCGCTGGGCATGGGCAAGAAGAGGAAACGCGATTTCGTATTGAGCCTTCCTTTGA
ATCTGCAACAACCCGAATACAATGATCAAGATAGCACCATGGGCGATAACGACAACGGCG
AGGATGAGGACAGTGACAGGCGAGAATCCAGGGAGGAAATTGTAGACGCACTGGAATGGA
ACTACGATGAAAACAACGTTGTGGAGTTTGATGGTATCGACATCAAGAGGCAAGGCAAGG
ATAATTTGCGATGCAGTATAACCATCCAGTTGAGGGGTGTGACGGTGGAAAAGTACAGT
ACTCGCCCAACTTAGCTACCTTGATAGGTATGCAACGGGCTCCGTTAATGACGCGGTTT
ATTGATCTACAAGTACATTTTGATCAACAATCTGTTTGTACGGAACAAACAGAGGCTC
AAGATGGTTCCAACGATGCCGAAGACAGCAGTAACGAGAATAACAATAAAAACGGTGCCTG
GTGACGATGATGGCGTCGAGGGAAGTACTCCAAGGATAAGCCCGAATTGGGTGAAGTGA
AGCTAGATTCACTCTTACAAAAGGTATTGGATACAAACGCCGCGCACCTCCCCTTGATGA
ATGTTGTGCAAAACCGTGAACAACTGGTATCACCCCTACCGCCCATCATCCTAGATTATA
CAATTGATCTTTCCAAAGATACCACCTATGGTGCTACCACCTTGGATGTAGATGTGTCGC
ACATTCTCCACCAGCCTCAACCCAGCCAAATTTACAAAAAGAGGAAGAAACAGATGCTG
AAGACACAGCAAAACTACGTGAAATCACAAAGCTTGCCCTTGCAAGTTGAAGTCTAGTGCTC
AAAAATACCAGTTTTTCCACGAAGTCTTTTGCATCCAAGAGAAACGCTGACTCACTACT
TATGGTCTTCCAAGCAAAACGAGCTTGTGCTGCAGGGCGACCAATACTTCAATGAAGATG
CTGCAAGAACGAGTGACATATACAGTAACAACAACAAATGACAGGTCACTAATGGGCAATA
TCTCACTACTGTACTCCCAAGGAAGACTATAA

YCR052W, 483 aa (SEQ ID NO 28)

MVTQTNPVVPTYPTDAYIPTYLPDDKVSNLADLKKLIEMDSRLDLYLTRRRLDTSINLPT

NTKTKDHPNKEMLRIYVYNTTESSPRSDSGTPADSGKTTWTLRIEGKLLHESANGKHPF
SEFLEGVAVDKRLKPLGMGKKRKRSSLSLPLNLQQPEYNDQDSTMGDNDNGEDEDSDAE
AESREEIVDALEWNYDENNVVEFDGIDIKRQKDNLRCSITIQLRGVDGGKVQYSPNLAT
LIGMQTGSVNDVYSIYKYILINNLFVTEQTEAQDGSNDAEDSSNENNNKNGAGDDGVE
GSTPKDKPELGEVKLDSLLQKVLDTNAAHLPLMNVVQTVNKLVSPLPPIILDYITIDLSKD
TTYGATTLDDVDVSHILHQPPQPNLQKEEETDAEDTAKLREITKLALQLNSSAQKYQFFH
ELSLHPRETLTHYLWSSKQNELVLQGDQYFNEDAARTSDIYSNNNNDRSLMGNISLLYSQ
GRL

YCR064C, 911 bp, CDS: 501-911 (SEQ ID NO 29)

AGGTTTAAACGCGTTATCTTTGTTCCGAAAAAACGGAATAATATTTTTTTC
GCGTCGCGTTCTCGCGTCTGTTTGTGTTTTTCGCGTTCCAATGACCAAAATGGGAAAGTG
GTCGTCCTTGACGAAGGAGACGAAAACCTCTTCTAAAACGTTGGGAGAGAGATAATTACA
TGGCCAGAACAATACTGCAACGTGCATATAGTCGTTAGTCTGTGCTTGCACATCCACGGC
AGCCGCGAGTGGACGCACTGATGGAAGGACACCTGTGTGCCCTTTTTGCGTGTCTCTCCT
CTAACTGTGCACGAGGACCCCTGCAGATGCAAGTGCTACCGTTGTTAGTTTCGTTCTTTTT
GAATGCAGCGCAGACAGCACAGTTTTTCATACCCGGTTTTGCGCCATTTGGCAATTAGCA
ATTTATCAGCATACTTTTCCTTTATCAACCAATCGTAAAGGTCTTTGGAGATGGCCTTTC
TCTTGTAGTACAGAGTATATATGTATCTAGAGCGCTGGTGGTGGAGTTGCATTATCTCCC
AGAGCTGCTCATTTGGACTTTGCTGCGAGCTTAGACGACTTGTCTTTTTGGGCATCTCTGA
GTTGGATTTGAAATCTGTGAGGGTTGGCTTGATTTTTTCGAACCCGTCAGGTGCAGGCT
TGGATCTTCTGGTCTTTATGCGCGGCATGTCGTTTTGTGAGGTGAGCTTTGCTAGTCTTG
ACGGCTGTAGAGGTGTTTACATTGATGATGAGTCCCTAAGAAAATTTTTCTTTTTTTTC
AGTATTTCACTTTCCGTTGTGAACGACAAATGTACTATGCGTTCAAGAGCCAACGCAGTA
TCATCGTCAAAGTTCTTACCACAACGCGTGTGATTGATCTTGTACTGGTTGTAAATGTGC
TAAGTCTGTGA

YCR064C, 136 aa (SEQ ID NO 30)

MYLERWWWSCIISQSCSLDFAASLDDLFSWASLSWISKSVRVGLIFSNPSGAGLDLLVFM
RGMSEVVSFASLDGCRGVYIDDESLRKFQYFTFR CERQMYAFKSQRSIIIVKVP
TTRVIDLVLVNLSL

YCR073W-A, 1448 bp, CDS: 501-1448 (SEQ ID NO 31)

GTTTATGGCTGGAATGACTTGATAATCTCTTACGAGCTTACTTGAGATGGTATGAGGAG
CCAGAACTCTCCCGCTTCAGCCGCTTTTGTGTGCTGTATTAGTATATCCATCATCA
TTTTCACTTACAGGAACCTACCTTTATAGCCACCCTAAGTAAACAACATTAGCTTAGC
ATCCTCAATTCTTATCGTATGTTGTTGCTGCTATTTTTATCCTATTGTTCTTGGCATCGC
TTTTTTACATAAGGTACCAAGGCAAGAGAAAAGACCCGCGAAATTTCAATTCGAGACAT
AGGGTTAAATACGAAATATGTTAAGGTCTAGTTTCCAAAAAATGAAGAAAATGTGATTAGA
CATCCTGGGGAAATTAGGTTTAAATAGGGCGGGCGCTACAGGGGTTTTCTTAACAAATTT
CAATGATAATAGTGGCATCATCATCTCATATCCAGTGTAGGTATGGACTAGAACAGAAA
GCAATTTGCAGCAAGACAATATGACTACGACGGTACCCAAGATATTCGCGTTTCACGAGT
TTTCAGACGTGGCAGAGGCGTAGCTGACCATGTAGTCCACGCGCAAGACGGTGCATTGG
CTCCAAAGAACGAGAGGAAACACTCTGTTCCCAACATCAGCATGAATGCACTGGATATGA
CGAGAGAGGCCTCTTGCAAAAGCACAGCATCTGCCGCGGAAGGAAAAGTGGTAGCAGTG
GTAGTGGCAGTGGTAGCAGTAAGCCCAAAAAGGAGAAACGGTTCAAGATTGCTCTCTCCG
GTGGGTGATGATCGAAGTGCTACACGAAGGTCTGCTAAAACGAGACGATGTACGGTGGG
GAGACTGGGACATTTACTTTGCAGACGAGAGACTTGTACCCTTCAGCTCGAATGAAAGCA
ATTATGGATGCGCCAAAAGGAAGATTTTGGACCTGATAGACACGGCGAAGTATGGAATC
CGAAGGTGTACCACATTGACGAGTCATTGATTGACGACCCGCAAGAATGCGTTGATAACT
ATGAAAAGGTGCTAATCCGCGGGTTTGCCGGTAGAGATTCCGTCAAACCTCCGATGTTCCG
ACTGTGTTCTGCTTGGTTGTGCCCCGATGGTCATATCGCATCACTCTTCCCTAACCTCC
AGGACAATCTACGTGAGAAACTTGCATGGGTGGTGCCCGTGGAGAACGCTCCTAGTGGGC
CCTCGACCAGAAATTCGCTGACTATACCTGTAATCTGCCATTCTCACAGGGTTACTTTCCG
TTGTGCAAGGTGCAACCAAGGCGCCCATCATCAAGACCATTATGGAAGGCCGTGAAAAGG
GCCTACCTAGCAGTATTGTCAACGAAGGTGCTGCTGGTCTGTATCATGGTTTGTGACG
ACGATGCTCTTACGGACGTCCTCGTCACCAAAAAAAGTATAAATTCACCAAGGTTTGT
CTATTTAA

YCR073W-A, 315 aa (SEQ ID NO 32)

MTTTPVKIFAFHEFSDVAEAVADHVVHAQD GALAPKNERKHSVPNISMNALDMTREASCK
STASAAEGKSGSSGSGSGSSKPKKEKRFKIALSGGSLIEVLHEGLLKRDDVVRWGDWDIYF
ADERLVPFSSNESNYGCAKRKILDLIDTAKYGTGPKVYHIDESLIDDPQECVDNYEKLIR
GFAGRDSVKLPMFDLFLLCAPDGHIALSPNFQDNLREKLAWVVPVENAPSGPSTRISL
TIPVICHSHRVTFVVEGATKAPIIKTIMERPEKGLPSSIVNEGAAGRVSWFVDDDALTDV
LVTKKKYKFHQGLSI

YDL010W, 1196 bp, CDS: 501-1196 (SEQ ID NO 33)

TAGTAATTAGTTTCTTATGATGGATTAAATGGCGTAGTTCATCCGCGTTTAATTTAACTA
GAGGATAATCTACTTGCAGCATGAATGAAAATAGTAAGCCAGTAAGGATGCACTGACAGA
CTCAGCTACCGATTAGTGTGTTGACTTTTCCGCAAGATCCTTTCTCCCTCTTTGGACC
TAGTCATCCCTCCACACAAGATTCGCTCTTAAGTAGTGGCGCAGGCTGTTGCTTTTAAAG
CATAGTGCTTAATGTGCAAGGCTTTATAGATCCCAAATACTACGCCTTGAGAAATTGAAT
GCATAGCAGTTAGTTAACTTTCTGGAACGCGCATGACGCGTCCCGGGGCGCTGAGGCG
GAGCGTTCCGCGAAATCGGGAACATTTATCTGGGAAAGATCACTATCTATTCTCTAAAT
GAACTTTAAAGCAAATTATCGTAAGATAGAAAAGACGAAACCTTAGCAACCTAGCGGTTT
AATATAGAAACAAATTTTATTATGATACCTTCCAATAAGAGAAATGCTAGAATTTTAAAGCA
TTACAACGCTATTATTTGTTGTTAGTGTGTTTTCGTAGCGCAAATGCGAACTTCTTGACGG
TAGAGATAAAAAGAGGAACTTCTAAAGCATTTAGTACTAATATGGACAATATGGCTGGAG
GATCTTCCAGGGAATATGCTGCTATGCGGACTTCTACCACGAATAAGGGGAGCTCTGAAG
TAGACGAAAGAAATTAATGAAATAAAAACAGAAGGTGGGACTCCAACAGCCCATAGCATCGG
TTGATGATAGTTTGTGCGCCATTAAAAACGATAAAGGGTCGCGAATAACCAAAGCTTTTA
ATGTTCAAAAAGAACTCTCCCTCATACTAGACTTGTCTCCGATTATAATATTTAGTAAAA
GCACCTGTTTCATATAGCAAGGGCATGAAGGAACTGCTTGAAAATGAGTATCAGTTTATCC
CAAACCTACTATATTATAGAACTTGACAAACATGGACATGGGGAAGAGCTGCAAGAATATA
TCAAGTTGTGTGACCGGTAGAGGAACTGTTCCAAACCTTTTGGTTAATGGAGTATCAAGAG
GAGGTAATGAAGAAATCAAGAACTGCACACTCAAGGGAACCTTTTAGAATCATTACAAG
TCTGGAGTGATGGTAAATTCGCTTGAGCAACGTGAAAAACCTTCCAATAATTGA

YDL010W, 231 aa (SEQ ID NO 34)

MIPSNKRNARILSITLLLLLVFVAQNANFLTVEIKEETSKAFSTNMDNMAGGSSREYA
AMPTSTTNKGSSEVDEEINEIKQKVLQOPIASVDDSLSAIKNDKGSRITKAFNVQKEYS
LILDLSPIIIFSKSTCSYSKGMKELLENEYQFIPNYIIELDKHGHGEELQEYIKLVTGR
GTVPNLLVNGVSRGGNEEIKLHTQKLLLESLQVWSDGKFSVEQREKPSNN

YDL036C, 1889 bp, CDS: 501-1889 (SEQ ID NO 35)

TCAAATCCAGCTTCTTTCAAGCAATATTGTACACAAACGATGATGAGAATAGCATTGAAG
AGGATAAGAAATTTACGCTATTTCAGATGCTAGTGCATCTGAAAATTATCTGGTCAAGCCCA
CAATACCAGGTACGACTCCTGATCCAATAATTGAGGCGCAGAACGATAATGATAGTAGTG
ATAGTAGCGGCATAGATTGATAGCCTTCTTAAGAAATGGACCATTATAAAGTTTTTGTA
TCGCGATGTTTGAAAATGGAAGTAAGGAACGTAATACAAATTGACAAGTAGCCGACATG
AATGACGCTCACTTCTCTTATATATGTTAGGTAGTATATGCATTATAGAATTTATTTCATT
GAAGCAATGTGATTCCCTCGATAAGTAAGCTTTTTTCTGTCTGGCGGCGAACCATTAGAG
AACAAAAGACCGAGTTAAGAAAAAGTTCATAAAAAACCTTTGAAAATGGATGAGTGCTCG
TATAATGGAAATAGGAACTTATGCAAAGAAATAATAGGTTAAGAAATTTGTTTACAGTGC
CAGTAATAATGGCTCGACAACCTCAAAGGAATGCATTATCTGCAGGTCTTGCTTTTGCAG
GTAATGCAACCTCAAATGAGTTTGATGAACATTTGCAAAATGAGGTTGAAAGAGAGAGGG
AAATTCAAAAAGAAAAAATAAAGCGAACTCAATCAAAAAAATCGCCAGATTTGATTA
ATAAATCTACTTTTCAATCACGAACGATAGGCAGCAAAAAAGAGAAACATAGACAACCTAG
ATCCAGAGTATGAAATGTGATCGATGGCCCTCTAAGGAAAATCAAGCCCTACCATTTTA
CGTACAGGACCTTTTGCAAAAGAGCGTTGGAGAGATAAAAAATTTGGTTGATGTCTTTATAT
CTGAATTTGAGATCGTGAATCTGAATATTATAAAGAACAATCGAAAACGGGGACGTTT
ATATAACGATGAAACTGCGGACTTATCTACTGTAATTCGCAATGGTGACCTGATCAAGC
ATCAGGTACATAGACATGAACCTCCAGTCACTTCCAGGCCTATCAAAGTTATTTTGAAG
ATGATAACATAATGGTTATTGATAAACCGAGCGGTATACCTGTTACCCAACTGGCCGAT
ATCGGTTCAATACAATTACGAAAATGCTTCAAAATAATCTCGGATTTGTTGTGAACCCAT
GTAATAGGTTAGATAGGCTTACAAGTGGAATTAATGTTTTTGGCAAAAACCTCCGAAGGGAG
CCGATAATATCGCGCATCACTAAAAGCTCGAGAAGTCACTAAGGAATACGTGGCCAAAG
TAGTTGGAGAAATTTCCAGAAACGGAAGTAATGTTTGAAAAACCTCTAAAACCTGATCAGAGC
CAAGGCTTGCTCTTAATGCAGTTTGTCAAAATGGACGAGAAAGGAGCCAAACATGCAAAAA

CTGTTTTTAAACAGAATCAGCTACGACGGTAAAACGAGTATTGTAAAGTGCAAACCGCTTA
CCGGGCGATCACATCAAATTAGAGTACATTTACAGTACTTAGGCCACCCAATTGCTAACG
ATCCTATTTATTTCCAATGATGAAGTATGGGGTAACAATCTCGGAAAAGGCGGCCAGGCTG
ACTTCGATATAGTTATTACTAAGCTAGACGAAATAGGGAAAAGAAAACCTGCTAAAAGTT
GGTTCCATAGTAATGGCGGGTACGGTGAGGTATTAAGGCAAGAAAAATGTTCTATTTGTG
AATCTGATTTGTATACTGATCCTGGCCCCAATGATCTTGATCTGTGGTTACATGCCTATC
TATACGAATCAACTGAGACTGAAGAAGGAACCGAAAAGAAAAAGTGGTGCTACAAAACAG
AGTATCCAGAATGGGCTCTGAGAAGATAG

YDL036C, 462 aa (SEQ ID NO 36)

MQRNNRLRNLFVTPVIMARQLKRNALSAGLAFAGNATSNEFDEHLQNEVEREREIQKKK
IKRTQSKKSPDLINKSTFQSRITIGSKKEKHRQLDPEYEIVIDGPLRKIKPYHFTYRTFCK
ERWRDKKLVDFVIFSEFRDRESEYKRTIENGDVHINDETADLSTVIRNGDLITHQVHRHE
PPVTSRPPIKVIFEDDNIMVIDKPSGIPVHPTGRYRFNTITKMLQNNLGFVNVNPNRLDRL
TSGLMFLAKTPKGADNIGDQLKAREVTKKEYVAKVVGEFPETEVIVEKPLKLI EPRLLALNA
VCQMDEKGAKHAKTVFNRI SYDGKTSIVKCKPLTGRSHQIRVHLQYLGHPIANDPIYSND
EWWGNLKGQADFDIVITKLDEIGKRKPAKSWFHSNGGYGEVLRQEKCSICESDLYTD
PGPNDDLWLHAYLYESTETEEGTEKKKWCKYKTEYPEWALRR

YDL083C, 1364 bp, exon1: 501-909, intron1: 910-1341, exon2:
1342-1364 (SEQ ID NO 37)

TATTCGACTAGAAAAAATTAATTTTCTAACTACAAAAAATTGCCTGCATATATGTAA
GGATGTAAACAGGAATGTATGGGTCACATATTAATAGCTTGTTTTACTCCATAAAAGAGT
CTGATATTTCAGAAAAAACCCCATACATGTTGAAAAATAATGCATTGTGAAAAAAGTGG
TTGAAAAATGTATGCGATCTAGGAAAAACTGAATTTTCTTAGGTTGTGCTCCTCCTCT
AGAAGGATGCTGTGGCCTTTGACCTGGGCGGAAATTCTCTCTGTTTCCCTCTAGCTGAGG
GAAACAGAACTGGTAGCAGTTTCGTTCCGGCCAGGCCGCGTGAGCCTATACCACCGAATAT
TATCCTAGCGCAGAGAGTAACACTGGCAAAGTCAAAAGTAAATGCCATGTAAATGTATA
GGTTACGCAGTAGACTATTTAATATATACCTTTTTTATTAGCAGTGTTTCGAAAAATACA
GCAAGAGAATAAGCAACAAGATGTCTGCCGTCCCAAGTGTCCAAGTATGTTAAATAATTT
AAACGATGTCACGAATTTGTGAGGGATATTGAAACCATGCAGTGAGATAATTTCAATTTA
AGAACCATATCACCTGAATAAGACGGGTGGGGCAAGCACTAGATGCGAATCATAGTTTTTA
GAACAACGGATCACCATTTACACGTTAAAGACCGAGTAGAAATAACCAATAAATTGTGT
GGGAAAAATATTACTTAATTTCTCTGTGGAGTAAAGTAATGAGCGTCTTTTGCGGTCTT
ATTTATTTCATTTCGCTCCCTTTGCAATGAATTTTGAACAGAATGCTCCAAAGAGGAAGTGC
CAGGTTACCTCACTTGTTTACCCCTTTTACACAGTTTCATAATTTTTTGAGGATTTTTGAA
TTTCTGTTTTTACTAACATGTGACACGAAATGTTTTTCATTTTTTGTTTTATAACAGACTT
TTGGTAAGAAGAAATCAGCTACCGCTGTTGCCACGTCAGGCCGCTAAGGGTTTGATTA
AGGTCAACGGTTCTCCAATCACTTTGGTTGAACAGAAATCCTAAGATTCAAGGTCTACG
AACCATTATTGTTGGTTGGTTGGACAAGTTCTCCAACATCGATATCAGAGTTAGAGTCA
CTGGTGGTGGTCATGTTTCTCAAGTCTACGCCATCAGACAAGCTATTGCTAAGGGTTAG
TCGCTTACCACCAAAAGTACGTTGACGAACAATCCAAGAACGAATTGAAGAAGGCCTTCA
CCTCTTACGACAGAACTTTGTTGATCGCTGATTCTAGAAGACCAGAACCAAGAAATTCG
GTGTAAGGGTGCTCGTTCTAGATTCCAAAAATCTTACCGTTAA

YDL083C, 143 aa (SEQ ID NO 38)

MSAVPSVQTFGKKKSATAVAHVKAGKGLIKVNGSPITLVEPEILRFKVYEPLLLVGLDKF
SNIDIRVRVTGGGHVSQVYAIRQAIAGLVAYHQKYVDEQSKNELKKAFTSYDRTLIIAD
SRRPEPKFGKGARSRFQKSYR

YDL125C, 1088 bp, exon1: 501-597, intron1: 598-708, exon2:
709-1088 (SEQ ID NO 39)

TTCAAAATACGAGTAAAGGAGATCCTAGGTGTGGATTAGTAAGGGGAGTGTGGCAACTTC
CTTTTTCCGGTTAATTCTCCGCGCTTTTCGTTAGACTATTTTGCAAGGACCCAAATAGGAG
ACGCATGGAGGCTTCTACAAAACAGCGTGCCGTTTTGATGGCATGAGCAGGGGGCGCAA
GGAAACACCGGTAAATCGCGCAAGACCTTGTTGGCCACGTAGCCTCAAAGGTTGAATTGA
CACTTGTCTACAGAACTTGAAGTACAAAAGGAGGTACATAAAAACAGTAAGCTTGAGA
AGCTTTAAGATATGGTGCGAATCGTTACAGAATATTCTTGCAGAAAATAATGGCGGGTCC
GTTCTCTTCTGAAGAAGTTACCGCCCTACTGAAGCATTGCTGTACGATCGTGAATGTGA
TGTGTGTTCTGACTGGAAAGCGGAGAACATTATGAAGTAAAAGGACAATCAGCACGCCTTC

CAGACTTTTAAGAAACATTGATGGAGCCATTGATATCGGCACCGTACCTAACAACAACAA
AAATGTCTGCTCCTGCTACGCTTGATGCTGCCTGTATTTTTTGCAAGATTATTAAGTA
TGTCACATTACTAATAAAGAGCTTACACTCACACCAATGATGGCGATAGTCTCTATGTAG
TACATATACATAAAGCAGAATACTAACAATCGATCCGCTATGCAACAGGCGAAATCCAT
CCTTCAAATTGATTGAAACAAAGTACTCGTATGCTTTCTTGGACATCCAACCTACTGCTG
AAGGTCATGCTTTAATCATTCCTAAGTACCATGGTGCGAAGTTGCATGACATCCCGGACG
AATTCCTTACCGATGCTATGCCGATTGCCAAGAGACTGGCCAAGGCAATGAAGTTGGACA
CTTATAATGTGTTGCAGAATAATGGTAAAATTGCGCATCAAGAAGTCGACCACGTCCACT
TCCATTTGATTCCTAAGAGAGATGAGAAAAGTGGTTTGATTGTAGGGTGGCCAGCCCAAG
AAACGGACTTCGATAAGTTGGCAAGCTACACAAGGAATTGCTTGCCAACTAGAAGGCT
CCGATTAG

YDL125C, 158 aa (SEQ ID NO 40)

MEPLISAPYLTTTKMSAPATLDAACIFCKIISKSEIPSFKLIETKYSYAFLDIQPTAEGHA
LIIPKYHGAKLHDIPEFLTDAMPIAKRLAKAMKLDTYNVLQNNKGIAHQEVDHVHFHLI
PKRDEKSLIVGWPAQETDFDKLGLKHLKELLAKLEGSD

YDL133C-A, 578 bp, CDS: 501-578 (SEQ ID NO 41)

AAAGGTGGTTGGAGACTTTGTGTTGTAGCTTAGAATTTCTTCCACTATATGAAAGCCAAG
ACCTCTTCTCCTCTTTTCGACACTTCGTTTATTTCCTTCCCTTATTTAGTATTCATCG
TTCAGAATGCTTTCTTTTATTTACGACGGTTACCACACCCGTACACCCTTATCTCATTTT
ACCAGTACCTTTCTTATTTAGATTCATCTTATTTTATTTTAGGATTTTATAGGTCATTGTA
CGACGCGTGTGCGACCATGGAAAAGGTGTGCGAGCTGCGATGCTATCCATTTACCCGTCA
TCATTGCTGGCAGAAATCCCATCTTCTCTGCTGGGGTGATTTATATATATGGAGAGTTA
ACGAATGTAATATTTCTGAATGTTAAATAATTGTTATCCGTCATTATTGTTTCACTTCTC
TCTTTGAAATTTTCGCTTGTCTTCTGTTTTCATCTTATATTTTACTTCAATCCTAAGTAG
TCATATCGACTTAATTCCAATGAGAGCTAAGTGGAGAAAGAAGAGAACTAGAAGACTTA
AGAGAAAGAGACGGAAGGTGAGAGCCAGATCCAAATAA

YDL133C-A, 25 aa (SEQ ID NO 42)

MRAKWRKKRTRRLKRRRRKVRARSK

YDL136W, 1268 bp, exon1: 501-503, intron1: 504-908, exon2:
909-1268 (SEQ ID NO 43)

CATGCGGACCTTGTGTGTTTGTCTAGATTGTTTTATTTTTATGATTGTTGAAGATAT
AAACCACGTATAGTTGTATAAGATAGGATAATGATGGTGCCTGAAATAAACTTACTA
GCTCTTTAATATTGCAACGGCTTGTAAACGGGCGCCATGATGACATTGAGAATTATACCAC
TACTATATGAAAAATGAAAAGAGGCCCTGCTTTGAACCCGTACATTTTATTCTATAATA
TTGCATCTGTGGTTTGCCTGACGGCAGCGAGTCCAACACAAAGTCTGGCATATGCTACGA
ATTTTCCACCATGGATTTCAGCACCCAAACATTTGAATTTTTTTTCATGTGCGATTGTGAAA
TTTTACTGAAGATGAGGGTAAATAGAGGCCCTGCAATCGTCATCATATGAGAAATGGATAT
ATTGAAAATCTACTCACATCTCTTTTTTGGGGGTTTGGTAGTACAGTGAGAACACGATAA
AGAACCAAATAGGACTAAAAATGGTATGTAGAGATGAATATACATGAAACGGACGTGATA
TAATGTGCTATGGAAGAAAAAGTCTCCTTTAATGTCTGCAGGATAAATAATCAAGTGGT
CTGAAGAAAATTTACAGCTACAGTATTACTGCAAACCTTGCAGGCAAATATCAGAGAGAT
CTCACCAGCTACAACCTGGTAAACAGAAATTTATAAGTTTATGGCACTTGTTAAATTTGTT
TGGAAGTTTTTCGAAATTATAATATTGGTCTTCAGAAACCTGGAACCATGTGAACATTAT
TTTTTTGGATAATGCATTGCACAGAGCGTATTAGTGTATACGAGAATCTAAAAATTTGAA
ACTGGCTCATAAAAACAGGAACTTTTACTAACAGTTATGATTTTTTTGTTCCCATTTTCTT
ATCAATAGGCCGGCGTTAAAGCTTACGAACTAAGAACCATAATCCAAGGAACAATTAGCTT
CTCAATTGGTTGACTTGAAAAAGGAGTTGGCTGAATTGAAGGTCCAAAAGTTGTCCAGAC
CATCTTTGCCAAAGATCAAGACCGTCAGAAAGAGTATCGCCTGTGTCTTGACCGTCATCA
ACGAACAACAAGAGAAGCTGTTAGACAATTATACAAGGGTAAGAAGTACCAACAAAGG
ACTTGAGAGCCAAGAAGACCAGAGCTTTGAGAAGAGCTTTGACCAAATTCGAAGCTTCCC
AAGTTACCGAAAAGCAAAGAAAGCAAATCGCTTTCCCAACAAAGAAAGTACGCTATCA
AGGCTTAA

YDL136W, 120 aa (SEQ ID NO 44)

MAGVKAYELRTKSKEQLASQLVDLKKELAEKLVQKLSRPSLPKIKTVRKSIACVLTIVINE
QQREAVRQLYKGKKYQPKDLRAKKTRALRRALTKFEASQVTEKQRKKQIAFPQRKYAIKA

YDL167C, 2660 bp, CDS: 501-2660 (SEQ ID NO 45)

TGGGTGTCGTCAAACAGGATGCCGTGGAATCATACGAACCGCACATTGTGGTAGAGCTAC
AAAGCGATACGAAAGAAGATATGGTATCTAACGTATCCCGTATTGTTGCTTGGGAAAAGA
TGTGGTTAGAACAAACATCCAGATGGAGTCAAAATGAATATCAAGGGCCTCGTAGCGATG
ACGAAGACGATGAAGACAGTGAAGTAGGCGTTCCATAACTTTGTGTATCTACATATATACA
TATATAATTGTAAATTAGTAACAGTAGTAATAGTAGTGCCTATTATAAAGGGTTTCTTT
AAGTAATGTCATGTACTTGTTTAATGTGACTTTGGTAATATATTTTCATTCTCCGATGCC
GATGCCAGTGGAAAAGTTTAAAGTGAAAAATTTTCAACACATACAAGTTTAATAAGTT
GGTTTTGATGCAAATAGCATTACTAAAGAAGAGCGCTAGGATAATTGTGCATTGCTATTG
TGATTTTTGATACAGAAATTATGCACTATGTGGTACTAGAGCTGCAAGTTGCGCATTTCG
CAGATACCCCCAAGGATCAATGTCCGATTGCGAATATAGCATTTCAAATTGTGAATGCTG
AAACATTAGTATGCCATTATGGGACCAATCTTTACCGAGCATTGAAGTAAACGGGACGA
CAAAGAGTTTGGAGAGTGCAATGGTGCAATTGGACAAGGATATTCATGACGTTATTGGTA
ACGACGACTTTGTTCCTGTTCCTTCCCTGTATTCAACATGGCATATCCGTGTTACCTTACCAC
GTCAAGCGAGAGATGATGGGTTTATTCTTACTTCTTATTTACAACATCCGAAAGTATTTG
ACTTATGGAAGGAATTTCGATAGATGGTGTGTCAACCATCCGGAGATTTTGGGACAAAAGA
AAGCAATCTCCAACAACAATTGTAATACTAAAAGTATTAGTATTAATGCAGCCAAAAATA
CGAAGGATTTGGACGAAATAGTTAGAATATTGGAAGTTTCAATCCCAACTGAAGAGGCAG
GCTCTGTTCAGAGATATACTCTCTTTTAAAAAGGACAACGGATATATTAATACAATTGC
ACAAAAAGTGTACTTCCCCTGAAGATATGGAATCTGTCTTAACAAAACCATATGACTCAC
ACACCGATATTAGAGCGTTTGTGCAAGAGAAATCTAAGATTTTGTACATGAACAATTTAC
CGCCCGACACAACCTCAAAGTGAGTTGGAATCATGGTTTACCCAATATGGTGTAGACCAG
TTGGGTTTTGGACTGTCAAAAACATCGTAGAAGATACGTCTAACGTTAATAATAACTGGA
GTCATAAATAACAGTCCCTATGTGGAAGATCAAGATAGTATCTCAGGATTTGTGTCTTCC
AAACACATGAAGAAGCAACTGAAGTACTAGCGTTGAATGGGAGATCAATCCTATCTAATC
TGGCAAACACTAAGCAACCAAGGGTGGTGAACATGTCCTTGAGCTTCAACCTTCTTCCA
CCGGAGTACTCGATAAGGCTCAAGAAATTTATCGCCTTTCCCTCAAAGTAAAAACAAAC
CAAGACCAGGTGACTGGAATTGCCCATCTTGTGGTTTTTCAAACCTTCAAAGACGTACTG
CATGTTTTAGATGTTCTTTTCCGGCACCATCAAATAGTCAAATACATACTGCGAACTCAA
ACAATAATGTTAACAGTAGTAGAAATAATTTAAACAATCGCGTGAACCTCGGGATCTTCAA
GCAATATTAGTAACACTGCAGCGAATCACCCCTATGGTGCCCTGAGTTCAACATGATTG
CTAACAACACGCCAGCAGCTTTAACATACAATAGAGCTCATTTTCTGCAATTACGCCAT
TGTCGCGACAAAATTCATTGAACATGGCACCATCGAACAGTGGGTGCGCGATAATTATAG
CGGATCATTTTTCGGGAAATAATAATATAGCCCCAAATTATCGTTATAATAATAATATTA
ACAATAACAACAATAATATTAACAATATGACCAATAATAGATATAACATTAAATAACA
TCAACGGTAATGGGAATGGTAATGGGAACAACAGTAATAACAATAACAATCATAATAACA
ATCATAATAACAATCATCATAATGGTAGTATCAATAGTAATAGTAATACCAATAATAATA
ATAATAATAACAATGGTAACAATAGTAATAATTGTAATTCGAATATCGGTATGGGAGGAT
GTGGCTCCAACATGCCATTTAGAGCAGGAGATTGGAAGTGTTCACGTGCACGTATCATA
ACTTTGCTAAAAACGTAGTGTGCTTACGCTGTGGTGGTCCAAAATCAATAAGCGCGATG
CAAGTGAAACCAATCATTACATAGATTTCATCAACATTTGGACCAGCGTCGCGTACTCCCA
GTAATAACAATATTCTGTTAATACTAATGGTGGTAGCAATGCTGGTTCGACCGATGGGA
ACGATAACAAAGGTCGTGATATTGATTTGATGGAATTTATGTACCACCGTTATCGATGG
CAACAAAGTCAATGAAGGAGGGAGATGGGAATGGTAGCTCGTTTAAACGAGTTCAAAGTG
ACAAAGCTAACGTTAATTTTCCAATGTTGGTGATAATAGCGCTTTCGGTAATGGTTTTA
ATAGTTCAATACGTTGGTAG

YDL167C, 719 aa (SEQ ID NO 46)

MHYVLELQVAHLPDTPKDCRIANIAFQIVNAETLVCHYGTNSLPSIEVNGTTKSLESA
MVQLDKDIHDVIGNDDFVLVSLYSTWHIRVTLPRQARDGFIILSYLQHPKVFDLWKEFD
RWCNVNHPILGQKKAISNNNCNTKSI SINAAKNTKDLDEIVRILEVSIPTTEEAGSVPEIY
SLLKRTTDILIQLHKKCTSPEDMESVLTKPYDSHTDIRAFLQEKSKILYMNLPDPTTQS
ELESWFTQYGVPRVGFVTVKNIVEDTSNVNNNWSLNNSPYVEDQDSISGFVVFQTHEEAT
EVLALNGRSILSNLANTKQPRVVEHVLELQPSSTGVLDKAQEILSPFPQSKNKPFRPGDWN
CPSCGFSNFQRRTACFRCSFPAPSNSQIHTANSNNNVNSSRNLLNNRVNSGSSSNISNTA
ANHYPYGAPEFNMIANNTPAALTYNRAHFPATPLSRQNSLNMAPSNSGSPII IADHFSGN
NNIAPNYRYNNNINNNNNNINNMNTNRYNINNNINGNNGNNGNNSNNNNNNNNNNNNHH
NGSINSNSNTNNNNNNNNGNNSNNCNSNIGMGGCGSNMPFRAGDWKCSTCTYHNFAKNVV
CLRCGGPKSISGDASETNHYIDSSTFGPASRTPSNNNISVNTNGGSNAGRTDGNNDNKRDR

ISLMEFMSPLSMATKSMKEGDNGSSSFNEFKSDKANVNF SNVGDNSAFNGFNSSIRW

YDL184C, 578 bp, CDS: 501-578 (SEQ ID NO 47)

AACAAGAAAACCCCTTCCGTTGATCTTAGATTTCTTAGAGGTTTCATGAAGTAAAGCGAC
TTGAACAAAGTCATCCTTCAAGAATCGAAATCTCAAGAGAAAAACAAAATTTAATGTAGA
TTGTCCACTATCTCATGTAAATATACATAACAGGTATTCTGAGCGTTTCGAAAATTAGAC
TGTAATTTTCTGATGCGCTCCCGTACACCTTTGACATATACAAACATCCGCACATTTTAT
AGCTTTCTTTCTAGAATTTTTCACGCGCTCTCGATCAATGAACCTTTAAAAGTAACTG
ACCCCTAACTTTTTTCCCAGGCAAGGCTGGCCTCATTACCTACCCGAAAAGTTTCACTTTA
CCCCATGGCAGATGGACGATATTTTAAACAAGACGAAACTGACCTCGTCTTCTATAAACT
GGACTTCTAAGCAACTCTCATTTATCTTATATCCGTTCCATTTTGTACTAAAAGAACCAG
ACCACATCGATTCAATCGAAATGAGAGCCAAGTGGAGAAAGAAGAGAACTAGAAGACTTA
AGAGAAAGAGACGGAAGGTGAGAGCCAGATCCAAATAA

YDL184C, 25 aa (SEQ ID NO 48)

MRKWRRKRTRRLKRRKRRKVRARSK

YDL191W, 1354 bp, exon1: 501-503, intron1: 504-994, exon2:
995-1354 (SEQ ID NO 49)

TATTGACGTTTCGCTCTCAGGTCCACCGTGTCTCAAAAGTAACTTTTAAAACCTAAAAC
ACACGAAATCATATTATGATAATTCAGAATGATAGTGTGGTACTGTGTCAATTGACTGTT
CAAGACTGAAGAGGATCTTTGATTTGTTGTTACTCAACAAATAATCTTCACGAAAACCTTT
CTCAATCTGGGGACTGTATTAATCTCAGACCCATACATATCTACACCCATAACTTTTTAC
ATTTAATTTTTTATCACAATAAGGTAGCTTAAATTTGTAAAGTCGCAAAAAAAAAATGGCA
GCGCAGCCTCTCCGGGTGAACCCACGACAACTTACCTGGCACTCCATGCCTAACGGGC
GGGTTTGGGCAAGGATTCAGCATCAATTTTGCAAAATTCACACCTGAGTAATTCATATAT
GTAATATAATGTTAAGCATACGCTGTCTGATTAGCACTATTATTGACCGTAGAATAGGTAC
AGTGAGACAGTATATTCGAAATGGTATGTTTGAGATGAACAAAATAATAAAGACTGACAA
CTGCAGAACAGAGAGGATCATAGCAACCTAGTGCAAGAAAGAGCCTCGAAGCGTTAAACT
TTTGGAACGTAATTCATCCGTTGGCTATGTCTATTCAATACAGTTAGAATACGAAAGCTG
TAATCAAGTATATCGGATTTATTCGCAAGCAAGAATCAAGGAAAAGAAAGTGAAAATAGC
ATACATCTTTAAATTCAGAGGTTTTGCTGAATTTTAATAGGGAAGTTTACGTTATGATTG
TTGGCCGTAGATCGCCTAGCGTTTGACCAAATTTAATCTCCTAATTTTTTTTATTGTA
AAAGCCTTCCAACGAAATAAATTAAGTTATTTGTTTCTCTGTTACGAGGGATATAT
GATGCCGTGTGCTTGTAGTTCAATTATAAGTGCTAATAAAATACTAACGTTAATAAAAAAT
TGGAATATTATTTCATTTTTATCCTATTAATAGCCGGTGTAAAGCTTACGAACCTAAG
AACCAAATCCAAAGGAACAATTGGCTTCTCAATTTGGTTGACTTGAAAAGGAGTTGGCTGA
ATTGAAGGTCCAAAAGTTGTCCAGACCATCTTTGCCAAAGATCAAGACCGTCAGAAAGAG
TATCGCCTGTGTCTTGACCGTCATCAACGAACAACAAAGAGAAGCTGTTAGACAATTATA
CAAGGGTAAGAAGTACCAACCAAGGACTTGAGAGCCAAGAAGACCAGAGCTTTGAGAAG
AGCTTTGACCAAATTCGAAGCTTCCCAAGTTACCGAAAAGCAAAGAAAGAAAGCAAATCGC
TTTCCCAAAAGAAAGTACGCTATTAAGGCTTAA

YDL191W, 120 aa (SEQ ID NO 50)

MAGVKAYELRTKSKEQLASQLVDLKKELAEKLVQKLSRPSLPKIKTVRKSIACVLTVINE
QQREAVRQLYKGKKYQPKDLRAKKTRALRRALTKFEASQVTEKQRKKQIAFPQRKYAIIKA

YDR103W, 3254 bp, CDS: 501-3254 (SEQ ID NO 51)

ATCAAGTTTCCTTTAAAGGGATATATAACAGATTCTAAACTGACAGAAATATTTTCGAGT
GAAGAAGAAGCGTTAAATATTGGATCTTTCCGCAAGTTCTACTCTGATACATTTTTGAAGT
AGGAGAGTCATTTAGAAGGCGTATTGCTCAATAGTAGAAAGCAGGCCTGTGCACATGAAT
TAATTAATAAATAAAGGTAGTGTAGACGACACATGTCCATAGGTAACCTGTCTATAA
TTTTGAACAATTTCCCTTCTTTTCTTTTTTTTTTTGGGTGCGGCATATGTAGCTTGT
AATTTACACATCATGTACTTTTCTGCATCAAAATATGAAAGGCGATAGTAGCTAAAGAAA
ATACCGAGAATTTCTCGAAAAGTTGACGACAAAAGAAAGGCATAAAAAAGTAATTTGAA
AATATTTTAAACTGTTTAAACCATCTAGCATCCGCGCTAAAAAGGAAGATACAGGAT
ACAGCGGAAACAACTTTTAAATGATGGAAACTCTACAGACAATATAGTTTCCCTTTTC
ACAATTTTGTAGCTCGACACAATATAGTGGTACCTTGTGCGAGAACTCCCAACCAATAA
TAGAGCTAGAGAAGCCAGTACTCTATCCCCATTGTCAAGAGGAAAAAATGGACGGAAA
AGTTAGCCAGGTTCCAAAGAGTAGTGCTAAAAAGAAAGATTCTCACCTTCTCCTATTT

CCTCCTCTACATTTTCGTTCTCACCCAAATCTAGGGTCACTTCTTCAAACCTCTTCTGGCA
ATGAAGACGGTAACCTAATGAATACACCTTCTACGGTTTCCACTGATTATTTGCCACAAC
ACCCTCACAGAACATCGTCTTTGCCAAGACCTAATTCCAATCTCTTTCACGCAAGTAATA
GTAACCTATCCCGAGCAAATGAGCCCCCAAGGGCCGAAAATTTATCAGATAATATACCAC
CCAAGGTCGCTCCATTTGGCTATCCAATACAAAGAACCTCTATTAAAAAATCCTTTTTGA
ATGCTTCTTGTACGTTATGTGACGAGCCTATTTCTAACAGAAGAAAGGGAGAGAAAATTA
TAGAGCTTGCATGTGGCCACTTAAGTCACCAAGAATGTCTTATTATCTCTTTTGGCACCA
CTTCAAAGGCAGACGTTTCGTGCGCTATTTCTTTTGTACCAAATGTAAAAAAGATACTA
ACAAAGCCGTTCAATGCATTCCAGAAAATGATGAACATAAAGGATATTCTAATTTCTGATT
TTTTGATTTCATAAGATTCCCTGATTCTGAGTTATCAATCACACCTCAGTCCCGCTTTCTCTC
CTTATTCACCACCTCTTGCCCTCCTTTTGGGTATCCTATACACCTGTTGAAAGACAAACGA
TATATTCTCAAGCTCCAAGTCTAAACCCAAATCTCATATTGGCTGCACCCCCCAAGGAAA
GAAACCAAAATCCACAAAAAAATCAAATATACATTTTACATTACCCCTGGGGCACA
GAAGAATTCGTCGAGCAAACCTCTATCTTAGCAGACACCTCTGTAGCGTTGTACAGCTA
ATGATTCTATTTCTGCTGTTTCCAATTCCGTAAGAGCAAAGGATGACGAAACCAAAACAA
CGTTGCCGCTGTTAAGGTCATATTTTATTCAAATTCTTTTGAACAATTTCCAGGAAGAAT
TGCAGGATTGGAGAATAGACGGGGACTATGGATTACTAAGGTTGGTAGACAAATTGATGA
TTTCCAAAGATGGTCAGAGATATATACAATGCTGGTGTCTTATTTTGAAGACGCATTTG
TAATAGCAGAAGTGGATAACGATGTTGATGTTTGGAAATTAGACTAAAGAATTTAGAAG
TATTTACACCTATTGCCAACTTGAGAATGACTACACTCGAAGCTTCAGTACTCAAATGCA
CCTTAAATAAAACAACATTGCGCCGATTTATCAGATCTTTACATTGTTTCAGAATATAAATT
CTGACGAAAGCACAACTGTACAGAAATGGATATCAGGTATATTGAATCAGGATTTTGTAT
TCAATGAGGACAAATACCTTCGACCCTGCCTATTCTTCCCATTATAAAGAACCTTTCAA
AAGATGTTGGTAATGGTAGGCACGAGACGAGTACCTTTCTAGGTTTAAATCAATCCTAACA
AAGTTGTTGAAGTTGGAAATGTGCACGATAATGATACTGTAATCATAAGGAGGGGATTCA
CCTTAAATTCAGGAGAATGTTCTAGGCAGAGTACTGTGACAGTATACAATCTGTTCTAA
CCACGATAAGCTCAATTCCTTCCCTTAAACGAGAAAAACCTGATAATTTGGCAATAATCT
TACAGATCGATTTTACGAAATTGAAAGGAAGAAGACAGTTTAAATTGTTGTTTATAACAGTC
TAAAAGCTTTAACCATTAAATTTGCGCGTTCAGTTCGTTGTTGTTGATCGAAATAATT
ATGTTCTGGACTATGGATCGGTATTACACAAGATAGATTCACTAGATTCCATCTCAAATC
TCAAATCAAAGAGTTCCCTCGACACAATTTTCACCTATTGTTGGTTGAAAAATACTCTATATC
CCGAAAATATTTCATGAACATTTGGGTATTGTTGCTGTATCAAATAGTAATATGGAAGCAA
AAAAATCCATACTATTTCAAGATTACAGATGCTTTACAAGTTTGGGAAGAAGAAGGCCCA
ATGAATTGAAGATTAAAGTGGGCTATTTGAACGTTGACTACAGTGATAAAATTGATGAAC
TAGTCGAGGCCAGCTCCTGGACTTTTGTTTTGAAGAACTCTTTGCTACAGTTTCGGTCTAA
GTTTGTGATGAACATGATGACGATGACGAAGAGGATAATGATGATTGACCGGATAAGAAC
TTGATAATAGTTTCAGGATCACTGTGCGGATGCTGAATCTACAACCTACTATTTCATATTGATT
CTCCATTTGATAATGAAAATGCTACCGCAAATATGGTGAATGACAGAAACCTTCTCACTG
AGGGTGAACATAGCAATATAGAAAACCTAGAAAACCTGTCGCTTCTTCAGTACAGCCAGCTC
TGATTCCATAATATTAGATTTTCACTTCATTCTGAGGAGGAAGGTACTAATGAAAATGAAA
ATGAAAATGATAGCCAGTATTATTACTTAGTGATAGGATAAAGGAATCGATGGCATAA
CCAGACGCAGTTTCATTCTCGAGTCTTATAGAGAGCGGTAATAACAACTGTCCCTCCATA
TGGATTATATATAG

YDR103W, 917 aa (SEQ ID NO 52)

MMETPTDNIVSPFHNFGSSTQYSGTSLRTPNQIIIELEKPSLSPLSRGKKWTEKLARFQR
SSAKKKRFSPISSSTFSFSPKSRVTSSNSSGNEGDNLMTNPSTVSTDYLPQHPHRTSS
LPRPNSNLFHASNSNLSRANEPPRAENLSDNIPPKVAPFGYPIQRTSIKKSFLNASCTLC
DEPISNRRKGKIIELACGHLHQECLIIISFGTTSKADVRALFPFCTKCKKDTNKAVQCI
PENDELKDILISDFLIHKIPDSELSITPQSRFPYPSPLLPPFGLSYTPVERQTIYSQAPS
LNPNLILAAPPKERNQIPQKSNYTFLHSPLGHRRIIPSGANSILADTSVALSANDSISAV
SNSVRAKDDTKTTLPLLSYFIQILLNNFQEELQDWRIDGDYGLLRVLDKMLISKDQQR
YIQWCWCFLEDAFVIAEVDNDVDVLEIRLKNLEVFPTPIANLRMTTLEASVLKCTLNKQHC
ADLSDLYIVQNINSDESTTVQKWSGILNQDFVFNEEDNITSTLPILPIIKNFSKDVGNR
HETSTFLGLINPNKVVEVGNVHDNDTVIIRRGFTLNSGECRSQSTVDSIQSVLTTISSIL
SLKREKPDNLAILQIDFTKLKEEDSLIVVYNSLKALTIKFARLQFCFVDRNNYVLDYGS
VLHKIDSLDSISNLKSKSSSTQFSPIWLKNTLYPENIHEHLGIVAVSNSNMEAKKSILFQ
DYRCFTSFGRRRPNELKIKVGYLNVYSDKIDELVEASSWTFVLETLCSYFGLSFDHDD
DDEEDNDDSTDNELDNSSGSLDAESTTTIHIDSPFDNENATANMVNDRNLLTEGEHSNI
ENLETVASSVQPALIPNIRFSLHSEEGTNENENENDMPVLLSMDMDKIDGITRRSSFS

SLIESGNNNCPHMDYI

YDR238C, 3422 bp, CDS: 501-3422 (SEQ ID NO 53)

CCGTGTCAAGATCTAACACGGTAGTCAGCTACTACACAAGGTCTCAGAACAGAATGAGAA
GTGGAACACTGGATAATGATTACGTGAACAGACAAAAAGCTTCCTACACATATCTCTCTTC
AAGATTATCGTGATGCTAATGCTAGAAGTAATATATCGCGTCAGGACTCTGTCTCCACAA
CGAACTCTGATGTGGTAGACCTCAGCTATTCTCTGGGGCATGGCTTGCCTGTGGCAAACC
CTGATTACAGACCCAGAATGATATCCCTTCTCTGTAGTTTGTAGATGTCATATATGTACGT
TTATGGAACAGCATTTTAGAAAAAGTATTACCCAGCTTATCACTTCGTTTTTTTTTCTTT
CCGTGTACTCGCTACACGTAGAAAAGAAATCAGAAAAACAACAGCTCGACAAGTGAAATTTG
ACGTTTCATTAAAGACTCAGTTAAGATTGCCTTGAGAATAAAACAAAAGTAATCACAGTTAAC
TATTGAACAAGAGTGCACCTATGACTTCACTTTCTTCACAGCCAGCGTACACGTTGGTTTT
TCGATCCTTCTCCGAGTATGGAGACTTACTCGAGTACCGATTTCAGAAAGCTCTTGAAA
AGGGATCTGATGAACAAAAAATTGACACGATGAAATCAATTTTAGTTACAATGCTGGAAG
GAAATCCAATGCCGTGAATTGTTGATGCACATAATAAGATTGTGTCATGCCCTTCTAAAAATA
AGGAATTAATAAAGCTTTTGTACTTCTACTGGGAAATTGTTCCCAAAGTACTGAAAGATG
GAAATTTAGACATGAAATGATTCTTGTCTGTAATGCCATTCAACACGATTTCGAACATC
CTAATGAATATATTAGAGGTAACACATTAAGGTTTTTAACGAAATTGAGAGAGGCCGAAC
TCTTAGAACAGATGGTTCCCTCTGTCTTAGCGTGCTTGGAATACCGTCATGCATATGTTT
GTAAGTATGCAATCCTAGCAGTTTTCTCCATTTTCAAGGTGAGCGAACATTTACTTCCCG
ATGCTAAAGAAATCATCAATTCGTTTCATAGTAGCTGAAACTGATCCAATATGTAAGAA
ATGCATTTATTGGGTTAGCTGAATTAGATCGTGAAAATGCCTTACACTATTTAGAGAACA
ATATTGCTGATATAGAAAACCTAGACCTTTATTACAAGCTGTCTTTGTTCAATTTATCA
GACAAGATGCAACAGGACCCCTGCTTTGAAAGCCCAATATATCGAATTATTGATGGAAC
TGCTTTTCGACCACGACTTCCGATGAAGTCATCTTCGAGACCGCATTAGCCCTAACTGTGT
TGCTGCCCAATGCCAAATGCTTTGGTTCTGCGGTTAACAATTTGATTGACTTGGCCGTCA
AGGTTTCTGATAATAACATTAAAGTTAATTGTTCTAGACCGTATTCAAGACATCAATGCTA
ATAACGTAGGTGCTTTTGAAGAGTTAACCCCTGGATATTTTGAAGTCTTGAATGCAGAAG
ATTTAGACGTTTCGTTCAAAGGCGCTTGATATTTCAATGGACTTGGCCACATCCAGAAATG
CTGAAGATGTTGTTACGCTTTTGAAGAAAGAGCTGCAAAACAACCGTAAATAACCCAGATC
AAGACAAGGCAATGCAGTACAGACAATTGTTAATAAAAACTATTTCGTACCGTGGCTGTAA
ACTTTGTAGAAATGGCAGCAAGTGTGTTTTCGCTATTATTAGATTTTCATCGGTGATTAA
ACTCGGTTGCCGCCAGTGGTATCATTGCCCTTTATCAAAGAAGTGATCGAAAAATACCCAC
AACTTAGAGCCAATATCCTTGAAAACATGGTTCAAACGCTAGACAAAGTGAGATCTGCTA
AAGCTTACCGCGGTGCATTATGGATTATGGGTGAGTATGCTGAAGGAGAAAGTGAGATAC
AACATTGTTGGAAGCACATTTCGTAACAGCGTAGGTGAAGTTCTATCCTTCAATCAGAAA
TCAAAAAGTTAACACAAAAACCAAGAACACACCGAAGAAAATGAGGTTGACGCTACCGCCA
AGCCAACCTGGTCCAGTTATTCTACCAGACGGTACGTATGCCACTGAAAGCGCTTTTCGATG
TGAAGACTTCTCAAAGTCAGTTACCGATGAAGAACGTGATTCTAGACCTCCAATTCGCC
GGTTTGTTTTAAAGTGGTGATTCTTACACAGCTGCCATTCTGGCCAACACCATCATTAAAC
TTGTTTTTAAATTCGAAAACGTTTCCAAGAACAAAACGTGTCATCAATGCTCTAAAGGCGG
AAGCTTTTACTAATTTTAGTTAGTATTGTAAGAGTGGGTCAAAGCTCTTTGGTGAGAAA
AAATTGATGAAGATTCCTTAGAGAGAGTTATGACATCTATTTCTATTTTATTGGATGAAG
TTAATCCTGAGGAAAAGAAGGAAGAGTTAAACTTCTGGAGGTTGCATTCTTGGACACCA
CCAAATCCTCATTCAAGAGACAAATTGAAATTGCAAAGAAGAACAAGCATAAGAGAGCAT
TAAAGACAGTTGCAAAAACATCGAACCAATTGATACGCCGATTCTTTTCAGGCAATTTG
CTGGTGTGGATTCTACTAATGTGCAAAAAGATAGTATTGAAGAAGATTTACAACCTGGCAA
TGAAAGGAGATGCAATCCACGCTACTAGCAGCTCTAGTATTTTGAAGCTGAAGAAGATAG
TACCTTTATGTGGCTTTTCTGATCCAGTTTACGCCGAGGCTTGTTATACAAACAATCAAT
TTGACGTCGTATTAGATGTTCTTCTTGTAAATCAAACGAAAGAAACATTGAAAAACCTAC
ATGTGCAATTTGCAACTCTTGGTGATTGTAAGATTATTGACACACCACAGAAGACCAACG
TGATTCCTCATGGCTTCCACAAATTCAGTGTACTGTCAAAGTTTCTCTGCTGACACAG
GTGTCATTTTCGGTAATATTATTTATGATGGTGCGCATGGTGAAGATGCTCGTTATGTTA
TTTTAAACGACGTTTCATGTTGACATTATGGATTATATCAAACCAGCCACTGCTGACGATG
AACATTTCCGTACCATGTGGAATGCATTTGAGTGGGAGAACAAAATATCGGTCAAATCAC
AACTACCAACATTGCATGCTTATTTGAGAGAACTGGTCAAGGGAACATAATGGGTATTC
TAACACCATCAGAGTCGTTGGGAGAAAGATGATTGTAGGTTCTTAAGTTGTAATCTGTATG
CGAAGTCGTCTTTGGTGAAGATGCCCTAGCCAACCTGTGTATCGAAAAGGATTCCAAA
CCAATGTCATAGGTTATGTTTCGTATCCGATCAAAGGGAAGGTTTGGCTCTGTCCC
TAGGTGACAGAGTGGCATTGATTGCTAAGAAGACCAATAAACTTGCTCTCACTCATGTTT

GA

YDR238C, 973 aa (SEQ ID NO 54)

MTSLSSQPAYTLVFDPSMETYSSTDFQKALEKGSDEQKIDTMKSILVTMLEGNPMPPEL
LMHIIRFVMPSPKNKELKKLLYFYWEIVPKLAEDGKLRHEMILVCNAIQHDLQHPNEYIRG
NTLRFITKLREAELLEQMVPVSLACLEYRHAYVRKYAILAVFSIFKVSEHLLPDAKEIIN
SFIVAETDPICKRNAFIGLAELDRENALHYLENNIADIENLDPLLQAVFVQFIRQDANRT
PALKAQYIELLMELLSTTTSDEVIFETALALTVLSANPNVLPVAVNKLIDLAVKVSDNNI
KLIVLDRIQDINANNVGALEELTLDILRVLNAEDLDVRSKALDISMDLATSRNAEDVVQL
LKKELQTTVMNPDQDKAMQYRQLLIKTI RTVAVNFVEMAASVVSLLLDFIGDLNSVAASG
IIAFI KEVIEKYPQLRANILENMVQTLDKVRSKAYRGALWIMGEYAEGESEIQHCWKHI
RNSVGEVPILQSEIKKLTQNEHTEENEVDATAKPTGPVILPDGTYATESAFDVKTSQKS
VTDEERDSRPPIRRFLVSGDFYTAAILANTI IKLVLFENVSKNKTVINALKAEALLILV
SIVRVGQSSSLVEKKIDEDSLERVMTSISILLDEVNPEEKKEEVKLEVAFLDTTKSSFKR
QIEIAKKNKHKRALKDSCKNIEPIDTPI SFRQFAGVDSTNVQKDSIEEDLQLAMKGDHAIH
ATSSSSISKLKKIVPLCGFSDPVYAEACITNNQFDVLDVLLVNQTKETLKNLHVQFATL
GDLKI IDTPQKTNI PHGFHKFTVTVKVSSADTGVI FGNI IYDGAHGEDARYVILNDVHV
DIMDYIKPATADDEHFRMTMWNAFEWENKISVKSQ LPTLHAYLREL VKGTNMGILTPSESL
GEDDCRFLSCNLYAKSSFGEDALANLCIEKDSKTN DVIGYVRIRSKGQGLALSLGDRVAL
IAKKTNKLALTHV

YDR259C, 1652 bp, CDS: 501-1652 (SEQ ID NO 55)

AAACTTTGTTCAAGATTATGCTTTCTTTGTAATTTTAAACATAGTCTTGCACCTTATTTTT
ACTGCAATGTGGATAAAAGTTTTCGAATCGTTTGCAGGCAAATGTAAACTATTACTTTTT
AATGATTTCTGATACTCTTTGATTCCATTCTGTCTACTTTTTTCTGCATTTGAAACGCT
AATTAAGTATTTCTTGGCCCTGCTTCTTTCTTTGATTCTTTTTTTTATTCTCAAGTT
TTTAATTTCTGGAGAATCTCTTTTTTTGTTTATTGTTTAAACACAGTTAGTGGAGCCTTG
TAGTATCGAGAGTAGACTATCTTTGGAAAGCAATGCGAGTTGAGAGATTGTGGAGTGTAC
TACAGAACCAATATTAAACACAATCTTTCTCTCAAACTGTAACACCGAGTTTTTTTCCCCA
CCAATCGTGAATCCGATAGCATATACTTTTGTCTAGAAATTTCAATAAACAACAGAATAA
CGAAGAGTGCTAAGGGACAAATGCAAAACCCCTCCGTTGATTCTGTCCTCCGATATGTATAATC
AGGGAAGCAGCTCAATGGCTACTTATAATGCCTCTGAGAAGAATCTAAATGAGCATCCTT
CTCCGCAAATTCACAGCCCAGCAGCTCCCAAAAGTTACCTTATAGAATAAATCCTACAA
CCACTAATGGGGACACCGACATATCTGTTAACAGCAATCCTATCCAGCCTCCTTTGCCAA
ACTTGATGCATCTATCTGGTCCGCTGACTATAGATCGATGCATCAAAGTCTTATACATC
CATCTTATATCATCCCTCCGATTCAAATGAAAGAAAACAATCAGCTTCTTACAACAGAC
CTCAAAATGCTCATGTAGTATTCAACCTTCCGTGGTATTCCCCCCTAAAAGTTATTCCA
TATCTTATGCACCTTATCAAATAAATCCCCCTTTACCAAATGGACTTCCGAACCAGAGCA
TATCTTTGAATAAGGAGTATATTGCAGAGGAGCAACTATCAACCCCTCCCATCTCGCAATA
CCAGTGTTACTACTGCACCTCCTTCTTTTCAAAACAGTGCTGATACCGCTAAAAATTCAG
CTGATAATAATGATAATAATGATAATGTAACCAAACCTGTTCTTGATAAAGACACCCAAC
TCATAAGTAGTTTCAGGCAAACTTTAAGAAATACTAGAAGAGCTGCTCAAAATAGAACCG
CTCAAAAGGCATTTAGACAAAGGAAAGAAAAATACATCAAGAATCTCGAACAAAAATCAA
AGATATTTGACGATTTACTAGCAGAAAATAATAACTTCAAATCATTAACGATTCATTAA
GAAATGACAACAACATTTTAATAGCTCAGCATGAAGCTATAAGGAATGCAATTACTATGT
TAAGAAGTGAGTATGATGTCTTATGTAACGAAAACAACATGTTGAAGAATGAGAATAGTA
TAATAAAAAATGAACACAACATGTCAAGAAATGAAAATGAAAACCTAAAACCTTGAGAATA
AACGCTTCCACGCTGAATATATACGAATGATCGAGGATATTGAAAATACTAAAAGAAAGG
AACAGAACAACGAGATGAAATAGAGCAACTAAAAAAAAAATAAGATCCCTGGAGGAAA
TAGTAGGGAGACACTCGGATAGTGCCACGTAA

YDR259C, 383 aa (SEQ ID NO 56)

MQNPLIRPDMYNQSSSMATYNASEKNLNEHPSQIAQPSTSQKLPYRINPTTTNGDTD
ISVNSNP IQPPLNLMHLSGSPDYRSMHQSPIHPSYIIPHSNERKQSASYNRPQNAHVS
IQPSVVFPPKSYSISYAPYQINPPLPNGLPNQISISLNKEYIAEEQLSTLPSRNTSVTTAP
PSFQNSADTAKNSADNNDNNDNVTKPVPDKDTQLISSGKTLRNTRRAAQNRTAQKAFRQ
RKEYIKNLEQKSKIFD DLLAENN NFKSLNDSL RNDNNILIAQHEAIRNAITMLRSEYDV
LCNENMLKNENSIKNEHNMSRNEENENLKENKRFHA EYIRMI EDIENTKRKEQEQRDE
IEQLKKKIRSL E EIVGRHSDSAT

YDR294C, 2270 bp, CDS: 501-2270 (SEQ ID NO 57)

CCGACAGTACGACTTAAAAAACAAAAACAACGTCCAGGTGAAAAAGCTGCCGCAAATGG
TACACGGTTTAGATCAACAAGATCCAATACCCCTAATTACACATGAATGTGACGTTTCCT
AAAAGAAGTAGCCTGTATAATATAGAGAGATTTTATATACTTTCTTAATGAATTAGACTG
TTTCTACAAGTATTTGACACTGGAAAAAAGAGAAAGTACATAGAGATTGGCCAAATATT
TAAATCTACACAGTTGCCTATCGTTTATCGCCTTATTCTTCAGAAACATTTTCATCAACTA
CTCTGGTGCATTATTTTCATGTTAGTTACCATATATACCGGCCCGCCGCATCGGGGTTTTT
TGATTGAAAAAATTGGTATATTTTCAGTACACATATAAATAAAACCCCTCAATTTGCCCTCT
CCAACCGTTATACTATTCCAGATCCTCTTTACCGAGCAAGTAGGCTAGCTTCTGTAAAG
GGATTTTTCCATCTAATACAAATGAGTGGAGTATCAAATAAAACAGTATCAATTAATGGTT
GGTATGGCATGCCAATTCATTTACTAAGGGAAGAAGGCGACTTTGCCCAGTTTATGATTC
TAACCATCAACGAATTAAAAATAGCCATACATGGTTACCTCAGAAATACCCCATGGTACA
ACATGTTGAAGGATTATTTGTTTGTGATCTTTTGTTACAAGCTAATAAGTAATTTTTTTTT
ATCTGTTGAAAGTTTATGGGCCGGTGAGGTTAGCAGTGAGAACATACGAGCATAGTTCCA
GAAGATTGTTTCGTTGGTTATTGGACTCACCATTTTTTGAGGGGTACCGTAGAAAAGGAAG
TCACAAAGGTCAAACAATCGATCGAAGACGAACATAATTAGATCGGACTCTCAGTTAATGA
ATTTCCACAGTTGCCATCCAATGGGATACCTCAGGATGATGTTATTGAAGAGCTAAATA
AATTGAACCACTTGATACCACATACCAATGGAAGGAAGGAAAGGTCTCTGGTGCCGTTT
ACCACGGTGGTGATGATTTGATCCACTTACAAACAATCGCATACGAAAAATATTGCGTTG
CCAATCAATTACATCCCGATGTCTTTCTGCCGTACGTAATAATGGAATCCGAAGTGGTTT
CTATGGTTTTTAAGAATGTTTTAATGCCCTTCTGATACAGGTTGTGGTACCACAACCTCAG
GTGGTACAGAATCCTTGCTTTTAGCATGTCTGAGCGCTAAAATGTATGCCCTTCATCATC
GTGGAATCACCAGAACAGAAATAATTGCTCCCGTAAGTGCACATGCTGGGTTTGACAAAG
CTGCTTATTACTTTGGCATGAAGCTACGCCACGTGGAGCTAGATCCAACGACATATCAAG
TGGACCTGGGAAAAAGTGAAAAAATTCATCAATAAGAACAACAAATTTTACTGGTCCGTTCCG
CTCCAAACTTTCTCATGGTATTGCGCATGATATTGAAGGATTGGGTAAAATAGCACAAA
AATATAAACTTCCTTTACACGTCGACAGTTGTCTAGGTTTCCTTTATTGTTTCATTTATGG
AAAAGGCTGGTTACAAAAATCTGCCATTACTTGACTTTAGAGTCCCGGGAGTCACCTCAA
TATCATGTGACACTCATAAATATGGATTGTCACCAAAAGGCTCGTCAGTTATAATGTATA
GAAACAGCGACTTACGAATGCATCAGTATTACGTAAATCCTGCTTGGACTGGCGGGTTAT
ATGGCTCTCTACATTAGCAGGGTCCAGGCCTGGTGTCTATTGTCGTAGGTTGTTGGGCCA
CTATGTTCAACATGGGTGAAAAATGGGTACATTGAGTCGTGCCAAGAAATAGTCGGTGGC
CAATGAAGTTTAAAAAATACATCCAGGAAAAACATTCCAGACCTGAATATAATGGGCAACC
CTAGATATTAGTCATTTCATTTTCTTCAAAGACCTTGAACATACACGAACATCTGACA
GGTTGTCCAAGAAAGGCTGGCATTTCAATGCCCTACAAAAGCCGGTTGCACTACACATGG
CCTTCACGAGATTGAGCGCTCATGTTGTGGATGAGATCTGCGACATTTTACGTACTACCG
TGCAAGAGTTGAAGAGCGAATCAAATTTCTAAACCATCCCGAGACGGAAC TAGCGCTTAT
ATGGTGTGCGCCGGGAGCGTTAAAACTGCTGGCGTTGCAGACAAATTGATTGTGGGATTCC
TAGACGCATTATACAAGTTGGGTCCAGGAGAGGATACCGCCACCAAGTAG

YDR294C, 589 aa (SEQ ID NO 58)

MSGVSNKTVSINGWYGMPIHLLREEGDFAQFMILTINELKIAIHGYLRNTPWYNMLKDYL
FVIFCYKLISNFFYLLKVYGPVRLAVRTYEHSSRRLFRWLLDSPFLRGTVKEVTKVKQS
IEDELIRSDSQLMNFQPLPSNGIPQDDVIEELNKLNDLIPHTQWKEGKVS GAVYHGDDL
IHLQTIAYEKYCVANQLHPDVFPVVRKMESEVVSMLVLMFNAPSDTGCGTTTSGGTESLL
LACLSAKMYALHHRGITEPEIIAPVTAHAGFDKAAYYFGMKLRHVELDPTTYQVDLGKVK
KFINKNTILLVGSAPNFPHGIADDIEGLGKIAQKYKLPLHVDSCLSFIVSFMEKAGYKN
LPLLDFRVPGVTSISCDTHKYGFAPKGSSVIMYRNSDLRMHQYYVNPWTGGLYGSPTLA
GSRPGAIVVGCWATMVNMGENGYIESQEI VGAAMKFKKYIQENIPDLNIMGNPRYSVIS
FSSKTLNIHELSDRLSKKGWHFNALQKPVALHMAFTRL SAHVVDEICDILRTTVQELKSE
SNSKPSPDGTSALYGVAGSVKTAGVADKLIVGFLDALYKLGPGEDTATK

YDR430C, 3470 bp, CDS: 501-3470 (SEQ ID NO 59)

ACGTCATTTTGTCTTGTGGAGCTGGTGGTTCTTGTGGAGCAGATTCTGTGGAGCAGAT
TCCTGTGGAACCTTGTGGTTCTTGTGGAGCATCTGGAGCCTGTGGTGGTTCTTGGTGTCTGT
TCTTCCACTGGGGCATCGACAACAGATTCTGGTAGTTGCTCTACGTGAGTTTCTTGAGCT
TCAGACATTATCCTTATGGTTTTAGCGTAATTGCTTAATTTTGATTCTTTCAAAGGTATA
TATATTTAGAAGAGAGGAAATATTTTTCTCATGTCTTTTTAAATCCCTTTGGGTGGCG
AAAAAAAAGAAATGTAAAAAATTTGCCCTTCGTTTACAGTGATAAATATACGGAGGGGCT
CTATGATAAAGGTAGTAGTAAATCATTGAATTGTTGAACAAGCATTGACAGATATGATAA

CAAGCAATTGTAATCAATAAGCCACCAATTAGAAGGCTACTCAAAAGAATAAAGTTACTTA
TAAAATATACTGCGGTATATATGTTGCGGTTTCAGCGATTTGCGTCCCTCGTATGCCCCAAG
CACAGGCCGTTAGAAAATATCCAGTTGGAGGTATATTCCATGGTTATGAAGTGAGAAGAA
TTCTACCGGTTCCGGAGCTGAGACTCACTGCGGTAGATTTGGTGCACTCCAGACAGGAG
CCGAGCATTTGCATATTGATAGAGACGACAAGAATAATGTGTTTCAGCATTCGTTTTAAAA
CCAACCTCCAGATTCCACTGGGGTCCCTCATATTCTAGAGCATACAACGTTGTGTGGGT
CTGTTAAATATCCAGTTAGGGACCCCTTTTTTCAAATGCTAAATAAATCTCTAGCTAATT
TCATGAACGCTATGACAGGTCCAGATTATACATTTTTTCCCTTTTCCACTACGAACCCCTC
AAGATTTTCGCTAATTTAAGAGGTGTTTATTTAGACTCCACCTTGAATCCGCTACTTAAAC
AAGAAGATTTTGATCAGGAGGTTGGAGGTTGGAGCATAAAAACATCACAGACCCCGAGA
GTAACATTGTTTTCAAAGGTGTTGTCTATAACGAAATGAAAGGTCAAATATCAAATGCCA
ATTACTATTTCTGGAGTAAATTTCAACAGTCTATTTATCCTTCCCTGAATAACTCCGGCG
GAGATCCTATGAAAATTACAGACTTGAGATACGGCGATCTCTTGGATTTCCATCACAAAA
ATTACCATCCCTCCAATGCAAAAACCTTTCACGTACGGTAACCTGCCATTGGTGGATACGT
TAAAGCAATTTAAATGAGCAGTTTCAGTGGTTACGGGAAGAGAGCTCGAAAGGATAAGTTGT
TAATGCCTATTGATTTAAAAAAGACATAGATGTCAAGTTACTGGGTCAAATAGATACTA
TGCTTCCACCGGAGAAGCAGACAAAAGCCTCAATGACGTGGATTTGTGGAGCGCCACAGG
ACACATATGATACCTTTTGTAAAGTACTGGGGAATTTATTAATGGATGGCCATTCTTT
CTGTAATGTATCAAAAATTAATAGAATCAGGAATTGGTTTGGAGTTCTCCGTAAATTCAG
GTGTTGAACCAACTACAGCAGTAAATTTGCTAACTGTTGGTATACAGGGCGTGAGTGATA
TTGAAATATTTAAAGACACTGTAAATAATATTTTTTCAAACCTGTTGGAAACAGAACATC
CTTTTGACCGCAAGCGTATCGATGCCATAATTGAACAATTTGGAATTATCTAAGAAGGATC
AAAAGGCTGACTTTGGACTTCAATTACTCTATTCTATACCTGGTTGGACAAACAAAA
TCGATCCTTTTGAGAGCTTGTGTTTGGAGACGTTTTGCAAGATTTAGAGGTGACTTAG
AAACGAAAGGTGATACTTTATTCCAAGATTTAATCCGTAAATATATCGTTTCAAAACCTT
GTTTCACGTTTTTCCATTTCAGGGATCTGAAGAGTTCTCTAAATCTTTGGATGATGAAGAAC
AAACAAGACTGAGAGAAAAAATTACTGCCTTGGATGAACAAGACAAGAAAAACATCTTTA
AACGTGGTATACTGTTACAGGAGAAACAAAATGAAAAAGAAGATTTATCCTGTTTACCTA
CCTTACAAATAAAAGACATCCCCAAGAGCTGGTGATAAATATTCGAATCGAACAGAAGATA
ATACAATGTCTAGGATTACTGATACCAATGGTATCACATATGTCAGAGGTAAACGTTTAC
TAAATGACATAATACCCCTTGAACCTTCCCATACTTACCTTTATTTGCTGAATCGTTAA
CTAACCTAGGGACAACAACAGAATCCTTCAGTGAAATAGAAGATCAGATAAAATTACATA
CGGGTGGTATATCAACACATGTAGAGGTTACATCTGACCCTAACACCACAGAGCCTCGCC
TGATTTTTCGGGTTTGACGGATGGTCTTTAAATTTCGAAGACCGACCACATTTTGAATTCCT
GGTCTAAGATCTTACTAGAACTGATTTCCATAAAAAACAGCGATAAAATTGAAAGTTCTTA
TCCGCTTATTAGCATCTTCAAACACATCTTCTGTAGCAGATGCCGGTTCATGCATTTGCAA
GGGGCTATTCTGCCGACATTATAGATCAAGTGGAGCTATAAATGAGACCCTCAATGGTA
TTGAGCAACTACAATTTATAAATAGATTGCACAGCTTGTAGACAATGAAGAACTTTCC
AAAGAGAAGTTGTGCAAGCTAACTGAATTGCAAAAGTACATTGTTGATACCAATAACA
TGAATTTTTTTATCACCTCAGACTCTGATGTTCAAGCGAAAACAGTAGAAAGCCAAATTT
CAAAATTCATGGAGAGATTACCTCATGGCAGCTGCTTGCCCAATGGACCAAAGACTTCAG
ATTATCCTCTTATTGGATCCAAATGTAAACATACTTTGATAAAATTTCTTTCCAGGTCC
ATTACACATCCCAAGCTTTATTGGGTGTGCCGTATACACATAAGGATGGCTCTGCACTTTC
AAGTTATGTCAAATATGCTAACATTCAAACATTTGCACAGAGAAGTCAGAGAAAAGGGTG
GTGCTTATGGTGGTGGTGCTTCTTATAGCGCCTTAGCGGGTATTTTCAGTTTCTATTCCCT
ATAGGGATCCTCAGCCTTTGAAGAGTTTAGAAACCTTCAAGAATAGCGGGCGTTATATAC
TGAACGATGCCAAGTGGGGCGTCACAGACCTTGATGAAGCTAAATTGACAATATTTCAAC
AAGTAGACGCACCTAAAAAGTCCCAAAGGAGAAGGCGTGACGTATTTTCATGAGCGGTGTTA
CAGACGATATGAAACAAGCAAGAAGGGAACAACCTCTTAGACGTATCTCTCCTGGACGTTTC
ATAGAGTCGCCGAAAAATATCTACTAAACAAAGAAGGGGTGAGTACGGTCATTGGACCTG
GAATCGAGGGGAAGACTGTTTCACCAAATTGGGAGGTGAAGGAACGTGTAG

YDR430C, 989 aa (SEQ ID NO 60)

MLRFQRFASSYAQAQAVRKYPVGGIFHGVEVRRILPVPELRLTAVDLVHSQTGAEHLHID
RDDKNNVFSIAFKTNPPDSTGVPHILEHTTLCGSVKYPVRDPFFKMLNKS LANFMNAMTG
PDYTFPPFSTTNPQDFANLRGVYLDSTLNPLLKQEDFDQEGWRLEHKNITDPESNIVFKG
VVYNEMKGQISNANYFFWSKFQQSIIYPSLNNSGGDPMKITDLRYGDLDFHHKNYHPSNA
KTFTYGNLPLVDTLKQLNEQFSYGKRRARKDLLMPIDLKKDIDVKLLGQIDTMLPPEKQ
TKASMTWICGAPQDITYDTFLLKVLGNLLMDGHSVMYQKLIESGIGLEFSVNSGVEPTTA
VNLLTVGIQGVSDIEIFKDTVMNIFQNLLETEHPFDRKRIDAIEQLELSKKDQKADFGL

QLLYSILPGWTKIDPFESLLFEDVLQFRFGDLETKGDTLFDLIRKYIVHKPCFTFSIQ
GSEEFKSLDDEEQTRLREKITALDEQDKKNIFKRGILLQEKQNEKEDLSCLPTLQIKDI
PRAGDKYSIEQKNNTMSRITDTNGITYVRGKRLNDIIPFELFPYLPPLFAESLTNLGTTT
ESFSEIEDQIKLHTGGISTHVEVTSDPNTEPRLIFGFDGWSLNSKTDHIFEFWSKILLE
TDFHKNSDKLVLRLLASSNTSSVADAGHAFARGYSAHYRSSGAINETLNGIEQLQFI
NRLHSLLDNEETFQREVVDKLTQLKYIVDTNNMNFITSDSDVQAKTVESQISKMERL
PHGSCLPNGPKTSDYPLIGSKCKHTLIKFPFQVHYTSQALLGVPHYTHKDGSAQVMSNML
TFKHLHREVREKGGAYGGGASYSALAGIFSFSYRDPQPLKSLETFKNSGRYILNDAKWG
VTDLDEAKLTIFQQVDAPKSPKGEVTFMSGVTDDMKQARREQLLDVSLLDVHRVAEKY
LLNKEGVSTVIGPGIEGKTVSPNWEVKEL

YDR438W, 1613 bp, CDS: 501-1613 (SEQ ID NO 61)

CTTTTCTCAGCACCTGTCCAGAGACATAACATCACAATCACATCGCCCCAGTAAATGCA
TACGCAAGATAAGATACAACTGGCTACGGGAACACTACGCCAACGTGATTGGCAATTGT
GCTCTAATAGTTACTCTATTATTGCTGTTAATTGACAATGTTTAGTCACGTGCAACACAA
TTCAAGTCACGTGGAAAGGCCCTTCACATGGTGATCCATCTTCTACATCTTCATCGGTCCT
GCATAAAGTCATAATATGGGGCTACTGGAATGTATGCACTTAACAGTACTATTATATGGT
GAGGCTGTAATGCTTACCGTTTGTGGCTATTCTCGTATTCTGTAGGCCCCCATACAC
ATTTTTCGGTAACTGCGGCATATAGATGAAAGTTGAAATGAATATTCAAAAGAATATATA
TAATAATGCAGGAGATCAAGGAAGAAATAGATATGTATAAGAGTGATGGTAGAGGCAAAA
AATAAAAAGTTAAGCAGGAGAAATGAATCGTGTGGTATAGACGTAGATCATATGATAGGGG
TCCTGCTTCTGGCCGTAGTGGTGGTGTTTTGGGTGGCGCTTCGTGTTTGAATAATGAAT
TGCTCGAGACAAACGCGTACAATAAACCTTTCTTCTTACTTATCTAAACATATCATCGT
TTGCTCTTTATTGACGCCAGATCTATGGAGGATAATCCAATCAAGAAGGAAGAGCTTGC
AGGAACGGACAGAACGAACATTACCTATTACACACAAGAATCTTTTTCAGAGTTCTTAC
CTTTACTATCTTCAACTCCTTCTACTTCTTCAAATTTGTCTTCGATAGCGGACACGAAAG
TGAAGGATACAAATGAGGTTGAGTCTGCTATTTTGGCTCTTGTGGTTCGTGGCAAATTTGG
CGGCTAACGCTGCTTTTGTGCTATACCACAGTGGCTTCGTCAACAATTCTTTCATCGACAT
CCTCATTTTTTACCCTTATTTCTTGCCACTAGTCTAGGAATAGAACTTTTTTCGACAAAAA
AACTGCTGGGGTTATTTGTGCTCTTTGTTTGAATTTATCTTAATTGTGATGCAATCCTCGA
AGCAACAGGATTCTGTGAGTGTCTTCTCTTTTGGTAGGTAACACTTTAGCACTGCTGG
GGTCATTGGGTTTACAGTGTCTATACAACCTTTTGAATAACGAAATATCATCCAAAGGTC
TCAGACTAGACATTACAGATGTTTCTTGGTTATGTTGGTATCTTCACGTTTCTGTTGTTTT
GGCCAATTTTAAATAATCCTGGATATAACACATATGGAACTTTTGAACACCAAGTAACT
TCCACATTTCTTTCTTGTCTATGTTAAATTTGATCATTATCTTTGTTAGTGACTATTTTT
GGTGTAAGCCCTCATTTTGACATCACCTTGGTGGTTACCGTTGCCTTAACCTTTTACTA
TCCCGTTAGCCATGTTTCGCTGATTTTGTATGCGGAGAGGCATTTTTTACGCCTTGGTATA
TCATTGGTGTATTTTTCATTTTGTTCATTCTTTCTAGTTAACCATCGGGGAGAATCTG
CTGTTGAAAAGGACTGTGCTGCGGTTGAAAAGGACCTATCTTGGATGCCTAA

YDR438W, 370 aa (SEQ ID NO 62)

MNRVGIDVDHMGVLLLVVVVFWVGASCLTNELLEYNAYNKPFFLTLYLNISFALYLTP
DLWRRIQSRKSLQERTERTLPIHTQESFSEFLPLLSSTPSTSSNLSSIADTKVKDTMRL
SLLFCVLWFVANLAANAALSYTTVASSTILSSTSSFFTLFLATSLGIETFTSKKLLGLFV
SLFGIILIVMQSSKQQDSVSASSFLVGNLALLGSLGYSVYTTLLKYEISSKGLRLDIQM
FLGYVGIFTFLFWPILIIIDITHMETFELPSNFHISFLVMLNCIIIFVSDYFWCKALIL
TSPLVVTVALFTIPLAMFADFVWREAFTPWYIIGVIFIFVSFFLVNHRGESAVEKDCA
AVEKGPIILDA

YDR450W, 1376 bp, exon1: 501-547, intron1: 548-982, exon2:
983-1376 (SEQ ID NO 63)

CGGCCCATGAGCATAAATTGAGAACGATATTATTAATTCTAGTATATTTTTAGGAACAGCA
GGCATTATATATCCAAAACCTTTTTTAAATAGCATCCACATCACTTACTGGCGTACAGTTT
CGTGTCTGGCAACAAAAAGTACATTTAATTTCAATGATTAAAAAGACATTAAACATCCG
TACATTACGCACCCATGCATGCTATCTGAAAATATTCTACATGCTGCTTTTAGAAATTTG
AAGCGGCATATGGTGTTCCTTGCGGAGACGCGCTCAGGGGAACGCGATTCCGAAAG
ATGCCCTTTCCAGTCCCATATGCCCATCCCAAGATCATGCCCGGGAGAGCAAATGTCGCC
CCAGCCAGGTCGGACACATCTGTCAATTCGACCACTAAGTATTGTCAAAGCTAGGGTTAAT
TGAAGATAGCTCTACATGTTATTAGTAGAGTTTAAACGTTGAGATACTAGTGAACGTA
TACACAAGAGCGGATAAAAGATGTCTTTAGTTGTCCAAGAACAAGGTTCTTCCAACACA

TTTTACGGGTATGTTTATTATTACTAGTGAGCTATGACAAAATCGGCTAAAAACTTAAAAA
TATGACAGACAAGAAAGGAAATTCATTACCTCTTTAATCGTGGCGATTATTCGCTAACG
ACGTGATTAAATATAATAATGATGTTCCCGGGCTGGACTAAGAACGTAATAATAAGGCTG
ATGAACAAATTTATGGTATTATGCATCAAAAAGGAACATGAATTTGGCATAAGCGCACATA
ATTACGGAACATTGCAATAGCGGTCCGAGGTAAAGTACCGGGAATGCTTTACAATGAATC
AGCTATTGGCGGATATTGACCAACCAACTAAAATTTTATATCCTGCTCCGATTTTTGT
CTTGGCCGTGAAATCCATTATGCACATTTTTACTAACGTTTATCAATAAGTTCGGTTTC
CCGTCTAAATTTTTTACGCAGTTTGTGTAACACTAACGTTGACGGTAACATTAAGATCG
TTTACGCTTTTGACCACTATCAAGGGTGTGGTCGTCGTTACTCCAACCTGGTCTGTAAGA
AGGCTGATGTTGATTTACACAAGAGAGCTGGTGAATTGACCAAGAAGAATTGGAAAGAA
TTGTTCAAATTATGCAAAACCCAACCTACTACAAAATCCCAGCTTGGTTCTTGAACCGTC
AAAATGACATCACTGATGGTAAGGACTACCACACTTTGGCTAACAACGTCGAATCCAAAT
TGAGAGATGACTTGGAAAGATTAAAGAAAATCAGAGCTCATCGTGGTATCAGACACTTCT
GGGTTTTCGCTGTTAGAGGTCAACACACCAAGACCACTGGTAGAAGAAGAGCTTAA

YDR450W, 146 aa (SEQ ID NO 64)

MSLVVQEQQSFQHILRLNNTNVDGNIKIVYALTITIKGVGRRYSNLVCKKADVLDLHKRAGE
LTQEELERIVQIMQNPHTHYKIPAWFLNRQNDITDGKDYHTLANNVESKLRDLDLERLKKIR
AHRGIRHFWGLRVRGQHTKTTGRRRA

YDR486C, 1289 bp, CDS: 501-1289 (SEQ ID NO 65)

ACTGCATACACAATAACTGTAGATGTAGCCCAAGGCACTACCACAGGTATTTCTGCTCAC
GACAGGTCGATGACTTGTAGGGCTCTTGCAGACTCTTCTCTACGCCAAAATCATTTTTTA
AAACCAGGGCACATCTGTCCCTTGAGAGCCGCTGATGGCGGTGTTTTGCAGAGAAGAGGC
CACACTGAGGCGGTGTCGATTTGTGTAAACTAAGTGGACTAAGTCCCGTCGCTGTTATT
GGCGAATTGGTTAACGATGACGAACAAGGAACATGATGAGATTAAATGACTGCCAAGCG
TTTGGTAAGAAACATGGCATTCCTTTGATCTCCATCGAAGAATTGGCCCAATATTTGAAG
AAATAATCTGGTGAACATTTTCTCCATTCATCTATCACAACAGACTCACACATATATAC
ATGTATATATTTGTAACTTTGTATATATCTTTTGTTTTTTGACCTTTTTCTTCTCTATG
TTTTTTCAGCCATACAAAATATGGGATTTTTAGCAAGAGAAAAAGTACATCTAAAAAAG
TAGTAATAGGAGGAAGCCAAGATTGGTTGAAACACAGTTATAAACTCTTCAAGGCAATTA
TGAACAGGATTTTTCGGATATGGGAACAAAAAGAGCCATGATCAGCTCTTACAAGAGTCGA
ATCAGTCCATGAATCAGGCCCAACAATCACTATCGAACAGAATATCCCAGTTAGATACTC
AAATCGCCCAGTTAACTTCCAGCTGCAAAATATTCAAAAGAATTTGCAAAGATCAAACA
ACAAGCAACCCCTCGTTAAGAAAACAGGCTTTGAAGATTTTAAATAAACGTAACAGTTAG
AAAATATGAAGGATTTCTTTAGATTCTCAATCCTGGTCCATGACGCAAGCCCAATTAACAA
ATGATAACTTACAGAACACAATGATCACTATAAACCGCACTAAAGCAAACAAACAATGCCA
TGAAGGCTCAATACGGCAAGATAAATATCGACAACTACAGGACATGCAGGATGAGATGC
TGGATTTAATAGAACAAAGGGGATGAGCTGCAAGAAGTCTTGGCAATGAATAATAACAGTG
GCGAGCTCGACGACATTAGTGATGCAGAGCTGGATGCAGAGCTGGATGCTCTGGCACAAG
AGGATTTCACTTTGCCAACCAGCGAAAACCTATTAGGTAACGATATGCCAGTTACTTAC
TAGGTGCGAATGCGCCACCGGCTTTTATTGATGAAGAGCCAACTTAGATACTGAAGACA
AAAATAAAGCTTTAGAAAGCGCTCAGTGA

YDR486C, 262 aa (SEQ ID NO 66)

MGFLAREKVHLKKVIGGSQDWLKHSLFKAIMNRIFGYGNKKSHDQLLQESNQSMNQA
QQSLSNRISQLDTQIAQLNFQLQNIQKNLQRSNNKQPSLRKQALKILNKRKQLENMKDSL
DSQSWSMTQAQLTNDNLQNTMITINALKQTNAMKAQYKINIDKLQDMQDEMLDLIEQG
DELQEVLAMNNNSGELDDISDAELDAELDALAQEDFTLPTSENSLGNDMPYLLGANAPP
AFIDEENLDTEDKNKALESAQ

YDR471W, 1295 bp, exon1: 501-531, intron1: 532-915, exon2:
916-1295 (SEQ ID NO 67)

GGCAAATCAATTAAAATTCCTTTTCTCTCTACCTTTGCTAATATTAAAAACCATAGTTGT
AAAGGGTACTTAAATGCTATATTCCTGTTAAGTTTCCTATTTACCTTGTTTTTTCCAATT
CTTACCAATTTGAAGACTATGTTTTTAAACACCCAATCATTTTCCACCCACACATATATT
ACCCTTTTTTTGGGTGAAGAGAAGTAGTATTTGTTTTTTCATGGGAGTGGAAGTCCTTTTC
AAAATAATCCGAGCAGTAGTGCTGTCTAGCGGAGATTATTGAAAGTCGGCATTTGGCTG
CAGCTAGCGTTTTGTTTTTGGTACTACCTGTCAAACCCGGGCTCTGCCTAGATTGCGCGG
AGGGTACGTTGAAACTTTTTGCCTTTCCACGTCAGTTTATAATATCAAAGCAGCAATATA

CACATTTAATGGTTTGGCCCTTAGTGACTATTAGGGCGTTTTGGTGAAAAGAAAGAGTCGC
TCAAAGAAATCAATATAACCATGGCTAAATTTTTGAAAGCAGGTAAAGTTGGTACGTAAA
TTTAACAGAGCAAACGCTCTAATTAAGATATCGAATAAAAGGGGACTTTTCAGGTGCATAA
GATGGGAAATTTGTACAATCTGAGGGACAAACAATATGGAAAGCAGTACATGATTGTATTG
TCATTGTAGGAGGTACCAATTGTGCCAGTAAAAAGAGAGGGCCCCGGGAGCACCACATT
CACGACCAATCGTGTGATCTGCAAAAAGGCACATGGAAAATGTAATTTATCAGTGTTT
AACACTGAGTTGAACAGATAGCTATCTAATCAATGTAACTTTCCAGGGAACAAAAAGCT
AAATCCACTTCTCTTTTATTTCAAAATATCATTAGAAATAGAAAAATTTACTAACAATTT
TTCGTATTATCGTAGCTGTGCTGTTGTCGTGGTTCGTACGCTGGTAAGAAGGTTGTGATCG
TTAAGCCACACGATGAGGGTTCTAAATCTCATCCATTTCGGTCACGCTTTGGTTGCCGGTA
TTGAAAGGTACCCATCAAAGGTCACCAAGAAGCACGGTGCCAAGAAGGTCGCTAAGAGAA
CTAAATCAAGCCATTCACTCAAAGTCGTCAACTACAACCACTTATTGCCAACAGATACA
CCTTGGATGTTGAAGCTTTCAAGAGCGTTGTATCTACAGAGACTTTTGAACAACCATCCC
AACGTGAAGAAGCCAAGAAGGTTGTAAAGAAGGCATTTGAAGAAAGACATCAAGCTGGTA
AAAACCAATGGTTCTTCTCCAAGTTGAGATTCTAA

YDR471W, 136 aa (SEQ ID NO 68)

MAKFLKAGKVAVVVRGRYAGKKVVIVKPHDEGSKSHPFHGHALVAGIERYPKSVTKKHGAK
KVAKRTRIKPFIKVVNYNHLLPTRYTLDEAFKSVVSTETFEQPSQREEAKKVVKAFEE
RHQAGKNQWFFSKLRF

YDR499W, 2744 bp, CDS: 501-2744 (SEQ ID NO 69)

TAACAATAGAAAAAATACACACACATTAGATTGGAATTAGAGCTTAAGTGGTACAACT
AGGGCTAATAAAGAGGTAACGGTCGGTTCTCTACTAAGGTTTCGTATTGTGTGGCACC
GATTAAAGCACTTTTAAGCGGAATAACTCGAGTGGAATTTTATGTTTATGTTTACCT
TTGAATTTTAAAAAAGAGTCAGACAGGCTCGCTCTTCTCTACTAAATATTAGG
AGCAAAGCAGTAAAAAGTCTCTGAATAAGGATAGTAACCTGTAGTAACCTCAAAATTTAT
CTTACAAAGAGCTATTAGTATCTTGGTTCTTCTATTTCTTCGATTATTGGTGATTTTTC
CCGCTCTAGCCAAATCCGAGCGTTCCATCGATTTTGGGGAAAAACAGCACATGCAATA
AAATAAAAAGCAAAACAAATACGCGATAGTGCACGAAACGTCAACACAATCATCAAATCT
TTTGCAATTTTCTATTATAGATGAGACGAGAAACGGTGGGTGAATTTTCTTCAGATGACG
ATGATGATATTTCTTTTGGAAATTAGGCACCAGGCCTCCAAGGTTTACTCAAATACCGCCAT
CATCAGCAGCATTACAAACACAAATCCCCTACTTTGGAGGTTACAACGACCACATTAA
ACAATAAACAGAGTAAAAATGATAACCAACTGGTTAACCAACTGAATAAAGCTCAAGGTG
AAGCAAGCATGCTTCGTGATAAAATAAACTTTTGAACATTGAAAGGGAAAAAGGAAAAAGA
ATATTCAAGCCGTCAAAGTTAATGAATTGCAAGTCAAGCATCTTCAAGAGTTGGCTAAAT
TAAAACAAGAATTACAGAACTGGAAGATGAGAAGAAGTTCTTACAGATGGAAGCGAGAG
GAAAATCGAAAAGGGAAGTTATTACGAATGTAAACCACCGTCAACAACATTATCAACAA
ACACAAACACTATAACGCCAGATTTCGTCTCAGTTGCAATCGAAGCAAAACCTCAATCAC
CAATCAAAAAACGTAAGATAAGTGATAATTTACTGAAAAAATATGGTTCCCTTAA
ACCCAATAGGATTATTCCCGATGAAACGAGTTTATTTCTAGAGTCAATATTACTTTCATC
AAATAATAGGCGCTGACCTGAGCACAATAGAAAATATTAAATAGATTGAAGCTTGACTACA
TCACAGAGTTTAAATTTAAGAAATTCGTCAATTGCTAAAGGAGCCCCCATAGGGAAGTCCA
TAGTTTCTCTACTTTTGCGATGTAAAAAGACGTTGACCCTCGACAGGTTTCATAGATACTT
TGCTAGAGGATATAGCTGTTTGTATCAAGGAAATATCAGTTTCATCCAAATGAATCGAAAT
TAGCTGTCCCATTTCCTGTTGATGATGTATCAGATTGTACAATTTTCGTCTAGTGCCA
CTCATAATTTAGCACTGAAGGATTGTTTCTTTTATTTGCGATTTAATAAGAATCTATC
ATCATGTATTGAAAGTACCGATACATGAATCAAATATGAATTTGCATGTAGAACCTCAGA
TTTTCCAATATGAACTGATAGACTATTTGATAATTTTCGTATTCTTTGATCTCCTAGAAG
GTATATTAAGGGTACTGCAGTCGCATCCTAAGCAAACTTATATGGAATTTTTTGATGAAA
ATATTCTAAATCATTTGAATTTGTCTACAACTAGCACTAACCATTTTCATACAAGCCAA
TGGTAAATGTAATATTAGTGCAGTCGAGGTCGTTAATATTATCACTAGTATAATATTAA
ATATGGACAATTCCTCAGATCTGAAATCCTTGATAAGCGGTAGTTGGTGGAGAGATTGTA
TTACAAGATTATACGCTCTTTTGGAAAAGGAAATTAAGAGTGGCGACGTATATAATGAAA
ATGTGGATACTACAACCTTCATATGTGCAAGTACCATGACTTTTTTGGGTTAATCCGAA
ATATAGGTGATAATGAATTTGGGAGGATTGATATCAAAGCTGATTTATACTGACCGATTGC
AAAGTGTCCTCAAGGTAATTTCTAAAGAGGATATTGGGATGGATAGCGACAAATTCCTG
CCCCATAATAGGTTACAAGATGGAATAATGGCTTTTGAAGTTAAAGATGAAGTTTAA
ATATTTTGAATAATTTATTAATGATCTATGGAGACGATGCGACCATAGTAAATGGAGAAA
TGCTCATCCACTCCTCTAAATCTTATCCAGGGAGCAAGCGTTAATGATAGAAAGGTACG

TGGGACAAGACTCCCCGAACTTGGACCTCAGATGCCATCTTATTGAACATACTTTAACCA
TAATATATAGGCTATGGAAAGACCATTTCAAACAATTGCGTGAAGAACAATCAAGCAGG
TAGAAAAGCCAATTGATTATGTCACTATGGAGGTTTCTCGTATGCCAAACCGAAACTGTGA
CAGCAAACGAAAGAGAAATGAGAGATCATCGACACCTTGTAGATAGTTTGCATGATCTGA
CGATAAAGGATCAAGCCTCTTATTACGAAGATGCCTTTGAGGATTTACCAGAATATATCG
AAGAAGAAATTGAAGATGCAATTGAATAAAAGAACGGGGAGAATAATGCAAGTAAAGTACG
ATGAGAAATTTCAAGAAATGGCAAGAACTATTCTTGAGTCAAAATCATTTCGATCTAACCA
CACTAGAGGAGGCCGATTTCATTATATATCTCAATGGGACTGTAA

YDR499W, 747 aa (SEQ ID NO 70)

MRRETVGEFSSDDDDILLELGTRPPRFTQIPSSAALQTQIPTTLEVTTTTLNNKQSKN
DNQLVNQNLNKAQGEASMLRDKINFLNIEREKEKNIQAVKVNELQVKHLQELAKLKQELQK
LEDEKKFLQMEARGKSKREVITNVKPPSTTLSTNTNTITPDSSSVAIEAKPQSPQSKKRK
ISDNLKKNMVPLNPNRIIPDETSLFLESILLHQIIGADLSTIEILNRLKLDYITEFKFK
NFVIAKGAPIGKSIIVSLLLRCCKTLTLDRFIDTLLEDIAVLIKEISVHPNESKLAVPFLV
ALMYQIVQFRPSATHNLALKDCFLFICDLIRIYHHVLKVPIHESNMNLHVEPQIFQYELI
DYLIISYSFDLLEGILRVLQSHPKQTYMEFFDENILKSFEFVYKLALTI SYKPMVNVI FS
AVEVVNIITSII LNMNSSLKSLISGSWWRDCITRLYALLEKEIKSGDVYNENVDT'TTL
HMSKYHDFGLIRNIGDNELGGLISKLIYTDRLQSVPRVISKEDIGMDSDKFTAPIIGYK
MEKWLKLDKDEVLNIFENLLMIYGDATIVNGEMLIHSSKFLSREQALMIERYVGQDSPN
LDLRCHLIEHTLTIIYRLWKDHFQKQLRREEQIKQVESQLIMSLWRFLVCQTETVTANEREM
RDHRHLVDSLHDLTIKDQASYEDAFEDLPEYIEEELKMQLNKRTGRIMQVKYDEKFQEM
ARTILES KSFDLTTLEADSLYISMGL

YDR507C, 3929 bp, CDS: 501-3929 (SEQ ID NO 71)

CTCTTTTAAATATTCCTATGTACTTTGTGCAAAACATCATTGTCAACATAAATGCATTCCCT
ACTATTACTAACTTGAACCTCACTTCACTGGAAGAACTGGGTTATTCAAGGTAAAGAAAT
CATTGTGTTTTGCGCCAAGTTTCGTCTGACAAGAATTTTTTATTATTATTTCCCACTTTTC
ATCGAAGGAAACGCGTCAAATCCATTCTGTTACTACGCGCAATCTGCGTTATTTCTTTT
CGGCATACCATCGCGAAATATCAACGGCCACACCATAGATTCTTTTGATGTTAAATTAA
AAGCGACTLGAATGAAGTGCACACATTTTATTATTCTTCTTGATTCTTTCTTTCTATTGTG
TTTGCTTTCTCTTCTGTCGACAACGCTCTCAACTGTACTCACCATTAGTATTCTCGAAGGC
TTTAGCAGACTTGTGAATAATTAATTGCCACTTTGATCAAGAAAGATATTTCGCAGCACA
ATACAATAATAACATTCAAAATGGCAATCAATGGTAACAGTATTCTTGCATAAAGGATA
ATACCATCGGTCCATGGAACTAGGTGAAACTCTCGGTCTAGGGAGCACTGGTAAAGTCC
AGCTTGTCTCGTAAATGGATCCACAGGACAAGAGGCGGCAGTTAAGGTAATATCAAAAGCAG
TATTCAATACCGGTAATGTCAGCGGTACTTCGATTGTTGGCTCCACCACCCAGATGCTC
TACCATATGGTATAGAACGCGAAATAATCATTATGAAGTTGTTAAACCACCCAAATGTGT
TACGTTTTATATGATGTCTGGGAAACAAATACAGATTTATACCTTGTTTTAGAAATACGCGG
AGAAAGGTGAGTTGTTCAACTTATTGGTTGAGAGAGGTCTCTGCCAGAGCATGAAGCTA
TCAGGTTTTTTAGACAAATTATTATTGGTGTGTCGACTGTCTATGCGTTGGGTATTGTCC
ATCGTGATCTAAAACCGGAAAATCTATTATTAGATCATAAATATAACATCAAGATTGCAG
ATTTTGGTATGGCTGCTTTGGAACTGAAGGAAAGCTACTGGAGACGTCGTGCGGATCAC
CACATTATGCTGCACCAGAAATTGTATCTGGTATACCGTATCAAGGTTTCGCAAGTGATG
TGTGGTCAATCGGTGTGATCCTATTTCGCCCTTCTTACTGGTGGTTACCCTTTGACGAGG
AAGATGGAAATATAAGAACACTATTACTTAAAGTTCAAAAAGGTGAGTTCGAAATGCCTT
CTGATGATGAAAATTTTCGCGTGAAGCTCAGGATTTGATTAGAAAAATCTTAACCGTTGATC
CTGAAAGAAGAAATCAAGACCAGAGATATACTCAAACATCCGCTATTACAAAAATATCCAA
GTATAAGAGATTCTAAAAGTATTAGAGGCTTACCAAGAGAAGACACATATCTCACGCCAT
TATCAGAAAGTAATTCCTTCTATTGACGCTACGATTTTGCAAAATTTAGTAATATTATGGC
ATGGAAGAGATCCTGAAGGAATTAAGGAAAACTAAGAGAACCTGGCGCTAATGCAGAAA
AGACATTATATGCACTACTGTATAGATTTAAGTGTGACACTCAAAAAGAGCTTTATTAAGC
AACAGCAAGTTAAGAAGAGGAGTCAATTAGTAGCGTTTCTGTTTCCCATCTAAAAAG
TATCGACAACCTCCACAACGCAGAGAAATAGAGAATCTTTAATTAGTGTAACATCTTCTC
GTAAAAAGCCAATATCCTTCAACAAATTCAGTGCCTCCAGTGCCTCCTCCAGCAATCTAA
CTACACCCGGTTCTTCAAAACGCCCTTCAAAAACTTCTCTTCAAGAAGAAATTATCTA
CAATCGTTAACCAATCTTCTCCAACACCAGCATCACGTAATAAAAGAGCTTCGGTTATAA
ATGTGGAAAAGAAATCAAAAAAGAGCCTCTATCTTTTCTACTACCAAGAAGAACAAGAGAT
CTTCTAGATCTATCAAGAGAATGTCAATTGATACCAAGCATGAAACGTGAATCGGTGACAA
CAAAATTAATGTCAACATATGCGAAATGGCAGAGGATGACGATTGGGAATACATTGAGA

AGGAAACAAAGAGAACGAGCTCAAATTTTGCAACTTTGATAGATGAAATTTTTGAGTACG
AAAAGTACGAACAAATAAGGAAAGAGAAGGAAGAGCTAGAACGTAAAGTGAGAGAAGCAA
AAGCACGTGAAGAGCTGGAACGTAGAAGACGTAAACAAGAAGAAAAAGAACGTGCAAGAA
AATTACTAGAAAAGGAAGATCTGAAAAAGAAAACAGGAGGAAGCTCAAGAAGCAAATTGAAA
TTGATATAAGTGATCTAGAGCAAGAGCTGTCCAAACACAAAGAGGAAAAACTGGATGGTA
ATATTAGATCTATCTCTGCTCCTATGGAAAATGAAGAGAAAAATATCAATCATTTGGAGG
TTGATATTGACAATATTCTCCGTCGCCGCAACTTTTCTTTACAACTAGACCTGTGTCAA

GGCTTGATCCGGGTATAATGTTCTCCAGTCCAAGTGAAGTAAGTCCAGTGGAAACCAA
AGAGAACAGAAAATGAAAGACTTACAACAGAAAAGAAAAATTTAGAACTATCAGAAGAT
CAAAATTCCTTGGGTTCATCATTTAATATCGATAAAGAGTTGAAATTGTCTAAAATGGAAT
ATCCAAGTATAAATTGCACCACAAAGATTGTGAGAGGAGCGAGTGGTGTGAGATTCTAATG
ATGGATATGAATCTTTGATCCTCCCGAAGGATGGGAATGGCGTATCTCAATTAAAGGATA
GTACCGCAACAACTGCTCCCGTCTCTGATGGTAGGTTGAGGAAGATCTCTGAAATTAGAG
TACCACAATTTTACTAGAAAATCAAGGCATTTTAGTGAGTCCAATAAAAGGCTATCTGTCC
TGTCGATGTACTCTACCAAGGAGTCGTTTACCAACTGGTTGATATTTGAAAAACGGTA
ACCTTGATGTCAATAACCAACAAAGCCAAAGAATTCCAACACCAAGAAGTGGCGATGATT
CAGAAATTTCTTTTTGAACTGTCAACGAAGAAGCTGAATATACAGGAAATAGTTCTGAACG
ATGAGAGATTGTACGATGTCGGTGATTCCACTATCAAAGACAAATCCGCGTTAAAGCTGA
ACTTTGCGAGATCGTTTAAATGGATCGAACGAAGCGAAACAACTGATAACTTACATCTTTC
CGATCCTTCCCTCCGCTTAAATGGTGACAATGAATTGCGTAAACAGAATAGCCAAGAGGGTG
ACCAGGCACATCCAAAGATTAAATCGATGATACCAGAATCAGGCTCTTCTTCACATACTG
AAAAGGAAGAAGAAAAATGAGGAAAAGGAAGAGAAAAAGCCAGAACAACACAAACAAGAAG
AGGATCAAGAAAAAAGAGAGAAAGTAGTAGATGATATGGAGCCACCATTGAACAAATCTG
TGCAAAAAATTAGGGAATAAATGCTGGCTCGCAGGCAAAGGATCATTCAAAGATCACT
TAAAAGAGCATAAAGCAGGATAAAAATACAGCAATTGGAAATGGTTCTTCTTTAGAAAAAT
TCTCAAAATCTTCGGACAAAACAATGGAATTGTATGCCAAGATTTCTGCAAAACAATTGT
TTAATGGTTTAGAGAAGCTGTTGCGTGGTTGGACTCAGTATGGTTTAAAAAATATAAAAT
CGCACCCCAACAATCTGACCTTAACGGGTAAACTATCGAGTGATAATATATTCTCACTAC
GTTCAACACTCTTTGAGGTTAATATTTATCCGAGAGGTAAGATGAGCGTTGTGCAGTTCA
AGAAAGTTTCTGGTTCAATTCAAAGCTGTCAAAAAGTTGGTCAATGAAGTTGAGAACGTCC
TGAATAAGGAAGGCGTTCTACAAAAATAG

YDR507C, 1142 aa (SEQ ID NO 72)

MAINGNSIPAICKDNTIGPWKLGETLGLGSTGKVLARNSTGQEAQVAVKVISKAVFNTGNV
SGTSIVGSTTPDALPYGIEREIIIMKLLNHPNVLRLYDVWETNTDLYLVLEYAEKGELFN
LLVERGPLPEHEAIRFFRQIIIGVSYCHALGIVHRDLKPENLLLDHKYNIKIADFGMAAL
ETEGKLLTSCGSPHYAAPEIVSGIPYQGFASDVWSCGVILFALLTGRLPFDEEDGNIRT
LLLKVQKGEFEMPSDDEISREAQDLIRKILTVDPERRIKTRDILKHPLLQKYPISIRDSKS
IRGLPREDTYLTPLSESNSSIDATILQNLVILWHGRDPEGIKEKLREPANAETLYALL
YRFKCDTQKELIKQQQVKKRQSISSSVSPSKKVSTTPQRRRNRESLISVTSSRKKPISF
NKFTASSASSNLTPGSSKRLSKNFSKKKLSTIVNQSSPTPASRNKRASVINVEKNQK
RASIFSTTKNKRSSRSIKRMSLIPSMKRESVTTKLMSTYAKLAEDDDWEYIEKETKRTS
SNFATLIDEIFEYEKYEQIRKEKEELERKVREAKAREELERRRRKQEEKERARKLLEKED
LKRKQEELKKQIEIDISDLEQELSKHKEEKLDGNIRSISAPMENEKNINHLEVDIDNIL
RRNFSLQTRPVSRLDPGIMFSSPTEEVSPVEPKRTENERLTTEKKILETIRRSKFLGSS
FNIDKELKLSKMEYPSIIAPQRLSEERVVSDSNDGYESLILPKDGNVSQLKDSATTAP
VSDGRLRKISEIRVPQFTRKSRHFSSESNKRLSVLSMYSTKESFTNLVDILKNGNLDVNNQ
QSQRIPTPRSADDSEFLFETVNEEAETGNSSNDERLYDVGDSTIKDSALKLNFAFRFN
GSNEAKQTDNLHLPILPPLNGDNELRKQNSQEGDQAHPKIKSMIPESGSSSHTEKEEENE
EKEKKPEQHKQEDQEKREKVDDMEPPLNKSQKIREKNAGSQAKDHSKDHLKEHKQD
KNTAIGNSSFFRKFSKSSDKTMELYAKISAKQLFNGLKLLRGWTQYGLKNIKSHPNLTL
LTGKLSSDNIFSLRSTLFEVNIYPRGKMSVVQFKKVSFSKAVKKLVNEVENVLNKEGVL
QK

YDR515W, 1844 bp, CDS: 501-1844 (SEQ ID NO 73)

GAGTTGAATCTATGCGTAACCATTTTGACTACCGCTTCGTATGCTTTCTTGCACTTTGTG
GAGCTACTATACATAAGCTTATAATCTGTGTAGTCAAATATATACTAGGCAAATTACT
AGTAAATGCAGTATTCATATGTCTCAAAACCGTTTTTTGCACTATGTTATTGATCCATCG
AATCAAAATTTTTACCGCCAAGAGAAAAAAGATCTTACTATTTTGTGCTTATGAAAAAA

TTAGTAAAAGTAAAGCTGGAAGCACATACAAGCGCAGCTGAATCACAAAGGAAAATTGGC
ACATCCTTGGTTGACACTTGCTATTTATTTAAAAGGTTTAAAAAGTAGTGTTTCAGCAGT
TCTATCATATTTTTTTATTTAAAAAAAATACTGAGAGGAAGCGTATTGTTAAGACACAA
TTTAGGGTGGCGTTAAATAAACGAGAGAGCCCCAAAAATATAACCAAGATAAAGAAAAATCA
ATCATAAAGTGAATTCAAAAATGTCATCGCAAAACCTCAATGATAATCCAAAAATACAT
CCTCAGCAGCTGAAGATAAGAAGAAACAACTTCATCCTTAAAGTTGGCACCAATACCAA

CCACATCGCCATGGAAATCATCTTCGCCAGATAGCAATACAGTAATTCCTGTAGAGGAAC
TAAGAGATATATCAAAGACTGCAAAGCCAAGTAAAAATGGTTCGGGGTCAATTAATTA
CAAGCAATACCAAATGGACTCCAATTACGCCGTCTGTTATAATCTCAGGTTCCAAGGACA
CAAATTCAAAGTCAGGAAAGAACTCTAAAAATTCTAAGACTAATAAAAAAATGAAAAAGC
GTGGCAAATATAATAACGATATCAATAAAAAGGACTTTAACGGTCAAACCAACAGTACAT
CGGAAATAAGTAACGTTTCCAATCTTGAATCCAAACCTTTAGATGCTAACGCTAAAGTAA
ACATACATTCAAGCTCAGGAGCAACTGCCAATGGGAATATAAAGAGGATAACAACAACA
ACAATTCAACCAACCGGTAGACAAATCAAGAAATTATCAAAAACAGGAATGGCAAAACAAGAT
ACAACAACAATAGTAGACACAGTCAGGCGGCTAATAATGCCATCTCCTTCCCAAAATTA
ATCAGGCTAGACCTGAATATATTCCCAATGCCAGCCACTGGTTGAACAACAATTCAGAA
ATAGCTATAAACAACCTGTCATACTTCCGTCAACAGCAGTATTATAATAACATCAACTATC
AACAACAATTCGAAAACACCATATTTACTCAATGGAACCTATTTTTAAATCTATCGAAA
GTATCAAAAACCAAATGAATTCATTTTAGTGAAGAGAATTTGAAAACAGATGAATTTT
TAAGATCTAAATTCAAAAAAGCCAAATGACGGATTATCCCCATGAGTTTGATAGGAAAT
TTTACCGTATGGTTAATTTATCTCTTGGTGGAGACCCAAATTTAATTTTGGCATCTATGA
GAGAAGTTTTACAACATAAAGAAACAAACCATTGGAATTTGCCCTTGAAGCATAGAAG
GTGCTCAGAAGAACATGGCAGATGATTTCAATCCATTGGAAAACCTATTTTATTAGGCGCG
AAAATTGGGCTGAATACGCTATGGAAAGTAATTTTGATGAAAATGATGACGAAACTGAAA
AATACAACATTGAGAAACTATTGGGACCGAAGATTAGACAATTATTCTTATATGGGCT
ATCCAAACTTCTTTCCCAAGTAATGAAAATGGGAAAAAGAGTCAGAGCTATGACCAAGGTG
AAATTAGCAGGCAGTTTGAACAAAACCTTACAAATAAATGATTAA

YDR515W, 447 aa (SEQ ID NO 74)

MSSQNLNDNPKNTSSAEDKKKQTSLSKLAPIPTSPWKSSSPDSNTVIPVEELRDISKT
AKPSKNGSGSIKLTSTNKWTPITPSVIIISGSKDTNSKSGKNSKNSKTNKKMKRGRKYNNND
INKKDFNGQTNSTSEISNVSNLESKPLDANAKVNIHSSSGATANGNIKRITNNNNSTNGR
QSRNYQNRNGKTRYNNNSRHSQAANNALSFNNYQARPEYIPNASHWLNNNSRNSYKQLS
YFRQQQYYNNINYQQQLQTPYYYSMEPIFKSIESIKNQIEFYFSEENLKTDEFLLRSKFKK
ANDGFIPMSLIGKFYRMVNLISLGGDPNLILASMREVLQHKETNHLEIALGSIEGAQKNMA
DDFNPLENYFIRRENWAEYAMESNFDENDDETEKYNIEKLLGPNLDLNYSYMGPYNFFPS
NENGKKSQSYDQGEISRQFEQNLQIND

YDR518W, 2054 bp, CDS: 501-2054 (SEQ ID NO 75)

GCAGCAGGGGCAAGATGACAACCCTGTTCTGTTCTGTTCCAGTAGAATCTGAGACGGC
TTTTGTGCCATCAGCAATTCACAGCACCAGCGTGCCAACAAAGAAGAAATCAAAAAATA
AAAGGGTACCCAGCCATTGGCAATGGATGACTATTTTAATGAAGGCAGAGATAAGTCATC
TACCGCTGCGAAGTCAGCAGAATCTGACATCCTCGCCCCACCACCACAAAAACAGTCATC
CTCTGATTAACTTTCTCGTTAGTCTTTTGGTTTGTGTTTCATAGCAAAATTAAATATATA
TATATAAGCTTGCTTTCCCTTCAAAACACGTAAACGATAGTTGGCAATGTACGAAAAGTA
CCGAGACTTTTTTTCAAAGGCACGCGTGTCTTTTTTGTGTTAAGACAATAGATATTTTAGC
ATTGAGAAAGTTTCAATTTCCAAGACTTGACGTTTCAATTATATGGCAATCTCCCAACAA
GCACCCGCTCATATAATACCATGCAAGTGACCACAAGATTTATATCTGCGATAGTCTCGT
TTTGCCCTGTTGCTTCTTTACGTTGGCTGAAAACAGCGCAAGAGCTACGCCGGGATCAG
ATTTACTCGTTCTAACAGAGAAGAAATTTAAATCATTTCATCGAATCTCATCCGTTAGTCC
TCGTCGAGTTTTTGTCTCCATGGTGTGTTGCATTCTCAGATCTTACGCCCTCACTGAGAAG
AGGCGCCTCTATTTTAAAGGAGCATAAACGTCCCAGTTGTTCAAATTGATTGTAGGCTA
ACAGTATGGTTTGCCTGCAACAAACTATAAATACCTACCCAACCTTGAAAATCTTTAAAA
ATGGTCGTATTTTTGATGGTCAAGTCTATCGCGGTGTCAAGATCACCGATGAAATCACTC
AGTACATGATTACGCTATACGAGGCTTCTGTCAATTTATTTAAATTCGAAGATGAAATCC
AACCATACTTGGAAAATGCAACTTTACCAGTAGTAATAAACAGAGGCTTGACAGGCTTGA
ATGAAACGTATCAAGAAGTCGCACTGGACCTTGCTGAGGATTACGTCTTTTTATCCCTTC
TAGATTACAGAAGATAAGTCATTTATCAATCCACTTGCCAAACACTACAGAACCAATCTGT
TTGATGGAAATGTAGACTCTTTGGTCGGAAATTCGTTGCTCTAACTCAGTGGTTAAAAAG

TGGTAATTTTACCTTACTTTACCGACATCGAACCTGATCTCTTCCCCAAGTACATTTCTA
GCAATTTGCCGTTGGCTTACTTCTTTTATACTTCTGAGGAAGAATTGGAAGATTACACTG
ATCTTTTACGCAGTTAGGTAAGGAAAATCGTGGCCAAATAAATTTTCATTGCATTAACT
CTACAATGTTCCACACCCGTTAGATTCTTAAATATGAGAGAACAGTTCCCATTATTTG
CTATCCATAATATGATCAATAATCTGAAATATGGTTTACCACAACCTACCAGAAGAAGAGT
ACGCGAAATTAGAAAAACCACAACCACTAGACAGAGATATGATCGTTTCAGTTGGTAAAAG
ATTACCGTGAAGGTACTGCCAAGCCAATTGTTAAGTCAGAAGAGATTCCAAAAGAACAAA
AGTCCAATGTTTATAAAATAGTTGGGAAGACACATGACGACATTGTTTCATGATGATGACA
AGGATGTCTTGTCAAATATTACGCGACATGGTGTATTTCATAGTAAAAGGTTTGCGCCCTA
TTTACGAAGAAATTGCAAATGTCTTAGCATCTGATGAATCTGTTTCGCGATAAAATCTTGA
TCGCCGAAGTAGATTTCAGGGGCAAATGATATCTTAAGTTTTCTGTGACAGGATATCCAA
CCATTGCTTTGTATCCTGCCGAAATAACTCTAAGCCTATTATCTTCAATAAAATTAGAA
ATTTGGAAGATGTTTTCGAATTTATCAAGGAATCAGGTACACATCACATTGACGGCCAGG
CAATTTATGATAAATTGCACCAGGCCAAGGATTCTGAAGTGTCTACTGAAGATACCGTAC
ATGATGAATTATAA

YDR518W, 517 aa (SEQ ID NO 76)

MQVTRFISAIVSFCLFASFSLAENSARATPGSDLLVLTEKKFKSFIESHPLVLVEFFAP
WCLHSQILRPHLEEAASILKEHNPVVQIDCEANSMVCLQQTINTYPTLKIFKNGRIFDG
QVYRGVITDEITQYMIQLYEASVIYLNSEDEIQPYLENATLPVVINRGLTGLNVIQEV
ALDLAEDYVFLSLDSEDKSLSIHLNPTTEPILFDGNVDSL VGNSVALTQWLKVILPYF
TDIEPDLFPKYISSNLPLAYFFYTSEELEDYTDLFTQLGKENRGQINFIALNSTMFPHH
VRFLNMRQFPLFAIHNMINNLKYGLPQLPEEEYAKLEKQPQLDRDMIVQLVKDYREGTA
KPIVKSEEIPKEQKSNVYKIVGKTHDDIVHDDDKDVLVKYATWCIHSKRFAPIYEEIAN
VLASDESVRDKILIAEVDSGANDILSFPVTGYPTIALYPAGNNKPIIFNKIRNLEDVFE
FIKESGTHHIDGQAIYDKLHQAKDSEVSTEDTVHDEL

YDR519W, 908 bp, CDS: 501-908 (SEQ ID NO 77)

GGGGCAAATGATATCTTAAGTTTCTGTGACAGGATATCCAACCATGCTTTGTATCCT
GCCGGAATAACTCTAAGCCTATTATCTTCAATAAAATTAGAAATTTGGAAGATGTTTTTC
GAATTTATCAAGGAATCAGGTACACATCATTGACGGCCAGGCAATTTATGATAAATTG
CACCAGGCCAAGGATTCTGAAGTGTCTACTGAAGATACCGTACATGATGAATTATAATCA
ATAAATAAAGCATATATAATGCACATTTTAAACATCTGATTACTCGCATCGTTTCTGGAA
GAAAAATAGCTAATATTCTGTTATTTATGGCATCACGATTATTCTCACCAGTTACCCGTTTA
TGCTCTTGAAGAGATTAGCATTACTGCCAGCGCATCTTCAAATACAGGTTTATATGAGA
CCCATTACTATAACCCTAAGAAGAGAAAAAGGAGTGCCTTTCGTTTTCAATCACATTCTAG
TTTACAGTAATTGAGTCTCGATGATGTTTAATATTTACCTTTTCGTCACTTTTTTTTCCA
CCATTCTTGCAGGTTCCCTGTCAGATTTGGAAATCGGTATTATCAAGAGAATACCGGTAG
AAGATTGCTTTAATTAAGGCAATGCCAGGTGATAAAGTTAAGGTTTCATTATACAGGATCTT
TATTAGAAATCGGGAACGTGATTTGACTCAAGTTATTCAAGAGGCTCTCCTATCGCTTTTG
AACTTGGCGTTGGCAGAGTAATTAAGGTTGGGATCAAGGTGTTGCCGGCATGTGCGTTG
GCGAAAAAAGAAAGCTGCAAATTTCAAAGTTCTTTGGCCTACGGAGAAAGAGGTGTCCAG
GCGTCATTCTCCAAGTGCTGATTTGGTGTGTTGATGTGCAATTGGTAGACGTGAAATCAG
CCGCCTAG

YDR519W, 136 aa (SEQ ID NO 78)

MMFNIYLFVTFSTILAGSLSDLEIGIIKRIPVEDCLIKAMPDGVKVKVHYTGSLLSESTV
FDSSYSRGSPIAFELGVGRVIKWDQGVAGMCVGEKRKLQIPSSLAYGERGVPVGPVPPSA
DLVDFDELVDVKSAA

YER102W, 1103 bp, CDS: 501-1103 (SEQ ID NO 79)

CGAGCTTGCCAGCATTCCAATGCCCATCGTATTGTACTCAATGGTGAAACTTACCACCAT
ATTGTTAAAAGCTATTATTATGATTTTACTTACCAAACATTGAAAGGAGACTGAACAC
ACCACGATAAAACGTATGTTCTGATACCCAGCAAATGAGAAAGTAGAAGGAGAAACCTAA
AAACCTGTGGCGGTCAAGACTGCTAGCAAGATGGATATTTAGATCATAAATCTAACGCA
TGCACTCTGAGCAATGAAATCATGCAACCTAACATTTGAGGTTAATATATGAGAATTAAC
TAGCGTTGAGGAGGTACTGCAATTTAAAAGACCGAAGAATTATCGATGCAAGGAAAAATG
GGTCTTAGGATGAATACGAGCAATTGAAATACATTTGGAATACCTTGTGAAAAATACACAT
ACTTTCGCCCTTCTATCTCGATGCGTTATTACAAGAAAAATAGTTTTACTAACAAATTAACA
AAAAATAAAATAGTGTAATAAATGGGTATTTCTCGTGATTCTCGTCACAAAAGATCAGCCA

CTGGTGCATAACGTGCTCAATTCAGAAAGAAGAGAAAGTTTCAATTAGGTCGTCAACCAG
CCAACACAAAAATTGGTGCTAAGAGAATCCACTCTGTGAGAACTAGAGGTGGTAACAAGA
AATACAGAGCTCTAAGAATTGAAACCGGTAACCTTTCTTGGGCTTCTGAAGGTATCTCCA
AGAAGACCAGAAATTGCTGGTGTGTTTACCATCCATCCAACAATGAATTGGTTAGAATA
ACACTTTGACCAAGGCTGCCATTGTCCAAATTGATGCTACTCCATTGAGACAATGGTTTCG
AAGTCTACTACGGTCAAACCTTGGGTAAGAAGAAGAACGTCAAGGAAGAAGAACTGTTG
CCAAGAGCAAGAACGCTGAAAGAAAGTGGGCTGCTAGAGCTGCTTCTGCCAAGATCGAAT
CTTCCGTTGAATCTCAATTCAGCGCCGGTAGATTATACGCTTGTATCTCTTCCAGACCAG
GTCAATCCGGTAGATGTGATGGTTACATCTTGAAGGTGAAGAATTAGCTTTCTACCTAA
GAAGATTGACTGCTAAGAAATAG

YER102W, 200 aa (SEQ ID NO 80)

MGISRDSRHKRSATGAKRAQFRKKRKFFELGRQPANTKIGAKRIHSVTRGGNKKYRALRI
ETGNFSWASEGISKKTRTAGVYHPSNNELVRTNTLTAAIVQIDATPFRQWFEAHYGT
LGKKKNVKEETVAKSKNAERKWAARAASAKIESSVESQFSAGRLYACISSRPGQSGRCD
GYILEGEELAFYLRRLTAKK

YER153C, 1265 bp, CDS: 501-1265 (SEQ ID NO 81)

ACCTATATGGGAGGACAACCTCGCCCACTGTTTGGGTCGTGTTAGCGATAAGGTCCGAAG
TAGAAGCGGAAAGAGAAGAGCTGAAGAGGTTAATTCATCGATGGAAGGCAACTGGGTTT
GGATTTCCGAGACATCGTTGGCATTGTTGGGCCGCTCGAATTAAATCTTTTGGCCTGAAAAG
AGATCCATGACGGATGGGCGCGGGCAATACTATGGTTCGAGCGGTGGCCAGTCTGGAAG
AGGCAGCAAACCTTGACGTGACGAGTCGAGAGGTGAGTTTGAACATCGTCGGGGAGGTTA
TTCTGTGGCTCCGCTTGTACGTGAACAGATACGTATAGAGGGCGAGCCACTGGTTAAATT
TTTCATGGCTCGGATTACTTCCGTACTGCTGGCTAAAATCGAAATCTCGGCCTGCTGAGA
GTGTTTTGAGCAATCAAGGGAACATCTGAACGTGGAAGAGCAGACGAGGCATTAGCTCGA
ACATAAGAACGGAACACGTCATGTTGACTATCACGAAAAGACTGGTGACCACCGATGTGC
GGTCGCGAATACTGTTAAGCAGTTTAAACGGGAAAATGTCCGATGCACCTGGCGCTGCTGC
GTCAGCAGCAGCAGACCAGCGTGGATGTGGAGCTGCTGCACACGATGCTAGCGCGAGCCG
CTGCGCTTGCCCATGCCCAGACTATAGCATAACATGTGGTATCAGCATGTGATGCCACGCC
GGTTGCCAGTAGAGGGCCGCTGCTATGTGAAATGGCTGGCGTAGCATTGTACCGAGACA
GGCTCTTCTTACCCGCGCAGTTCTCCAGCACTACCAGGCGATGAATCGCGATCGTCGCA
CCAGCCCAGAAGATGAACTGATTGAGTATGAGCTTAGACGGATTAAAGTCGAAGCGTTTG
CGCGTGGCACAATGCACTCCACGGCGCTCAGGGAAAAGTGAAGGTATTCTTGCAGGAGA
TGGATACGCTACCAGGGCAGCGCCATTAAAGGCTGCGCGACTTCCCGCAAATGACCAAGG
CTATGGGCATAGCATTTGATGCAGCAAGATGAGCAAGCAGCTGCCCTGGCGTTGTTGGAC
GACAGCCCCTAGTGATAAAGAACGAATGGTCACTACCGCTACTACTGGCTGGTGTCTCTT
GGCATGTTCCCGGCCAGCGCAGGCGGACGTGTGCTGGCGGAGTTCCGTCAAAGTTATC
GCGGGCTGCCGCTGCTGGATGCCGAAGTAGTGATAAAGAGAAGAGGATTTGAAATCAACA
CATAA

YER153C, 254 aa (SEQ ID NO 82)

MLTITKRLVTTDVRSRILLSSLNGKMSDALALLRQQQOTSVDVELLHTMLARAAALAHAD
TIAYMWYQHVMPRRLPVEGRLLCEMAGVALYQDRLFLPAQFLQHYQAMNDRRTSPEDEL
IEYELRRIKVEAFARGTMHSTALREKWKVFLQEMDTLPGQPPLRLRDFPQMTKAMGIALM
QQDEQAAALALFGRQPLVIKNEWSLPLLLAGVLWHVPGPAQARRVLAEFRQSYRGLPLLD
AELVIKRRGFEINT

YFL014W, 830 bp, CDS: 501-830 (SEQ ID NO 83)

GGACTAGAAGCCAAAAGCCAGAGGCGGTAAAAATAGCAAGACTAGAATATTGCTGGCATC
TGTTAAGGGGATATGTTGCAACTTGCAGGGGCGGCACAAAATAACATAGAAACGTAGTA
AAGAGGGGAAAAGGAAAAGGAAAAGGAAAGGAAAAGGAAAAGGAAAAGGAAAAGGAAAAGG
TGAAAGAAGGAAAGGTATACGCAAGCATTAATACAACCCACAAACACAGACCAGAACAC
TCTAGACGGAGAGTAAGTAGATCTACAGCCCCGTAAGAAATCGTTTGGTCAACTTTGAGGT
TCCGGTTCGTCCCCCTCTTGATCTGAAAGGTCCTTCTCTAAATCTATATTTAAACGTATAA
ATAGAGACGGTGAATTGCGTTCTACTTCTCTCAATTGCGTTTGTATCTTATTTAATCTCTCTC
TAATATATAGAAAAAAACCCTCTGATTATTCGATAATCTCAAACAAACAACTCAAAC
AAAAAAACTAAATACAACAATGTCTGACGCAGGTAGAAAAGGATTCCGTGAAAAAGCTT
CTGAAGCTTTGAAGCCAGACTCTCAAAGTCATACGCTGAACAAGGTAAGGAATACATCA
CTGACAAGGCCGACAAGGTGCTGGTAAGGTTCAACCAGAAGACAACAAGGTTGCTTCC

AAGGTGTCCACGACTCTGCCGAAAAAGGCAAGGATAACGCTGAAGGTCAAGGTGAATCTT
TGGCAGACCAAGCTAGAGATTACATGGGAGCCGCCAAGTCCAAGTTGAACGATGCCGTCG
AATATGTTTCCGGTCGTGTCCACGGTGAAGAAGACCCAACCAAGAAGTAA

YFL014W, 109 aa (SEQ ID NO 84)

MSDAGRKGFGKASEALKPDSQKSYAEQGEYITDKADKVAGKVQPEDNKGVFQGVHDSA
EKGKDNAEQGESLADQARDYMGAAKSKLNDAVEYVSGRVHGEEDPTKK

YFL015C, 995 bp, CDS: 501-995 (SEQ ID NO 85)

GACCTTCAGCGTTATCCTTGCCCTTTTTCGGCAGAGTCGTGGACACCTTGGAAGACACCCCT
TGTTGTCTTCTGGTTGAACCTTACCAGCGACCTTGTCGGCCTTGTCAGTGATGTATTCCT
TACCTTGTTTCAGCGTATGACTTTTGAGAGTCTGGCTTCAAAGCTTCAGAAGCTTTTTCAC
CGAATCCTTTTCTACCTGCGTCAGACATTGTTGTATTTAGTTTTTTTTTGTGTTGAGTTGT
TTGTTTGAGATTATCGAATAATCAGATGGTTTTTTTTTCTATATATTAGAGAGAGATTAA
ATAAGATCAAACGCAATTGAGGAAGTAGAACGCAATTCACCGTCCTATTTATACGTTTTTA
ATATAGATTTAGAGAAAGACCTTTCAGATCAAGAGGGGGACGACCGGAACCTCAAAGTTG
ACCAAACGATTTTCCAGGGGCTGTAGATCTAGTTACTCTCCGTCTAGAGTGCCTTCTGGTC
TGTGTTTGTGGGTTGTATTAATGCTTGCGTATACCTTTCCTTCTTTCAATTTCTACGTCA
ATGGGTTTTTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
ATGTTATTTTGTGCCGCCCCCTGCAAGTTGCAACATATCCCTTAACAGATGCCAGCAAT
ATTCTAGTCTTGCTATTTTACCAGCTCTGGCTTTTGGCTTCTAGTCTTGTCCCAAGAG
CCAAGGGCCCGTCAACACGTCGTCAATTGCTACCGCCAGCTGGCACCCACACATCACCGAC
CCTTTTTTTTCCATTTTTCGGCTGGGCCGTTAGTGGGATCCGCCCGCTCCCGGAGATTTTCA
CTTGGAATTTGCGCGTCCCCTTTTTTTTCTTCTCTGACTCCCCCTACCTTCTCCCACT
TTTCTGTGTATCAAGAGGAAAAGAAGGAGAAAAGGAGAACTCCGAAAAATACCGAACAAAG
AGGGTAACAGAATGTGCATTTGGATGAGCGGGTAA

YFL015C, 164 aa (SEQ ID NO 86)

MLAYTFPSFNFYVNGFFSFLFLFLFLFPLSLLRFYVILCRPLQVATYPLNRCQQYSSLAIF
TASGFWLLVLVPRAKGPSTRRHCHYRLAPTHHRPFFSIFGWAVSGIRPLPEIFTWICASP
FFLHSLTPPTFSHFSVYQEEKKEKRRTPKNTEQEGNRMCIWMSG

YFR022W, 2702 bp, CDS: 501-2702 (SEQ ID NO 87)

CTGCCCTCCGTACGTCACACGCATACACAATATAGTTTATATAAACTCCTGCGTATAAT
CTATCCTTTTGCATAATATTTTCGTCACCATTATCTTGTTGCGGTGTTTTTATTTAAAC
AATAGAACTCGCCTAAAGGGGAAATTTTCGATATAAAAAATTCAAAAAAATGGCTTTTCATG
GATCGAGTATTTGTTTGTGCGAAAAAGGATCACTGGAGTGACGTTACTACGCTACGAAGCC
TCCTTCCGGCTTAGCCCTGTTGATTACGAATTTGGATCAGTTGGTATTTGATTCTCCTCGGA
AGAGTTAACTTCACGCGGGTAAATCACTTGTGATGCGGTATATTCTCTATACGGCTAATA
GATGAATCAGGGTGTTTTAAAGTGCGTATAAACCCCTTTTGCTATTTTCGTTTATATAATT
GGCGTTGATAAAGAGCCAATATCTATTGTTGCTACATAGAGGCAGCTCTCTTAGCAAAAT
AAAAATACAAAAAGTTTCGACATGGGCTTCAGTAGCGGTAAATCAACTAAGAAAAAGCCTC
TGCTTTTTCGATATCAGACTTAAAAATGTTGACAACGATGTAATACTCCTCAAAGTCCCTC
CAAACGAGGCCCTCGGTGCTTTTATCTGGTTGCATCGTTTTATCGATTAAACGAACCCA
TGCAGATCAAAAGCATATCATTGAGACTTTATGGGAAGATACAAATAGACGTACCATTAG
AGAGGCCCCAGGACGCTAGTTCTTCTGTCGTTGTCTTCATCGCCGCCAAAGATCAGAAAGT
ACAACAAAGTTTTTTTATAATTACGCATGGGATAATGTTAACTCAAGGAGTATCTGAGTG
GTTTAAAGAGGGCAATCTGGCCTTGCGGGCAGTAGCTCATCAAGTAATATCTTGGGCACCTC
GCCAAAGAGCTCAGTCCACAAGTCTTGAAGTCTTTAAAGGGGTCTCCTCACCTCTCTT
CATGTACTTTAGATAAGGGCAACTACGATTTTCCCTTTAGTGCTATTTTGCCTGTTTCGT
TACCAGAGAGCGTAGAATCTTTGCCAAATTGCTTCTGTGACATATAGCATGGAATCCGTTA
TTGAACGCAGCAAAAAATTATAGTGATTGTAGCTGTAGGAAAAATATTAGAGTTCTGAGAA
CCATTTTACCCGCGCAGCTGGAGTTATCAGAACTGTTTGTGTAGATAACTCATGGCCCG
ACAAAGTGGATTATTTCTATTTTCAGTACCCAACAAAGCCGTAGCTATTGGTTTCAGCCACCC
CTATAAATTTTCCATTGTACCTTTTCGAAAGGTTTGAATTTGGGCTCAATCAAAGTCG
TATTATTTGAGAATTATCAATATTGTGACCCCTTCCCTCCAGTAATTTCTGAAAATAGGC
AAGTGACAGAACTAAATCTTGAAGATCCCTTGAACGAGTCATCTGGAGAATTTAATGGTA
ATGGTTGCTTTGTAAATAACCCCTTTTTCAGCCTGATCATTCATTCCAAGACAAGTGGG

AGATTGATACCATCCTGCAAATCCCGAACAGCTTATCAAACTGTGTGCAAGATTGTGATG
TCCGCTCTAACATTAAGGTTTCGCCATAAGCTCAAATTTTTCATCATCTAATTAACCCAG
ATGGTCATAAATCTGAGTTAAGAGCGTCTTACCGATTCAACTTTTTATTTCACCATTTG
TGGCACTTTCAATAAAACCATTGTCATCCTCGAATTTGTATTCGCTTTTTAGCACCACCTA
ACCAGAAAGACGAAAACATCACAAGAAGAGGAAGAGGAATATCTGTTTTCTAGATCAG
CATCAGTCACAGGGTTGGAATTATTAGCGGATATGCGTAGCGGTGGCTCTGTTCTTACCA
TTTCAGACTTGATGACGCCCCCAAATTATGAAATGCACGTATATGATCGTCTTTATAGCG
GTTCTTTCACTCGCACGGCTGTGGAAACGTCTGGAACATGTACTCTTTGGGAAGCGAAT
GTTCCGACTGTGAGGATCAGCAACAGGATTTAGAAGATTACGTATACGGTTGACAAAAA
TTAGAAATCAACGTGACAATCTAGGGCTACCACCGTCTGCCTCGTCTGCTGCCGCTTCCA
GATCGCTATCTCCATTACTAAACGTTCCAGCACCAGAGGATGGCACGGAGAGAATCTTAC
CTCAGAGTGCTCTTGGTCCCAATAGTGGCTCTGTGCCAGGAGTACATAGTAACGTATCAC
CTGTTTTACTTTCAAGATCCCCAGCCCCAAGCGTGTGAGCCCATGAAGTGTACCAGTGC
CCTCGGGCTTAAATTATCCAGAGACTCAAAACCTGAACAAGGTTCCATCGTATGGCAAGG
CAATGAAATATGATATCATTGGTGAGGACCTTCTCCTTCTTACCCTTGTGCGATACAAA
ATGTGCAACCAAGAAAACCCAGTAGGGTACATTCAGGAACTCTTCGACAACATTGTCAT
CTTCTATACCAACTAGCTTTTCACTTCTCTAGTTTTATGAGTAGCACTGCTTCCCCTATTT
CCATAATTAATGGCTCTAGAAGTAGTTCTAGTGGGTATCTCTTAATACTTAATGAGT
TAACTTCGAAAACCTCGAATAACCCATCCAGTAATAGTATGAAAAGGTCACCAACAAGAC
GGAGGGCTACTTCTTTAGCTGGGTTTATGGGAGGTTTCTATCAAAGGGTAACAAACGAT
AG

YFR022W, 733 aa (SEQ ID NO 88)

MGFSSGKSTKKKPLLFDIRLKNVDNDVILLKGPPNEAPSVLLSGCIVLSINEPMQIKSIS
LRLYGKIQIDVPLERPQDASSSSLSPPKIRKYNKVFYNYAWDNVNLKEYLSGLRGQSG
LAGSSSSSNILGTRQRAQSTSSSLKSLKGSSSPSSCTLDKGNYPFFSAILPGSLPESVES
LPNCFVTYSMESVIERSKNYSDLICRKNIRVLRTISPAAVELSETVCVDNSWPKVDYSI
SVPNKAVAIGSATPINISIVPLSKGLKLSIKVVLFFENYQYCDFFPPVISENRQVTELN
EDPLNESSGEFNGNGCFVNNPFFQPDHSFQDKWEIDTILQIPNSLSNCVQDCDVRSNIKV
RHKLFKFIILINPDGHKSELRASLPILQFISPFVALSIKPLSSSNLYSLFSTTNQKDENS
SQEEEEEYLFSSASVTGLELLADMRSRGSVPITISDLMTPPNYEMHVDRLYSGSFTRTA
VETSGTCTPLGSECSTVEDQQDLEDLRLTKIRNQDNLGLPPSASSAAASRSLSPLL
NVPAPEDGTERILPQSALGPNSGSPVGVHNSVSPVLLSRSPAPSVSAHEVLPVPSGLNYP
ETQNLNKPSPSYGKAMKYDIIGEDLPPSYPCAIONVQPRKPSRVHSRNSSTLSSSIPTSF
HSSSFMSSTASPIIINGSRSSSSGVSLNLTNELTSKTSNNPSSNSMKRSPTRRRATSLA
GFMGGFLSKGNKR

YGL011C, 1259 bp, CDS: 501-1259 (SEQ ID NO 89)

AGACAATAAAATATGGAAAATAAAACGCTTAGCACAGCAGTCAATGAAATACTCTGATAT
ATTTTGACTCTGTGGAGCATACAGCTACCCTAAATAGGATTGTGGGGACAAATATGGAA
TGGATCAAAACGTTCTTAGGATTGTGGTGGTAAACTTGTAATCAAGCTGAGATCTT
AAATCCAGCAAACCTTCGCCCATATTTATTCTTTTATAACAGAAGAAGAGACTATATTCT
CAAAACCTCGTATATTTATATACATATCTCCAAACAACTCCCAAGTTTCACTTCTCTG
GATTTACCTTGGCATTCTTTTCCCCATCTCTTATAATGGTAATCGCGATCCTTAATTA
TGATATCACAAATAGACGAAGGGCACACACCAATTTGCCACCGTAAGGATAGAGTAAGTTA
AATGGCTAACTCATTATAATCTTCATGCTAAATCATATAAGGGCAGAGACGAAGCAAAGC
GAAAAAACATATTACAATCATGTGGGTGCTGCTGCTGCATCTGCTGCTGGTTATGACA
GGCACATCACTATCTTTTCCCCGAGGGTCGTTTATATCAAGTAGAATATGCCTTTAAAG
CGACTAATCAAATAACATAAACTCACTAGCGGTGAGAGGTAAAGATTGTACAGTGGTGA
TAAGTCAGAAAAAGGTCCCTGATAAACTGTTGGATCCAACCTACTGTTTCGTATATTTTTT
GTATTTCAAGAACAATTGGTATGGTAGTGAACGGACCAATACCGGATGCAAGAAATGCGG
CCCTAAGAGCCAAGGCTGAGGCTGCAGAATTCCGTTATAAATATGGTTATGATATGCCAT
GCGATGTATTGGCTAAGAGAATGGCTAACCTTTCCCAAATCTATACTCAAAGAGCATATA
TGAGACCATTAGGTGTTATACTCACATTTGTTTCGGTAGATGAAGAATTGGGTCCCTCCA
TTTACAAAACCTGACCTGCAGGTTATTACGTTGGCTACAAAGCTACTGCGACAGGACCAA
AACACAGGAGATCACAACAACTTAGAAAACCAATTTCAAAAAGAGTAAATCGACCATA

TTAATGAAGAATCATGGGAGAAGGTGGTAGAATTTGCTATTACTCATATGATTGACGCAC
TGGGTACCGAATTTTCAAAGAATGACTTGGAAGTCGGTGTGCTACAAAGGACAAATTC
TTACCTTGAGTGCTGAGAACATCGAAGAAAGGCTAGTAGCAATTGCTGAACAAGATTAA

YGL011C, 252 aa (SEQ ID NO 90)

MSGAAAAAAGYDRHITIFSPEGRLYQVEYAFKATNQTNINSLAVRGKDC TVVISQKKVP
DKLLDPTTVSYIFCISRTIGMVVNGPIPDARNAALRAKAEAAEFYKYGYDMPCDVLAKR
MANLSQIYTQRAYMRPLGVILTFVSVDEELGPSIYKTD PAGYYVGYKATATGPKQOEITT
NLENHFKKSKIDHINEESWEKVVEFAITHMIDALGTEFSKNDLEVG VATKDKFFTLAEN
IEERLVAIAEQD

YGL031C, 968 bp, CDS: 501-968 (SEQ ID NO 91)

CCAAGTTAAGCAAGACACCAAGACAATAACTTGAGAGGTATGTCCCTATATGATGATGAT
TCATAATTAATGGCGACCGAGGGCAGCGTTGTGCTAGAAAGCAATGTATTAATATATGAG
AGAGCTTCAGATAGCCAATACACCGGAATTTAGACTTTGACAGGATTGTGGCTTTGTTCCA
GTATAACTTATAATATATGTCAACCTTTGAGCAGGAAACCCAATGAAAATGCTTCATTAC
ATATATACGATATGGAGAAGCATGAAAAATAACAGCGTGAGATGTTATCCATGTTGCAAG
AACCTAGTAAATGAATTCCTGAATTTGCAAAAAGTCCATATTTCCACGTTCTCCTCTTCC
TACAATTTTGC GAACGCTGAACAACCATGCGGATTACCATTATTTATATTGACAAGATG
GCTACCTATGAAAAGCATAGACTTACTAACATTTTTTTTTTCAAATATGTTTGAAAAACG
TGGATTAATATAGTGATAAAATGAAGGTTGAAATCGATTCTTTTTTCAGGTGCCAAAATCT
ACCCAGGCAGAGGTACCTTGTGTTGTCCTGGTGACTCCAAAATCTTCAGATTCAAAAACT
CCAAATCTGCCTCTTTGTTC AAGCAAAGAAAGAACCCAAGAAGATCGCTTGGACTGTCT
TATTCAGAAAGCATCACAAGAAGGGTATCACCGAAGAAGTTGCTAAGAAGAGATCTAGAA
AAACCGTTAAGGCCCAAAGACCAATTACCGGTGCTTCTTTGGACTTGATCAAGGAAAGAA
GATCTTTGAAGCCAGAAAGTTAGAAAAGGCTAACAGAGAAGAAAAATTGAAGGCCAACAAAG
AAAAGAAGAAGGCTGAAAAGGCTGCTAGAAAAGGCTGAAAAGGCTAAGTCTGCTGGTACTC
AAAGTTCTAAGTTCTCCAAGCAACAAGCTAAGGGTGCTTTCCAAAAGGTTGCTGCTACTT
CTCGTTAA

YGL031C, 155 aa (SEQ ID NO 92)

MKVEIDSFSGAKIYPGRGTLFVRGDSKIFRFQNSKSASL FKQRKNPRRIAWTVLFRKHHK
KGITEEVAKKRSRKTVKAQRPITGASLDLIKERRSLKPEVRKANREEK LKANKEKKKA EK
AARKAEKAKSAGTQSSKFSKQQA KGA FQKVAATSR

YGL032C, 764 bp, CDS: 501-764 (SEQ ID NO 93)

CTCCCATATTTTTTTATTTCACAGGCTAGACAATGGTAATGGTGCTTTAGATGATTTCACT
GGATTACATTTCGCACAATAGATAAATGACTAATTTTCAAGAATTTGTTTCAACCTGCCG
GCATTCACTTATTATAAGTTATTGTTTGATGGTAAACTTCGCCATCACCGGTTGCTGCG
TTTATTGCAAAATTACTGAAACCATGTAATTTCCGAATACGGTAATTACACGCAGTTTGA
AATTGACATGCAAGTTTAACAAAAAACTTCTGTCCGCATCTAAAGCTTAATTAAGGGA
CTGTTTCATACCTTCAGATCCAATATACTGAATATCAGGCAATTGATTTCCCTTGTAAT
ATACAATATAAATAGTTGTAAGAAGAGGTGATATGTTAAGTTTCCATTTTGACGTATTCC
TCATTCTAGAATGATTGTAAGCTCTCAACAGTCACTTGTGTGCCAAAATATTATACCTAC
TTCATACATTTTCAATTAAGATGCAGTTACTTCGCTGTTTTTCAATATTTTCTGTTATTG
CTTCAGTTTTAGCACAGGAAGTGAACAATATGCGAGCAAATCCCCTCACCAACTTTAG
AATCGACGCCGTACTCTTTGTCAACGACTACTATTTTGGCCAACGGGAAGGCAATGCAAG
GAGTTTTTTGAATATTACAAATCAGTAACGTTTGTGTAAGTTGCGGTTCTCACCCCTCAA
CAACTAGCAAAGGCAGCCCCATAAACACACAGTATGTTTTTTTGA

YGL032C, 87 aa (SEQ ID NO 94)

MQLLRCSFISVIAVLAQELTTICEQIPSPLESTPYSLSTTTILANGKAMQGVFEYYK
SVTFVSNCGSHPSTTSKGSPINTQYVF

YGL043W, 1430 bp, CDS: 501-1430 (SEQ ID NO 95)

TCGGGATGGTGGGTTGTTCTGTACCCCGCATTCACACCGCTCTGCCTATTCAATTTATC
GTTTTCTGCTTTTTCTTTCAATGTATTGATAATTAACGTGTCTATGTGATGCTATTGGTAT
ATAGCCTTTCTTGATATCCCTCTAACAATTATTACAAGTGTCTGTTTAAAGCAAGTG
CTAGAAGTGACTCGGTTCTCTTAGGAAATCTAAACGCAAGATTTCTCTTATGGTGATTG
TAACAATTATGAGATACTTCACTAGCCACCTTAACTTTACGGACCTCTTTTTGAAACGA

TGCTTCGAATGACAACGCCCTTTTTGATATATAATATCCAATTTTATTATAGGGAATTTT
CAACTCTTACCCGCCCCACTGTGCTGATATGACCAAGTGATCACTCGATGATGGGACTAC
GTATTGAAAAATATTGAATGAAAAATTACTCAAGCAGCAGAACATTACAGTGTAGTCAG
TCCGCATAAGAGCATTTCATCATGGATAGTAAGGAAGTACTGGTACATGTGAAGAATCTAG
AAAAGAACAAAAGTAATGATGCTGCAGTTCTAGAAATCTTACATGTCTTGGATAAAGAAT
TCGTCCCCACTGAAAAGTTACTGAGAGAAAACAAAAGTTGGTGTGGAAGTCAACAAGTTTA
AAAAATCCACTAATGTAGAGATCAGCAAACTCGTGAAGAAAATGATTAGCTCTTGGAAAG
ACGCAATTAATAAAAAATAAGCGTTCCAGGCAAGCACAGCAGCATCATCAAGATCATGCCG
CAGGCAATGCAGAGGACAAGACAACCTGTAGGTGAGTCCGTGAATGGTGTTCACAGCCGG
CCTCCTCCCAGTCAGATGCCATGAAACAAGACAAGTACGTCAGCACTAAACCAAGAAATA
GTAAGAACGATGGTGTGGATACAGCTATATACCACCACAAATTACGTGATCAGGTACTAA
AAGCACTCTACGACGTTTTGGCCAAGGAAAGTGAGCATCCACCTCAATCTATTTTGCATA
CTGCAAAGGCCATAGAAAAGTGAATGAATAAAGTTAACAACCTGTGACACCAACGAAGCCG
CTTACAAAGCCAGGTATCGTATAATTTATTCAAACGTCATATCAAAGAATAACCCAGATC
TCAAACATAAAAATTGCCAACGGTGATATAACACCTGAATTTCTTAGCTACATGCCATGCCA
AGGATCTGGCACCAGCGCCCTTAAAGCAAAAGATAGAAGAAATTGCCAAGCAAACTTAT
ACAACGCACAGGGTGCCACCATAGAAAGGTCAGTCACCGATAGATTTACATGTGGTAAAT
GTAAAGAGAAGAAGGTATCTTACTATCAATTGCAAAACAAGATCTGCGGATGAACCATTGA
CCACTTTCTGTACATGTGAAGCATGTGGTAACAGATGGAAATTCTCTTAG

YGL043W, 309 aa (SEQ ID NO 96)

MDSKEVLVHVKNLEKNKSNDAAVLEILHVLDDKEFVPTEKLLRETKVGVENVKFKKSTNVE
ISKLVKKMISWWDKDAINKNKRSRQAQQHQDHAPGNAEDKTTVGESVNGVQPPASSQSDA
MKQDKYVSTKPRNSKNDGVDTAIYHHKLRDQVLKALYDVLAKESHPQPSILHTAKAIES
EMNKVNNCDTNEAAYKARYRIIYSNVISKNNPDLKHKIANGDITPEFLATCDADKLAPAP
LKQKIEEIAKQNLNAQGATIERSVTDRTCGKCKEKKVSYQLQTRSADEPLTTFCTCE
ACGNRWKFS

YGL102C, 929 bp, CDS: 501-929 (SEQ ID NO 97)

TGTTACGATCAACATTCTTGTCCGTAATCAGCATGGTAGTTAAACCCATTCTGTACATAT
GGTCAGATATACCTTTTCGCATGGGTCAATACCATGGTCAACCCAACCAAGTTCTTCTTTGCG
TTTTCAAAAGTTGTATAATATTCAAAAACGCTAACTGATAATTTGGGTGAGGTTTCGAAA
GAATTGCCAAAATCTCCCTAGGTATATTATCTTCTGGCTTCCAGATGTTAACTGCAGTCA
TTTTGTTTTTCTCGGTCTTTACCTCGAATAGGTTTCTTGTGTTTTGTTATTTGTTTTCTTT
TTGGACCCATATGTTTATATATGGATTTTGAAAATCTTTTAAAAAAGCGATAAAAGCGTTG
GGATCTGCCACTGGTAACCTTCAAAATAGACAAGACGAAAAAACGGTGAAAATGGGTGATA
GAAATAATACAGAAGTAGATGTTGAATTAGATTAAACTGAAGATATATAATTTATTGGAA
AATACATAGAGTTTTTTGTTGATGCGCTTAAGCGATCAATTCAACAACACCACCAGCAGCT
CTGATTTTTTCTTCAGCCAACCTTGGAGACGAATCTAGCTTTGACGATAACTGGAACATTT
GGAATCTTACCCCTTACCCAAGATCTTACCGTAACCGGTGCCAAAGTGTCAATAACTGGA
GCAGTTTCTTTAGAAGCAGATTTCAGTATTGGTCTCTCTTGTCTTCTGGGATCAATGTC
CACAATTTGTCCAAAGTTCAAGACTGGCTTCCAGAAATGAGCTTGTGCTTGTGGAAGTAT
CTCATACCAACCTTACCGAAATAACCTGGATGGTATTTATCCATGTTAATTCTGTGGTGA
TGTTGACCACCGGCCATACCTCTACCACCGGGGTGCTTTCTGTGCTTACCGATACGACCT
TTACCGGCTGTACAAAAAAATATTGTAA

YGL102C, 142 aa (SEQ ID NO 98)

MRLSDQFNNTSSSDFFFSQLGDESSFDNWNINWSTLTQDLTVTGCSVNNWSSFLRSR
FQVLVSLVFDQCPQFVQVQDWLPEMSLLLVEVSHNTLTEITWMVFIHVNSVVMLTGHT
STTGVLVSLDPTTFTGCTKKIL

YGL103W, 1461 bp, exon1: 501-549, intron1: 550-1060, exon2:
1061-1461 (SEQ ID NO 99)

AACAAGCTATAATATTGTTAAATATAGTTGATCAACAGCATTGTAATGATTACAAGAGAC
GAGGTGGAATGAACCTTATGAAATGCGTATTATATATAAACTGTAATAAGAGCTAAGTTG
AATTGAAATCTACGATACCTTGATGTTGACATTATAGCACTAGTTCCCAGGAAACCTTTT
GAAAAACACAGCAAAAACAAGAGTACTGTAACCAATGTAACATCTGTACACCAGGGACCC
ACACATTACCAAAAATCAAAATTTATTTTCTAATGCCTGTTATTTTCTATTTTCTCTCT
GGCGCGTGAATAGCCCGCAGAGACGCAAAACAATTTTCTCGCAGTTTTTTCGCTTGTTTAA
TGCGTATTTTCCCAGATAGGTTCAAACCTTTCATCTGTATCCCGTATATTTAAGATGGCG

TTTGCCTTTCTCCGTTGATTTTTTCTTCTTAGTGATTTTTTGCATTAAATCCCAGAAC
AATCATCCAACATAATCAAGAATGCCTTCCAGATTCACTAAGACTAGAAAGCACAGAGGTC
ACGCTCAGGTATGTAGTTCCATTTGGAAGAGGGAATGAAAGAACCAAGACGGTGACTTT
TTTTTTAGTGTTGTGCAACCAATATGTCGTGTGTATATCATGGTACAGGAGAATGTCAAT
CAGCTAAGTGTAACATATTTCTTTGTGTTTTGATTGCGAACTTTGTATTACCATCT
CACTGTTGAGACGGCTTATTTGAGGTAATAGCTCGAGTAAATGTACTCTTCCATCGCAAA
CTGAGCAAAAAGAAAGTGTGCATAGCCTTTGTCTACTTCTCCTTTATTATACCATGATA
TTCAGAACAGTCACTACTGTCTACTCATTTTACGGCTATAAAAGGTAACCTTCATTTAGAT
TATGGAAGCACTAATTTATCGCTGTATCAAATGGTTGTAGAGAGCGCAATTATGAAAAAG
AGTTACCACGTTTCTTTGTTTCGATAAAATGTCCAGTTGAAAACCTGTTTTACTAACGA
TTTAAAAATTGTATTTCAATTACAATATTTTTTTTTGTACAGCCGGTAAAGGTGCTATCGGT
AAGCACAGAAAGCACCCCGGTGGTAGAGGTATGGCCGGTGGTCAACATCACCACAGAATT
AACATGGATAAATACCATCCAGGTATTTCCGGTAAGGTGGTATGAGATACTTCCACAAG
CAACAAGCTCATTTCTGGAAGCCAGTCTTGAACCTGGACAAAATTGTGGACATTGATCCCA
GAAGACAAGAGAGACCAATACTTGAAATCTGCTTCTAAGGAAACTGCTCCAGTTATTGAC
ACTTTGGCAGCCGGTACGGTAAGATCTTGGGTAAGGGTAGAATTCCAAATGTTCCAGTT
ATCGTCAAAGCTAGATTCTGCTCCAAGTTGGCTGAAGAAAAAATCAGAGCTGCTGGTGGT
GTTGTTGAATTGATCGCTTAA

YGL103W, 149 aa (SEQ ID NO 100)

MPSRFTKTRKRGHVSAGKGRIGKHKHPGGRGMAGGQHHHRINMDKYHPGYFGKVGMR
Y FHKQQAHFVKPVLNLDKLWTLIPEDKRDQYLKSASKETAPVIDTLAAGYGKILGKGRI
PN VPVIVKARFVSKLAEKIRAAGGVVELIA

YGL130W, 1880 bp, CDS: 501-1880 (SEQ ID NO 101)

TTTTGGTACTTGAATTTCTCGTTTCTACTAGCTGGATTGCTTGTCTTTTACAATTCCTG
GGAGTTTGGCTATTGCTACCCTTGGTCTTAGCACCACCTTTTTTCCGCTATTTGTATTTGT
TGAACATAATTTAGTATCTATTTCCATTTCAATTATAATTCACGTTTTTAGCAGCCTCTCTT
CTTCTAGGTAATTTGAAATCTTCTTCTTTAGGCATAGCGTGACCAGCTGAAAGGCAGATG
ATCTCAAATATGTCCTCGATAGGCCAATTTGCCACCAGATAGTTCGATGGCATTTTATTTT
TAGTCTCTTTTGAAGCAATATCATAAATATATATAGTTCTCCATGATGTTCCGGTCACT
CGCTCCGAAGCGTAACCTAGTATAATAAATAGTTCATTGCAGAAAATAACGAAAGAAATG
GTGGAATACGATCTGTATATCTAACTAAAGCTAACTAACGGAATAAGCAAATACGAAT
CGACCGCTAATTTAACAAATATGGTTTATGCAATGGAAGTAGAGTGGCACCGGAAATTC
CTGGGCTCATTAACCTGGGAATGTCACGCAAGACTTGAAGATGATGGTCTGTAAATTTAT
TGAAATTTCCCAAAACCTACGAAAACATTTCCCTGGTTCCAGCCTGTGTCTTTTACGACTT
CTGATGTGGAAGAGAAGCTGCTTGCATGATTACTACGTTTGTGAGAAAACAGATGGTCT
TGCGGGTGTGTATGTTTATAGTGATAAATCCTGTGACGGGTGAGCAAGGATGCTTTATGA
TTGATAGGGAAAATAACTATTATCTGGTTAATGGATTTAGGTTTCCAGATTACCCCAAA
AGAAGAAAGAAGAGCTGCTAGAGACTCTTCAAGATGGCACCTTATTAGATGGTGAACCTG
TCATACAACTAACCAATGACAAAATTACAAGAGTTGCGTTATTTAATGTTCTGATGTC
TTGCTATCAATGGTAGATGTCTCACACAATCACCAACAAGTTCTAGACTAGCCCACTTG
GAAAAGAATTTTTTAAACCATACTTCGATTTAAGAGCAGCGTACCCTAATCGTTGTACTA
CTTTTCCGTTCAAAATTTCCATGAAACATATGGATTTTCACTTACCAATTAGTAAAGTTG
CTAAAAGTTTAGATAAACTACCACATCTTCTGATGGTCTGATATTTACTCCTGTGAAGG
CACCTTACACTGCCCGCGGAAAAGATTCAATTGTTATTAAAATGGAAGCCAGAACAAGAAA
ACACCGTGGACTTCAAAATGATTTTAGATATCCCAATGGTGGAGGATCCTTCTTTCGCTA
AAGATGATCGGAACAGGTGGTATTACAATTATGACGTTAAGCCAGTTTTTACGCTTATATG
TCTGGCAAGGCGGAGCTGATGTCAATTCACGTTTAAAACATTTTCGACAGCCTTTTCGATA
GGAAGGAATTTGAAATATTAGAAAAGACATACAGAAAATTTGCAGAGTTGAGCGTTTCAG
ATGAGGAATGGCAAAATTTGAAGAACCTAGAACAGCCATTAAATGGTAGAATAGTAGAGT
GCGCAAAAACCAAGAGACTGGGGCGTGGGAAATGTTAAGATTCAAGGATGATAAGTTAA
ATGGTAATCATACATCGGTGGTCCAGAAAGTTTTGGAGAGTATCAACGATTCACTTTCAT
TGGAGGACCTCGAGGAAATGTTGGTGTATTTAAAAGGTGCTGGGACGAGAGAAGAGCAA
ATATGGCTGGTGGTAGTGGGAGACCACTACCGTCTCAAAGTCAAATGCGACATTATCTA
CCTCTAAGCCAGTCCATTCACAGCCCCCAAGTAATGATAAGGAGCCAAAATATGTAGACG
AGGATGATTGGTTCGATTAG

YGL130W, 459 aa (SEQ ID NO 102)

MVLAMESRVAPEIPGLIQPNVTQDLKMMVCKLLNSPKPTKTFPGSQPVSFQHS DVEEKL

LAHDYVCEKTDGLRVLMTIVINPVTGEQCFMIDRENNYYLVNGFRFRLPQKKKEELL
ETLQDGTLLDGLVLIQTNPMTKLQELRYLMFDCLAINGRCLTQSPTSSRLAHLGKEFFKP
YFDLRAAYPNRCTTFPFKISMKHMDFSYQLVKVAKSLDKLPHLSDGLIFTVPVKAPYTAGG
KDSLLLKWKPEQENTVDFKLILDIPMVEDPSLPKDDNRWYNYDVKPVFSLYVWQGGAD
VNSRLKHFDQPFDRKEFEILERTYRKFAELSVSDEEWQNLKNLEQPLNGRIVECAKNQET
GAWEMLRFDDKLNGNHTSVVQKVLESINDSVSLEDLEEIVGDIKRCWDERRANMAGGS
RPLPSQSNATLSTSKPVHSQPPSNDKEPKYVDEDDWSD

YGL147C, 1076 bp, CDS: 501-1076 (SEQ ID NO 103)

CAATATTATAGTTACTACCTATTTGATTATTAAGATCAAAAGTAATCCTTCATCTCATAT
CAAAAAGAAAGGTTTGTAAAAGAGCATTGGGCAGAGAGTATTTGTCCTGCGTATAGAGGA
GAAAAAATGTACTGATGCTAATTTTGGTGTGCTTCTTCTTTTTTATTTTGTAAAGACTGT
TTTCCAGAAATGTTTGGGTTTATTTTTTAATTTTTTGAAACATTTTTTTCATCCTTTCTC
ATTTTGTCTCATTTTCTGTGGAAAATTTCACTGACGCGAAGAAGCGATGAAATTTTC
CAACATCCTCCCATCATCCCAATATTGGCATAACACACATGCAGCACAGCGGAACGCG
GAGGTGTCAGAGCAATGTGGCAGAGACGCTGGCGCGCCTGTATTGTATAATAGTATATTTT
ACACTCAATTCATTTTGTATATTAAATAGTGTGTAAAAAGCTTCTGAAATCAAGAAG
CCCGTACCAGAAGTTCAATCATGAAATACATCCAACTGAACAACAAATCGAAGTCCCAG
AAGGTGTCACGTGTCAGCATCAAGTCCAGAATCGTCAAGGTTGTTGGTCCAAGAGGTACTT
TGACCAAGAACTTGAAGCACATTGATGTTACCTTCACCAAGGTCAACAACCAATTGATCA
AGGTTGCTGTTTCAACCGGTGGCAGAAAGCACGTTGCTGCTTTGAGAACCGTCAAGTCTT
TGGTTGACAACTGATCACTGGTGTCAACCAAGGTTACAAGTACAAGATGAGATACGCTCT
ACGCGCATTTCCCAATCAACGTCAACATTGTTGAAAAGGATGGTGCCAAATTCATTGAAG
TCAGAAACTTTTTGGGTGACAAGAAGATCAGAAACGTTCCAGTTAGAGATGGTGTACTA
TCGAAATTTTCCACCAACGTTAAGGACGAAATTTGTCTTGTCAAGTAACTCTGTGCAAGACG
TTTCCCAAAACGCTGCTGACTTGAACAAATCTGTGCTGTGCAAAACAAGGATATCCGTA
AATTTTTGGACGGTATCTACGTTTCTCACAAGGGTTTTATTACTGAAGATTTATAA

YGL147C, 191 aa (SEQ ID NO 104)

MKYIQTEQQIEVPEGVTVSISRVKVVGPRGTLTKNLKHIDVTFKVVNNQLIKVAVHNG
GRKHVAALRTVKSLVDNMITGVTKGYKYMRYVYAHFPINVNIVEKDGAKEIEVRNFLGD
KKIRNVPVRDGVITIEFSTNVKDEIVLSGNSVEDVSQNAADLQICRVNRNKDIRKFLDGIY
VSHKGFITEDI

YGL213C, 1694 bp, CDS: 501-1694 (SEQ ID NO 105)

AATCAAAACGATCGTTATACAATTCATTGAGGAACCTCTCTAGTCCGATCCGCTCTTTCAT
CGATCATTTCCGGATCATCATATCTTCTTTGCCACCTCCTGTCCAATACACCGGGCTTTT
CAGGGAAGTCATATGGGATGGTGTCTTCTTACATCTCTCTCCAATCGTGTCTTCAGTTTCC
AAAACCTCGGAATACCTTTTGTAAAGGCGCTTGTGTTGGTGTACTAACACCGTATAAAACAT
ACTTGGGGTTGATTTTAACATCGTCCACCTTGATTCTTAACTTTTCACTCATTTTCCCTA
CAGAAATAGCTGCCATCAATATCAATTATCAACCTTATATGACTTTATTGTTTTTGTGTT
TTGTTGGCTAATTAATTGATACAAATCTTTAGGCGAAAAATAAAAAAATATAAAGTAAA
GAAGGAAAAATTAGGCGATATTAAACAAATCTAAAATAAAGACAAGAAACGAAAAAGAG
GTTAATCAAGTATTGGAATAATGTCCAAAGTGTATTGTTGTTGTTGTTGTTGTTGTTGTT
CTCATGACGCTGATTTTTCTCGGTTTCTGCTTGCAATTCATTTACGGTAAGTTGTTTACG
GTGACGGTTACTTAAAGGTGTGGGATAATAAGCTGTTAGATAATGAAATCCAAAAGATA
AGTCATATTCTCACTTTGTCCATAAGTCCGGATTGCACCATGTGATGTCTTGCAGGCTA
TTGAGAGAGATGCATTTGAATTATGCCTTGTTGCTACCACTTCATTTTCTGGCGATTTAC
TCTTCTATCGTATCACTAGAGAAGATGAGACTAAAAAAGTTATATTGAGAAATTTGGATC
TTCTAGACTCAGACATGAAAAAGCATTCTTTTGGGCATTAAAAATGGGGTGCCTCAAATG
ACAGACTACTTTCCCATAGGCTGGTTGCTACAGACGTCAAAGGGACCACTTACATTTGGA
AGTTTCAACCGTTTGCAGATGAGTCAAATCTTTAACAATAAATTGGAGCCCCACGTTAG
AATTACAAGGCACTGTGCAATCGCCTATGACTCCAAGTCAATTTGCCACTTCTGTGGATA
TCTCTGAACGAGGACTAATTGCCACAGGTTTAAATAATGGAACAGTACAAATTTCAGAAC
TATCTACATTACGCCCCGTGTACAATTTTGAATCTCAGCATTCTATGATTAATAATTCTGA
ATTCCATCAGATCGGTGAAATTTTCTCTCAAGGATCCTTATTAGCCATTGCTCAGGATT
CAAAATCATTTTGGTTGCATCACTCTATATGAAACTGAATTTGGTGAAAGAATAGGCTCCT
TATCCGTACCAACCCATAGCTCGCAGGCAAGTCTGGGTGAATTTGCACATTTCTAGCTGGG
TCATGAGTCTATCGTTTAAATGATTCTGGTGAACATTATGCAGTGCCGGATGGGATGGTA
AATTGAGATTTTGGGATGTAAAAACAAAGGAAAGAATCACTACATTGAATATGCATTGTG

ATGATATTGAAATTGAAGAGGATATCTTAGCTGTTGATGAACATGGAGATTCTTTAGCTG
AACCTGGTGTCTTTGACGTGAAGTTTTTAAAAAAGGTTGGAGATCTGGTATGGGAGCTG
ATTTAAATGAAAGTTTATGCTGTGTTTGTTTAGATAGAAGCATCAGGTGGTTTAGAGAAG
CTGGCGGTAAATAA

YGL213C, 397 aa (SEQ ID NO 106)

MSKVFIA TANAGKAHDADIFSVSACNSFTVSCSGDGYLKVWDNKLDDNENPKDKSYSHFV
HKSGLHHVDVLQAIERDAFELCLVATTSFSGDLLFYRITREDETKKVI FEKLDLLDSMDK
KHSFWALKWGASNDRLLSHRLVATDVKGTTYIWKFFHFADESNSLTNLNWSPTLELQGTVE
SPMTPSQFATSVDISERGLIATGFNNGTVQISELSTLRPLYNFESQHSNNNSNSIRSVK
FSPQGSLLAIAHDSNSFGCITLYETEFGERIGLSVPTHSSQASLGEFAHSSWVMSLSFN
DSGETLCSAGWDGKLRFWDVKTKERITTLNMHCDDIEIEEDILAVDEHGDSLAEPGVFDV
KFLKKGWRSGMGADLNESSLCCVCLDRSIRWFRREAGGK

YGL235W, 1037 bp, CDS: 501-1037 (SEQ ID NO 107)

CTGGTTCCAACCATATCTTATGGGAAGATCTATCAGGAAACCTTAGAATCTTAGCTTCGA
TGGAGGGACAATAGCGGGGGCCCTTGATGGTCTGTCTGAATATGAATGGATTGATGCA
AGTTATTGCGCAAAAAGTCGTGCATTTGAGGTGTGGTATGTGTGCCAAAGCAATCCAGTT
GCTTCGTGGGTTCGACTGACACGGTTTCATTCAGAAAACCTCATAGGGACAGGCAACGCAT
CTCCCTTCTGGACCTCCAGAGCGCTGAAATCAATGGATTCTTGGCCAGCCTAGCCGGAG
TGCCTGTCTTCAACGCGCCCTAACTGAAAGCCCACTCATTTTGTAGAGTATTGCTGATCC
CATATGTTGGCTGCTCGCCAATTCCTCTGCTGCAATACGCTTGTGCGCGATGTGAATTT
CTGCACTGAGAAACGTACCTGTAGTATTATGACCTGATCTGCCCCAACCTGGGTACCGT
CATCCAGAACCACACCTTTTGATGACCTTGTGGCCACATCCGGGGTCATACAAGATCAAGT
CAGCAACTTTGTTCTGACAGCAGAGACAAGTTGGGGTGTGCTTTCTTGTGCGAAAGTTCCC
TTTGCATGTATTTCTTATATAACTCTCTGTCTATCTGGGCTCTGGGCCCCACACAGCAG
GACCTTGTCTTCTGTTTCAGCATTTTGAATTGCACTCCAGCGAGATCAGTTACTTTGCCCA
TCAGCCCATCGAGAGCGTCGATTTCTTTACAAGGATGCCCTTACCCACTCCACCAATAG
AGGGGTGTCACGAACACTTACCAATATCTGTTAACGATGGTGTAAATGAGAGTAGTATGCG
CACCAGTCCTAGATGACGCAGCTGCAGCTTCGCAGCCTGCATGTCCAGCACCGATGACCA
CGACCTGTCTTTGGTTGTGGTTGGAAGCTTGTCAAAGAAGATATGGTCAACCGCCTCC
TGAGGACCTGTAAAGGAAATGAAGTACACGAAGACGCCAAGGTTGTTACACGCAGCATCG
TTCTTTGGGGCGTTTAG

YGL235W, 178 aa (SEQ ID NO 108)

MTLWPHPGSYKIKSATLFCSRDKLGCAPLSESSLCMYFLYNSLSI WALGPHTAGPLLLFS
ILNCTPARSVTLPISPSRASISFTRMPLPTPIEGLHEHLPI SVNDGVMRVVVCAPVLD DA
AAASQPAC PAPMTTTCVLVVGWKL VKEDMVNRLRLRTCKGNEVHEDAKVVTRSI VLWGV

YGL260W, 731 bp, CDS: 501-731 (SEQ ID NO 109)

TACCATGGAACACCGGTGATCATTTCTGGTCACTTGGTCTGGGGCAATACCAGTCAACATG
GTGGTGAAGTCACCGTAGTTGAAAACGGCTTCAGCAACTTCAACTGGGTAGGTTTCCGTT
GGGTGGGCGGCTTGGAACATGTAGTATTGAGCCAAGTGAGCTCTGATATCAGAGACGTAG
ACACCTAATTCAACCAAATTGACTCTTTCTGTCAGACTGAGCTAGAGTGGTGGTTGCGGAA
GCAGTAGCAGCGATGGCAGCGACACCAGCGCGATTGAAGTTAATTTGACCATTGTATTT
GTTTGTTTTTTTAGTGCTGGTATAAGCTTAACAGGAAAGAAAGAAATAAAGATATATTCT
CAAAAGCATACAGTTGAAGCAGCTCTATTTATACCCGTTCTCTATCAGTCATCACTACT
TAAACGATTCTGTTAACAGATGCTCATTTAGCACCTCACATATCCTCCATATCTCATCTTT
CACACAATCTCATTTACTATGGAGATGCTCTTGTCTTCTGAACGAATCATACATCTTTC
ATAGACTTCGTATGTGGAGTATTGTATTATGGCACTCATGTGTATTCTGTATGCGCAGAAT
GTGGGAATGCCAATTATAGGGTGCCGAGGTGCCTTATAAAACCTTTTCTGTGCCTGTGA
CATTTCTTTTTTCCGTCAAAAGAATATCCGAATTTTAGATTTGGACCCCTCGTACAGAAG
CTTATTGTAA

YGL260W, 76 aa (SEQ ID NO 110)

MEMLLFLNESYIFHRLRMWSIVLWHSCVFVCAECGNANYRVPRCLIKPFSVPVTFPFSVK
KNIRILDLPRTAYC

YGR085C, 1025 bp, CDS: 501-1025 (SEQ ID NO 111)

TCCTTACTTTTAGTCTATTATCAATATCTCTCCCCCTCCTAAATATGTACTCTTTTATTT

TTTTTAATTGTGAAGGAACAATTCAAGTTAGAACTCTTTTGATAGGAAACATTATTTCCCT
GTGTAGCCTAATGTTTAAATGCCTAATTTTTTCTAAAATGCAGCAACATACATATGTTGA
GTCGTATAGACATCTATATATAACAAGCACAGAACCGTCTAATTGGTATTTTTTCAGGACA
TTTTAAACATCCGTACAACGAGAACCATACATTACTTTTTTTAATATTCCTTTTTGTTTT
CACCGCCTTCTTTTTATTTTTATCCGAAGATCTTTTGGAACCCGCTCTGCGAATAGCGAA
GCTAGGATACCAAATTGAACTTGGACATAACTCATCTAATAAGAAGTATACTGTTAAGA
GAGGCATTCATTTTCGTGTATTATAACGTTTAGCATCAGTTACCCCTGAAAGCCCCAACATA
TACAAAAATACGCGTCCAAGATGTCTACTAAAGCCCCAAAACCTATGCGTGATTTGAAGA
TCGAGAAATTGGTCTTGAACATCTCCGTTGGTGAATCTGGTGACAGATTAACCAGAGCCT
CCAAGGTTTTAGAACAAATTATCTGGTCAAACCTCCAGTTCAATCCAAGGCCAGATACACTG
TCAGAACTTTTCGGTATCAGAAGAAACGAAAAAATTGCTGTTACGTTACCGTCAGAGGTC
CAAAGGCTGAAGAAATTTTGGAAAGAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACA
GAACTTCTCTGCTACCGGTAACCTTCGGTTTCGGTATTGACGAACACATTGACTTGGGTA
TCAAGTATGACCCATCCATCGGTATTTTCGGTATGGATTTCTATGTCGTCATGAACAGAC
CAGGTGCTAGAGTCACCTAGAAGAAAGAGATGTAAGGGTACTGTTGGTAACTCCCACAAGA
CAACTAAGGAAGACACCGTCTCTTGGTTCAAGCAAAAGTACGACGCTGATGTGCTCGATA
AATAA

YGR085C, 174 aa (SEQ ID NO 112)

MSTKAQNPMRDLKIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRFTGIR
RNEKIAVHVTVRGPKEEILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSI
GIFGMDFYVVMNRPGARVTRRKCKGTGNSHKTTKEDTVSWFKQKYDADVLDK

YGR118W, 1258 bp, exon1: 501-565, intron1: 566-885, exon2:
886-1258 (SEQ ID NO 113)

AGCCATGTCGGTTCGCACTAGACTTTTCTTCTACTGTCACTTACCTGTTTGAAATCATGT
CCTTTTTTTTTTTTGCCATTCTTATACATTTTCTTTCTTCTGAAATTAACGTACACCCA
TACCTATATACACCCATACCCATATTTTAAATATAAAAAGTAACTTCATTTTGAAAGA
CCACTCTGCATCAGCACGCGGGCTCTGGAAGGAAGAAATGACGTTTCGGCGGAATACCCCT
TTCAGAAGGTCTGCTCTTGTGGCTGGTTTCATGGGAGACACCCAGCGGAGCTCCTCCCCGAG
AAAGCCCCCTTCATCTCTGCGGATTGCTGACGGAAGCAGTAGCGGAGGTTTGAGTTCTC
TACGCCGAGAGTACACTGCCGTAATATCACAATGTTTTCGACTAACGGTTACAGTACGTTA
AATTAGATACTGCCTATGAATTGACATATTAGATAATGTCAAATTTTACAAAAACCTAAG
ACAACAGGAAATAAAACAAAGATGGGTAAAGGTAAGCCAAGAGGTTTGAACTCTGCTAGAA
AGCTACGTGTCCACAGAAGAAACAAGTATGTTGACTATTTCAAATTAACAAAAAATATC
AACCCTATTGTGATATCGTTTATAGGTGAAGGAATGTTGTGAGCTCTGGAGTGATAAA
TTTATCAAGTAACATATCCTGGCGCAAATCAGTTTGGAGAGGCTTAAATGACACGTCAC
AGTGATAAAAAGTAATGAATAGTGAACGGTCAGCTTCGGCCATTCTTCCCAATCTATAGT
GTGGAATAAACCCTTTTCTTCCCAAAATAACTCAGAAAGTCACAGGAGGCCGTTTTTTTA
CAACGGAATCATTTTTTTACTAACAGTTTTTTTTTATTATTATAGCCGTTGGGCCGAAAA
CAACTACAAGAAGAGATTGTTGGGTACTGCCTTCAAGTCTTCTCCATTCCGTGGTTCTTC
TCATGCCAAGGGTATCGTCTTGGAAAAAATTGGGTATCGAATCCAAGCAACCTAACTCTGC
TATCAGAAAGTGTGTTAGAGTTCAATTAATCAAGAACGGTAAGAAGGTCACGTCTTTCGT
TCCAAACGATGGTTGTTTGAACTTTGTGCGACGAAATGATGAAGTCTTGCTAGCAGGTTT
CGGTAGAAAGGGTAAAGCTAAGGGTGATATCCAGGTGTTAGATTCAAGGTCGTTAAGGT
CTCTGGTGTCTCCTTGTGGCTTTGTGGAAGAAAAGAAGGAAAAGCCAAGATCATAA

YGR118W, 145 aa (SEQ ID NO 114)

MKGKPRGLNSARKLRVHRRNMRWAENNYKKRLLGTAFAKSSPFGGSSHAKGIVLEKLGIE
SKQPNSAIRKCVRVQLIKNGKKVTAFPNDGCLNFVDENDEVLLAGFGRKGKAKGDI PGV
RFKVVKVSGVSLALWKEKKEKPRS

YGR142W, 1733 bp, CDS: 501-1733 (SEQ ID NO 115)

GGACTACTTTACAGGGTAATGAATATTTGGGCGTTTTTCGCTATTTTAGCATGCTGTAGT
GTATGTACTGTGCATCGTCATGTAGCACTATTTTCAGCCGTATTTTCTTTTTTTCTTTTCG
CACCGTCTGTGGTTGTAAAGTTACTGACACTTTTTTTTCTAGAAAGTTCCGGAAAAATTGC
GACACTCGGTGGAGCTCGAGAGTTGTATCCAGTTTCTTGTTCGGCGATATCCGAACCA
GGTCGGGTTGGGCTAACAGCCGCCGAGATGGAAGAATTAAGAATTCATAGAACCTTTC
AGTTCTTGGCGAAGTAAAGTGGCAAAACAAATGGAAGATCTATTGCATTACATATATAAA
AGCATTAGAACAATCTTTCTCATTGACAGGTATTCTCATTGCTCTATATATATTTTCTT

CTTCTTGAAAGAAATATCAGTATTACAATCATAACAACAACCAAAAGAAAATAACTAATA
GACCCCATTTACAAATATAGAAATGTTTTCCATATTCAATTCACCATGTGTTTTGAACAGC
TGCCATCTTTTAGTCAGCCCTACATTCGCGTTATTTTGATTGCAGTTCCTCCAGTGAGCT
ATTATCCAGAAATGTAAAAGGAGGAAAAGCAATAAAAGCTAACCTAAGAGCTCCAAAAAAA
GCGATGCAAATTTGTTGAGAACCTTTGAGGTATGCACTTGCTGAAACACCAATGGTTATA
CATTAAGCTTGTCTAAGCGGATTCCATATGAACTTTTTTCAAAGTACGTTAATGAGAAAT
TAGGTGAGCTAAAGGAGAACCATTACAGACCAACTTACCATGTTGTCCAAGATTTTTTTG
GAAACCAGTATTATGTTGAAGATGAAGCGGATGAAGATGCTCTATTGAGATCTGCATTGA
AAGATCTGGATTTTAGAGCCATAGGAAAGAAAATTGCTAAGGATCTTTTCCAAGACTACG
AAATAGAATTGAATCATAGAGGTGATGAATTGAGCATATTGAGTAAGAAGGATAAAATCT
TTAAGGAATTCTCTCTAGACCAAGTGTGTTGAAGATGTTTTGTTATTGGCTGTGGAGTTG
AAAACATAGATGATGGCTCGAGAGAAAATATGCACTTTTAAAGATTGGTTTAGTTAAGC
ATGAGGAAGAAATTTCCGAAGGTGGCATCAACGAACCAAGATGCCAATAATTGAATCCA
AAATAGACGAGTCTCAGGATGATGTTAATCATGCTGAATCTTTGAAGGAGGAAGAAGCGG
AGAAAGCGAAAAGAACCACTAACCAAGAAAGACCAAAATAAAAAAATGGATAGAGGAAGAAA
GATTGATGCAGGAGGAAAGCAGAAAATCAGAACAGGAAAAGCTGCCAAGGAAGATGAAG
AAAGGCAAAAGAAAGAGAAGGAAGCCAGATTGAAGGCAAGGAAGAATCTTTGATAAATA
AGCAAAAACCAAGAGGTCCAGCAAAAAAATTGCAAAATTCCAAATCATTCGCTATCT
CTGAGATTGAGGCCAGCAATAAAAAATAATAGCAATTCTGGTTTCAGCAGAAAGTGATA
ATGAAAGTATAAACAGTGATTCTGATACGACTTTGGATTCTCTGTGTCTGGTAAATACAC
TAAAAAACACGCTTCACCCCTATTAGAAGACGTTGAGGATGAGGAAGTTGACAGATACA
ACGAGTCCCTAAGCAGATCTCCAAGGGAACTCTATTATTGAGGAGATATAA

YGR142W, 410 aa (SEQ ID NO 116)

MFSIFNSPCVFELPSFSQPLHSRYFDCSSPVSYYPECKRRKAIKANLRAPKKS DANCSE
PLRYALAETPNGYTL SLSKRIPYELFSKYVNEKL GELKENHYRPTYHVVDFFGNQYYVE
DEADEDALLRSALKDLDFRAIGKKIAKDLFQDYEIELNHRGDELSILSKDKIFKEFSLD
QVFEDV FVIGCGVENID DGSREKYALLKIGLVKHEEEISEGGINEPKMPIIESKIDESH
DVMSESLKEEEAEKAKEPLTKEDQIKKWIIEERLMQEESRKSEQEKAKEDEERQKKEK
EARLKARKESLINKQKTKRSQKKLQNSKSLPISEIEASNKNNSNSGSAESDNESINSD
SDTTLDFSVSGNTLKKHASPLLEDVEDEVDYRNESLSRSPKGN SIIIEI

YGR236C, 890 bp, CDS: 501-890 (SEQ ID NO 117)

CAAAAAGTTTTTCGGATGAACCGGATTAATACAAGTAAATCAGCAAAGATATAGAAGAC
AAAATAAGCGTGAAAACAATCATAAACCACTCACACGGGGGTTTTTCAGCTGTTACTCCT
CCATATACATATTTTGATAAAGATATAATGTTATATTCTTTTCGTAATTTTGTTTACT
TCGGTTTGCTCTATAGATTTTCATCAGCCGACCGAAAAGGGAGATCAATAAGGTACCCCT
TAAAAGGGATAAGAAGCCTACATCACCCCAATAAATGGAGTAATGGCCAGCATTTGGATGA
AGAGAAGAAATTACGGGATACTGGGATAACACTGTTAAAAAATGCTTCGCGACGTGAGGGT
CTTCTTCATATAAATTGAACTGCCAAATCTCTTTACATTATCCAGGATAGTTTGGAAATG
TGTTGTTACTGAAGGATCAGAATCAATAAATACAATCAATACAAATATTTAGCGCATAAAA
TTCAAACAAAGTTTACTGAAATGAAGTTAGATTGAGGAATATACTCAGAGGCACAAAGAG
TTGTGAGAACTCCAAAGTTTAGATATATTATGTTAGGGCTGGTGGGCGCTGCTGTGGTAC
CGACCGCATACATGAGGAGAGGCTATACGGTTCTGTCACATAGCTTAGACAACATCAACG
GCGTAGACACAACTAAGGCGTCTGTTATGGGTACAGAACAGAGAGCAGCTATGACGAAGG
GTAAGAGTTTACAAGAGATGATGGATGATGAAGTAACGTATTTGATGTTCTCTCTTCA
ATCATGTAAGGGAAATTTGTACTTGGTTCCCTGCATTTATGTTCTTTGCATTTTGTTCG
CATTTAATCATAGTACGACAAAACGGGGAAGGGGATTGTGATTTTACATAA

YGR236C, 129 aa (SEQ ID NO 118)

MKLD SG IYSEAQRVVRTPKFRYIMLGLVGA AVVPTAYMRRGYT VPAHSLDNINGVD TTKA
SVMGTEQRAAMTKGKSLQEMDDDEV TYLMFLFNHVREFVLGSLHLC SLHFVFAFNHSTT
N GEGDCDF T

YGR277C, 1418 bp, CDS: 501-1418 (SEQ ID NO 119)

AATCTTTGCGATTGAATTGCTGCACGAACATTAAACATTAGTTCTTTTGCTAAAGTTTCTC
CAATATCTGGAATATCAGAAATTTAGCAAGGCAATCAAAGCGGATAAAGCAGGGATTAGCC
TGCCATTCTGTTTGTTCAGAGTAAATCCACAACATTTTACAAATTATGTTGCGGCCAA
TAAGTATATTGACTTGAAATAAGTCTCTGTGCGATTCTGTAAAGTTGTCCATTGTTAAAT
TGGATATTATGGGTGAAACGTGTGACCTTATCATTTCCAGTTTTCTCTCTGAAATTTAA

TGTCTTCATCCTGTATGGTAGCGGTAGACATGCTGGTTTGTAGCCTTTTTATTCCTTTTT
AGGTTTCTTACTCACAATGCCAAAATAAATATCAGTGTAATATAATTTTTCAAGAGTACG
TAATGGAAAAAGATAAAAAATAAGGACCGTCATAAAAAGAGACGTGATTAAACCTAAAAAT
CTAAAGTAAAGAAGTGTAAGATGGTTGAGGAAAATTCCAGAGTTTTGATTGTTCTTCCTT
ATACACCGCCTAGTGCTACTTTGCAGAGGATTATAGGGCAAATATTCCGTTCTTAAGAG
AATGTCAAAGTCAACTAGACATCGTGATTGTACCTGAATTCAAAACCTCATTCCAGTTGG
ATTCTGCGCTAGGGAAGATGTACAGTATTACCAGGGATGTCTTTTTGGGGCTATGGAATGA
TCAACAGCGGAATCAACATCATATTCAACAATATTCAATTCGTCGAGAGTAATTTGCAAT
GGAAAGTGGTTTATTTGCCACAGGAATCCACTTTTGAAACTTGGAAGCTAGAGTTGGGAC
AAGGACAATACCATAGTATAGAACATTATGCATTACACGATAATATAATGGAAGAGATAG
AAGGTCCCAAAGATGCTAACAAATTTTATGTACCCGATTGGGGCGGAACGTTCCGACCACA
TTCACGATGGACATAAAATATGTGTGAGCGTCTCTACATTCATCACGTCACAAAGGTTAA
TTTGTGGAATTAAGTGCAGTGTGAGCTCTTGCAAAACAAGAAATACAAAGAGTTGATTGAAC
CTTATGATACACGATGCAGGCACGTACATCAATTCATCAAGTTGTTAAAACCGGATCTCT
CCGTAGAACTAGTTCCCTTAAGGGACGTGTGCGGCCCCACAGGGAAAGTACCCGAGATAG
AATGTTTGTGTGAGTAGAGAAACCGTCAGTGGGGCAGAGACTGTGAATAAGACTAGGA
TTGAAAAAGGCATGAGCCCATTTGGCAGTACATGTGGTTAATGTACTTGGAGGAAGGGAGG
AAGACGCGTGGAGCGGAGAAGTTAAGCAGCACGGAAATCAGACGCCTACTTAAGTCTCTG
CTTCGCCAACGTGCACTCCACAAAACCTTGCGTATAA

YGR277C, 305 aa (SEQ ID NO 120)

MVEENSRVLIVLPYTPPSATLQRIIGQTIPFLRECQSQLDIVIVPEFKTSFQLDLSALGKM
YSITRDVLLGYGMINSGINIIFNNIHVESNLQWKVLLPQESTFETWKLELGQGYHSI
EHYALHDNIMEEIEGPKDANKFHVTAALGGTFDHIHDGHKILLSVSTFITSQRLICGITCD
ELLQNKYKELIEPYDTRCRHVHQFIKLLKPDLSVELVPLRDVCGPTGKVPEIECLVVS
ETVSGAETVKNTRIEKGMSPHAVHVVNVLGREEDGWSEKLSSTEIRRLKSSASPTCTP
QNPCV

YGR284C, 1433 bp, CDS: 501-1433 (SEQ ID NO 121)

AGAGAGCCATCCGTAACCTCTGCTAAGGAAGCTGACTACTTTGGTGATGCTGACAAGGCCA
CCACGATTGACGAACAAGTTGGTTTGATCCGTTGACAGTTTGAATGACGAAGAGTTAGTGT
CCACCGCCGATAAGATCAAGGCCAATGCTGCTGGTGCCAAGGAAGTTTTGAAGGAATCTG
CAAAGACTATTGTGCTGATTCTGGCAAATACCATCCAGCTTGTGTCTTACTTCGTGTGAA
TACCGTAAGAAATGGAATAGAAATATATACGAATGTATACGAATATTATAGAGAACGTTCT
CTTTTATTTCTATAATGAATAGGTTCCGGTAACGGTTCCCTTTTTTAGGTATTTCTAGAAG
ATGAGAGAAGGGAATAATGAGAAAGGCCAAAAATAAAGGACACCTTTAACGAAAGATC
AAAGGTGTCCTTATTTACTTACAATAGCTGCAATTAGTACGACTCAAAAAAAGTGAAGAAC
AAAAGTGAAGGATAGATCAATGTCTTACAGAGGACCTATTGGAAATTTTGGCGGTATGC
CAATGTTCATCATCGCAAGGACCATACTCTGGCGGTGCACAATTCAGATCAAACCAGAAC
AATCCACTTCTGGCATCTTAAAGCAATGGAAGCATTCTTTTGAAGGTTTGCCTCCAGAA
TTGAGGGGCTCACTGACAATGCAGTTGTTTATAAATTGAAGCCTTACATTCCAAGTTTGT
CAAGATTTTTTCAATTGTGGCCACCTTTTATGAAGATTGCTTTAGGATCTTATCACAATGGT
CAGATCAAATTTTTTATCTGAATAAGTGAAGCATTACCCATACCTTCTTTGTCTGTTGTGT
TTCTAGTGGTTGTTACCGTTTCCATGTTGATTGGCGCCAGTTTGTAGTTTAAAGAAAGC
AAACCAATTATGCCACCGGTGTGTTATGTGCTTGCCTTATTTCTCAAGCATTAGTTTATG
GGTTGTTTACGGGTTTCATCATTTGTCCTAAGAACTTTAGTGTATTGTTGGGTTGTTAA
TTGCATTACAGCGATTCAATTGTTCAAAACAAGACAACATTCCGTATGCTTCCTGAATTAA
ACAGCAAAAACGACAAAGCGAAGGGTTACCTGTTGTTTGCTGGTAGAATTTTAAATTGTTT
TAATGTTTATCGCTTTTCACTTTTCACTAAATCATGGTTTACTGTTGTTTGTGACCATTATCG
GCACAATATGTTTCGCCATTGGTTACAAGACAAAATTTCGCATCCATTATGTTGGGTTTGA
TACTAACTTTTTACAATATCACGCTAAACAACCTACTGGTTTATAACAATACTAAGAGAG
ATTTCTTGAAGTATGAGTTTTACCAGAACTTAAGCATCATTGGTGGGCTTCTATTAGTTA
CTAATACTGGCGCTGGTGAATTATCCGTTGATGAAAAGAAGAAGATTACTAG

YGR284C, 310 aa (SEQ ID NO 122)

MSYRGPIGNFGGMPMSSSQGPYSGGAQFRSNQNSTSGILKQWKHSFEKFASRIEGLTDN
AVVYKLPYIPSLSRFFIVATFYEDSFRILSQWSDQIFYLNKWKHPYFFVVVFLVVVTV
SMLIGASLLVLRKQTNATGYVLCACVISQVGLFTGSSFLVRNFSVIGLLIAFSDSI
VQNKTTFFGMLPELNSKNDKAKGYLLFAGRILIVLMFIAFTFSKSWFTVVLTIIGTICFAI
GYKTKFASIMLGLILTFYNITLNNYWFYNNTRDFLKYEFYQNLIIIGLLLVNTGAGE

LSVDEKKKIY

YGR285C, 1802 bp, CDS: 501-1802 (SEQ ID NO 123)

CATTTAGTTCTGATTACAGCAGAAATCGTAGCGGATGAGACATTTTCATCAAATGGCCTT
TTTTTTTTGGGCAATTTTTTATATCTTGAAATGATAGTTGCCCTTGACTTTCAACCGTT
CATTTTCATTAAGAACTTGACTAAATATGAACATTTCTTAAAAAAAAGGTTGACATATAAA
AATAATCGAATATAAACGATGGAATTTTTATAAAATTAAACACATATATATATATATT
AACTATAAATATGTCAAAGAAACCATAACAATCATAGATTTATAACTATCTTTTGGATGAC
ATTAATGAACATAACGCTCCTAATACAAATGTCCAAAAAATATTACCCGCAAATACGAAT
CTTTTTTTTTCTCGATGAAATTTTGCAAAGAGTTCGAAATTTTTATTTCAGAGCTGGT
AGAGAAAATTTTCATAAGGTTTTCTACCGATGCTTTTATAAAATCTTCGTTTTGTCTCAC
ATATACCAACAAGAGTAACGATGTTTTCTTTACCTACCTAACCTCAGACATCACTGTTG
AAGTCAACAGTTCGGCTACCAAAACCCCATTCGTCGGTCGTCGGGTCGAACCGGTTGGTA
AGTTCTTTTTTGCAACATGCTCAAAGAACTTTGAGAAACCACACCTGGTCTGAATTTGAAA
GAATTTGAAGCTGAAAAGAAGCTCAAAACCGTTGATGAATCCAATGTCGACCCAGATGAGT
TGTTATTTCGACACTGAATTGGCCGATGAAGATTTACTGACTCATGATGCTAGAGACTGGA
AAACTGCCGATTTGTATGCTGCTATGGGTTTGTCTAAGTTGCGTTTCAGAGCTACTGAAA
GTCAAATCATCAAGGCTCACAGAAAACAAGTTGTCAAGTACCATCCAGACAAGCAATCTG
CTGCTGGTGGTAGTTTTGGACCAAGATGGCTTTTTCAAGATTATTCAAAGGCCTTTGAAA
CTTTGACTGATTTCCAACAAGAGAGCTCAGTACGACTCATGTGATTTTGTGCCGATGTTG
CTCCTCCAGAAAGAAGGTACCGATTATGACTTTTATGAAGCTTGGGGCCCCGTTTTTCGAAG
CTGAAGCTCGTTTTTCTAAGAAGACTCCTATTCTTCTCTAGGTAACAAAGATTTCTCCA
AGAAGGAAGTTGAACAATTCTATGCTTTCTGGCACAGATTTGACTCCTGGAGAACCCTTG
AGTTCTTGGACGAAGATGTCCCAGATGACTCTTCTAACAGAGACCACAAGCGTTACATTG
AAAGAAAGAACAAGGCCGCAAGAGACAAGAAGAAGACTGCTGATAACGCTAGATTGGTCA
AACTTGTTGAAAAGAGCTGTCAGTGAAGATCCCCGTATCAAATGTTCAAAGAAGAAGAGA
AGAAGGAAAAGGAAAAGAAGAAAATGGGAAAAGAGAAGCCGGTGCCAGAGCTGAAGCTGAAG
CTAAGGCCAAGGCCGAAGCTGAAGCGAAGGCTAAAGCTGAATCTGAAGCCAAGGCTAACG
CCTCCGCAAAAGCTGACAAAAAGAAGGCTAAGGAAGCTGCTAAGGCCGCCAAGAAAAAGA
ACAAGAGAGCCATCCGTAACCTCTGCTAAGGAAGCTGACTACTTTGGTGATGCTGACAAGG
CCACCACGATTGACGAACAAGTTGGTTTGATCGTTGACAGTTTGAATGACGAAGAGTTAG
TGTCCACCGCCGATAAGATCAAGGCCAATGCTGCTGGTGCCAAAGGAAGTTTTGAAGGAAT
CTGCAAAGACTATTGTGCGATTCTGGCAAACCTACCATCCAGCTTGTGTCTCTACTTCGTGT
GA

YGR285C, 433 aa (SEQ ID NO 124)

MFSLPTLTSDITVEVNSSATKTPFVRRPVEPVGKFFLQHAQRTLNRNHTWSEFERIEAEKN
VKTVDESNDPDELLFDTELADEDLTHDARDWKTADLYAAMGLSKLRFRAESQIIKAH
RKQVVVYHPDKQSAAGGSLDQDGGFKIIQKAFETLTDSNKRAQYDSCDFVADVPPPKGT
DYDFYEAWGPVFEAEARFSKKTPIPSLGNKDSKKEVEQFYAFWHRFDSWRTFEFLDEDV
PDDSSNRDHKRYIERKNKAARDKKKTADNARLVKLVERAVSEDPRIKMFKEEEKKEKERR
KWEREAGARAEAEAKAEAEAKAESEAKANASAKADKKKAKEAAKAAKKKNKRAIRN
SAKEADYFGDADKATTIDEQVGLIVDSLNDDELVSTADKIKANAAGAKEVLKESAKTIVD
SGKLPSLLSYFV

YHR010W, 1472 bp, exon1: 501-531, intron1: 532-1092, exon2:
1093-1472 (SEQ ID NO 125)

GACTCGGACGGAACCGTCTCATATTATACGTTCAAGTGAATATTTTTCACGGAAGAATGGA
AAGGGCCTCGAAAGACGTTAATGCATCCGTACACCTACATCTTTACATTTTTTGTGTTG
CACCTACACTGTTTTTTTTTTTTTTCACCTTATGAGTCCTGTATTTCTTGAAAGAGCCGAT
AACAATATTCCAGGTGGAGTCCCGAGGCAGAATCAAGGCTGCGGAGAGAAGTTCCCTCTCA
AACTAATGGGAGTGATCCGCTCAGTTCTCCCATCACGACAGAACTGTCTGAGACAAAGTC
TTTCCAGCAGAGTCCGCTACGCTCTTGCTGCAGAGATTCGCCCGAAGGCAGGTTTCCTG
AAATTCTTTTCACTAGTAAAGTGTTTCGTTTCATGTAAACATACTGCCGTAGTTTTGAGCT
AAAATTAAAGATATATTAGATTTTTAGAATTTCTTAGATAGTCTCAACGTGTTAAAACAA
AAGCATAACCAAAGAAAAAATGGCTAAGTTCTTGAAAGCTGGTAAAGTTGGTACGTATC
ATTTTCAGTTTTTGGACATCAACAAAAAACCGTGAACCTGTGGTATTAGAAATCCAAGTT
ATTAGCAGTTGATGTTGTATAATTTGAGTTTGAATTCGAGTATTGTATCTTCATATGGGA
GTAGGGAGGAAAAAGCGTGGAGATGTTAGATCTGGGAAAAAACCTTTAAATTTGAATGAT
AGCTTATTAATAGAAATATTGGACAAAAAGATGAATGATTTAGGAGCGAAACTAACGATT

ATTCATATTCATTGAGCTATACGAGGCAGTGGAAAGGGTTATCAAAAAGTTGTAATTTAAA
AGAAAAAGCATCAATAGCCACCAAATAAGATGGTGAAAGTTCCGCGATATATTTGCTAA
GACCATAGGCACATGTACGCAGGCGACCAGGGCCTTTTATTTACTGTAGTTCTTTCCATG
CCCTATTAATAAATTCGTGGGCCATGATAATTTTTCTCTCCCTAGTATTGAAGAACAAAA
TTGAGAATTCGCCAAACTTTAAGAAGGGTTCACATTTACTAATATTTCTTTTCTTCCT
TTTTTTACACAGCTGTCGTTGTCCGTGGTTCGTACGCCGGTAAGAAGGTTGTTATCGTTA
AACCACATGATGAAGGTTCCAAGTCTCACCCATTTGGTCACGCTTTGGTTGCCGGTATTG
AAAGATACCCATTGAAGGTCACCAAGAAGCACGGTGCCAAGAAGGTTGCTAAGAGAACCA
AGATCAAGCCTTTTCATCAAGGTCGTCAACTACAACCATTTATTGCCAACCAAGATACACTT
TAGATGTTGAAGCTTTCAAATCCGTTGTTTCTACTGAACTTTTGAACAACCTTTCCCAAC
GTGAAGAAGCTAAGAAAGTCGTCAAGAAGGCTTTTGAAGAAGACACCAAGCTGGTAAGA
ACCAATGGTCTTCTCTAAGTTGAGATTTTAA

YHR010W, 136 aa (SEQ ID NO 126)

MAKFLKAGKVAVVVRGRYAGKKVIVVKPHDEGSKSHPFGLVAGIERYPLKVTKKHGAK
KVAKRTRKIKPFIVVYNHLLPTRYTLTDLVEAFKSVVSTETFEQPSQREEAKKVVKAFEE
RHQAGKNQWFFSKLRF

YHR021C, 1299 bp, exon1: 501-503, intron1: 504-1053, exon2:
1054-1299 (SEQ ID NO 127)

TTACTTACGTCTATTATAACCTTCCGCGTAAAAAAGAAATATTGACATCCTTTCTTGTAT
TTAGCCCATACATTTTCACCCATGCACCATTTGGATTATAAAGAAAAAATTTAATAAAAA
TCTGCCGGGGAATTTTCAGAAGAAAAAAGGAAGGTGTGTTTCGCATTTAACACGGGCCACC
ATAAATCTTTGTTTGCACCCATCTAGACGGGATCCGCCCGCCCAAGGCTCTCTTCCTC
TAGCTAGGCAATGTGGCTCTCGGAAAGGAACTCCCACCAGGACGTGGTGGAATGCGAG
CAATTCGCCCTCTGCTTCCCCTGACCTTTCTTGGGCCAGTTTAGTAAGTATGCTCTCAT
CTTTCATGTGTGCTGTAACCTTGCAAGTCATTAACACTATCTATAATTGATATTAGACGTT
AAAAGTTCTATATAGCATTTGCTTTTATTTAGAGAATACGAAAACACACCAGATAATTAG
TGCATATATATTAGATCAATATGTTATGTGAAAGAGATATTAAACATAAGATGTGAAGGA
AACAGAAGAGAACAAATTTTGAGGAATGAATTCGGATGAAATCTTAGTAGAAGAAAAAG
CCTAAAAATAAAAGAAAGAAAGGAAAAATAAAGCAGTAATCAACCTCTGACATTTGATAGG
AGTATGCGTTTCCGCAAAATCAACAAATCATGCATTAACCTGGTAACGGAGACTTTAAAG
ACGTGCAAAGAAAGCAATTAATTTTATAGATAGGAATTGAAAGGCTCTGTATAGCAGAAA
ATTTGAGATCTACTGTGAGATAAGCATATGGTGTGAGTTATGGGTAATCTAACAAATAA
TAGAACTTATAGCAGTTGAAGATGGCGGATCATGATGCCGGATACGTGCTGGGTAATGAT
TTATCTTCTTTTGGAGCACAATGCTCACTTTTCTGTCTCTCTTAACCTTTTCTG
ATGTATACCAACCCCTACAGTTTCAAATTAACATCAATTTTTTTTGTGAACGA
CTTTCGTTTTCTGTTCTATTTATTTTATTACAGGTTTATAGTTCAAGATTTGTTGCACCCA
ACTGCTGCTTCTGAAGCCAGAAAGCACAAGTTAAAGACTTTGGTTCAAGGCCCAAGATCC
TACTTCTTGGATGTCAAATGCCAGGTTGTTTGAACATCACCAGTGTTTTTTCTCATGCT
CAAACGTGCTCACTTGTGAATCATGCTCTACTGTCTTATGTACTCCAACCGGTGGTAAG
GCCAAATTATCTGAAGGTACTTCTTTCAGAAGAAAGTAA

YHR021C, 82 aa (SEQ ID NO 128)

MVLVQDLLHPTAAASEARKHLKTLVQGPRSYFLDVKCPGCLNITTVFSHAQTAVTCESCS
TVLCTPTGGKAKLSEGTSFRRK

YHR141C, 1262 bp, exon1: 501-504, intron1: 505-945, exon2:
946-1262 (SEQ ID NO 129)

TAAAACATGGCATTTTAAATAGTACTGCCAAAATTTAATGCAATGGCAATTAGTTGGCTA
TGTTGCTACATATTATTTCCATAGCATTTCTGTGCACAACTTCAAAATAAAGACAGT
GACATCCGAACATCCGATACACCCATACATCATGAAAATAAATCCTGACATTGGAAGAAG
TCTTGATACAAAAAAGATCGCTGTCAAAAATGCGGCCAGACTGCCGCTGCATCGTACCA
ACAGTGCGTATGTTTACAGCGGAGAGACGACCTCTAGAGAGACGTCCGTCCGTGCGGCAAC
GCTGACGGTTTAGTTGTTGACGGGATGATGGGTTCCGCCAGGGGGAGGGAAGGCTTTCC
ACCAAGAGAGGTAAATTTATTCGTGCAAAATGAACTCAGAGATACATCCATATTGTTGACA
ATGTATATCTTAATTGATGTGGTATTTTCACTGTTTTAACGTAAATTGAAGGAGATTAAAG
CAAAAAACAAATCAGTAATAATGGGTATGTGGACGATTAGGAATAGACAAACCATGTTAT
TTATCTCCATTAGGGCGTGAGAGTGAATTAGTACACAGGTACTACTAGAATGCTAAAGA
ACTTTTTAAATATCTGAATCGTAGGGCAATCCATGTCAAGCAAGAACTAATAGTTA

TTAAACTTCATTTACTTTTGAGCTAGTTAAATATTTTCATCATTTCCCTAAAGTACTGAAC
ACCTGAATGATACTTTTATTGGCCCTTTTAATAAGAACTCTGGTTAGAAAATATATTGAG
GATATCATTTAGTAATACTCATTAGATATTTGTGAATTTAGCCGTTTCCCCATTACAGAAA
AAAGATACACTAATTACATGTGCAGTCAAATTACTTTTTTTTTTAAGATCAATTACTAAC
AATCAACTATCATGCTAAATTTGCTGTGATATCATTTTGAACCAGTTAACGTCCCAAAGA
CCAGAAAGACCTACTGTAAGGGTAAGACCTGTCGTAAGCACACTCAACACAAGGTTACTC
AATACAAAGCTGGTAAGGCTTCCTTGTTCGCTCAAGGTAAGAGACGTTATGACCGTAAAC
AATCTGGTTTCGGTGGTCAAACCAAGCCTGTTTCCACAAGAAAGCTAAGACTACCAAGA
AGGTTGTTTTGAGATTGGAATGTGTCAAATGTAAGACTAGAGCCCAATTAACTTTGAAGA
GATGTAAGCACTTCGAATTGGGTGGTGAAAAGAAGCAAAAGGGTCAAGCTTTGCAATTCT
GA

YHR141C, 106 aa (SEQ ID NO 130)

MVNVPKTRKTYCKGKTCRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGFGGQTKPVFHK
KAKTTKKVVLRLCEVKCKTRAQLTLKRCKHFELGGEKKQKGQALQF

YHR217C, 962 bp, CDS: 501-962 (SEQ ID NO 131)

CATCGCTTGATTTCCGGCCTGCAAAAATAAAGTAGTCGGTACGTACTTTTCGTTTTCAATT
TCCATGGTGCACAGTATCTTAACTATCTGCTTAGTCGAGGAGAACCAGGATTCTGTTTCGT
TGCTCAGCCGCTTCGTGGATATTCTCTTGGATACTTTAAACATGGACCTACGTTCCGCTC
TCGAAAGACCAATATAAATAAAGTTATAAATTACATTTTCCTTATTAGGTATACGACCT
CGCGCTTCGAAGTAGAGGAGCCCTTTTTGGCGTACCTACATATGGCGCGTCAGACAGACA
AACTTCCCCCAAAAATGTATTACCCCGCCGAATAAGAAAACAGACCCATTACCCACGAC
GTATCAAGTTACTTCTTGGTGCAATGTCCCACTATAAAAAAATTCCTTGACGCTAGATC
GTTGGACTAAAAATCTGCGTCACAATCGCCTAAACAGGAAATATTGCCTATTTTCGTACAA
GGTTACTTCTTAGATGCTATATGTCCCTACGGCTTGTCTAACACCATCCAGCATGCAAT
ACAGTGACATATATATACACACACACCCACACCCACACCCACACCCACACACACACCCCA
CACACACACACCCACACACACCCACACCCACACCCACACCCACACACACACACACACCC
CACACACACACCCACACCCACACCCACACCCACACCCACACACACACACACCCATCTA
ACCTGTCTCTTAACCTACCTCACATTACCTACCTCCCCACTCGTTACCTGCCCCACT
CAACCATAACCACTCCCAACCAACCATCTCTCTACTTACTACTACCATCCACCGCCCA
TCATAACCGTTACCTTCCAATTACCCATATCCAACCTCCACTACCATTACCCTGTATTAC
CCTACCATCCACCATGTCTACTCACTGTACTGTTGTTCTACCCTCCATATTGAAACGTT
AA

YHR217C, 153 aa (SEQ ID NO 132)

MSLRPCLTPSSMQYSDIYIHTPHPHPHPHPTPTHTHPHTPTPTPHPHPTPHPHPTPTPT
TPHHTHTPHTTSLNLSLNLPSHYPTSPLVTLPHSTIPLPTTIHLSTYYYHPPPIITVTLQ
LPISNSTTITLLLPYHPPCPTHCTVVLP SILKR

YIL112W, 3752 bp, CDS: 501-3752 (SEQ ID NO 133)

TTCCATAGGGCTTATTTCCAGTTGATGGAATGGGAGGTTGCTCTTAACGCGAAGACTAA
CGTGCAAGCCAAACAGTTATAGAAAAGTACCGTGAGAGAGAAAAAAGATATAGCA
TTCAATGAGGCTTTATTGAGGGGCACGATGCTCTTTTTTCTTCTGTACTTTATAAATAA
TTCCGTATTTCTTCGCTTGTTCATGCTCTGTTCTGAGCTTTTAGTTTCTCTTATTGAG
AGCCTTTTCCAAATCAAGGCTCAGGAAGTGACTCGTCTTAGAAGAACAAGGTTTGGATT
TGGTAGGGTCTTGTACGAAGTTCTCAATATAATTTGCGCATTTACTGTACGGTTCATAC
TAGTTTATTTCCGGGTAACAAGTTTCTTGTGATGCTAAATCAATGTGTATATTGAGAAAA
CTATGTAGTAAGTTACACAAAAGCAACAAAGGATATTATTATATGTGACAGAGAAGAATTG
CTGTAGAGATTATGACAATATGAATGAGACTACTACAAAACAGCCGCTAAAGAAAAGGT
CCCTGAGCAGCTATCTTTCAAACGTGAGCAGAGACGGGAGGAGCTGGAAGAAAGTTTCTA
AACAAAGAAACATCCGAAGAGGAAGATACTGCCGGCAAGCATGAACAAAGGGAAACACTGT
CGGAAGAAGTAAGTGATAAGTTTCCAGAAAATGTTGCATCGTTTCGCTCACAGACTACAA
GCGTTGCATCAAGCCACCCAAAATAACCTGAATGCAAGGAATCCGAAGACCTGGCCCAT
AGAATGATGCGAGTTCACACGAAGGAGAGGTTAATGGGGACAGCCGTCCGGACGATGTTT
CTGAAACGAATGAAAAAATAAGCCAAGCAATACGAGCGAAAATTTTCGTCATCATCATCAT
CACCAATGTACGTAATGTGATATCCAAAACCATCAACCTTTTTTCGAGAGACCAACTTC
GAGCGATGTTGAAAGAACCAAAAAGGAAAACCTGTTGATGATTTCATAGAAGAAGAGGGTT
TGGGAGCTGTTGAAGAAGAGGATTTAAGTGATGAGGTACTTGAAAAAATACAAACAGAAC
CAGAAAATGTGGAAAAAGATATAGAGTATAGCGACTCAGATAAGGACACAGACGATGTGG

GAAGCGATGATCCACGGCACCCAACTACCAATAAACTTGGTCGTCGCAAACTGGTTA
GAGGTGACCAACTTGATGCAACAACAAGTTCCATGTTTAATAACGAATCAGATTCTGAAT
TATCAGATATCGATGATAGCAAGAATATTGCTTTATCCAGTAGCCTATTTAGAGGCGGTT
CTTCACCTGTGAAAGAGACAAACAACCTTTCAAATATGAATTTCCACCAGCACAAA
ATCCAAAAAGGGGTTCTGTCTCCAGGAGTAATGATAGTAACAAGAGTTCTCATATAGCTG
TTTCCAAGCGCCCCAAACAGAAGAAGGGCATATATAGGGATTCTGGTGGTAGAACAGAC
TACAGATTGCCTGTGACAAGGGCAAATATGATGTAGTCAAAAAGATGATTGAAGAAGGAG
GTTACGATATTAATGACCAAGACAATGCTGGTAATACAGCATTGCATGAAGCGGCGTTGC
AAGGTCATATTGAGATTGTGGAACGTGTGATAGAAAATGGTGCAGATGTAAATATCAAGT
CTATTGAAATGTTTCGGCGATACTCCCTTGATCGATGCTTCGCCAATGGACACTTGGATG
TTGTCAAGTATCTTCTTAAAAACGGTGCGGACCCAACTATACGTAACGCTAAAGGGTTAA
CTGCGTTTGAATCTGTGATGATGAATCTGAATTTGATGATGAAGAAGACCAAAAGATTT
TGCGTGAAATAAAAAAAGGTTGAGTATAGCCGCTAAAAAATGGACTAACAGAGCAGGAA
TTCATAATGACAAATCTAAAAATGGCAATAATGCTCACACAATAGATCAGCCACCTTTTG
ATAATACCACAAAAGCCAAAAACGAAAGGCGCTGACTCACC'TTCAATGGCTTCCAAATA
TTGATGAGAAAAGCTCCGGAAGAGGAATTCTATTGGACAGATGTTACTTCTAGAGCGGGAA
AAGAAAACTGTTTAAAGCTTCGAAGGAGGGACATTTACCATACGTTGGTACGTATGTAG
AAAATGGTGGTAAGATAGACTTAAGGTCATTTTTCGAAAGCGTTAAGTGTGGCCATGAAG
ATATTACAAGTATCTTTTGGCATTCCGATTTCCTCGTAAATCAAAC'TTCAAGGGATAATA
AAACATCCGCTTTAATGGTAGCTGTGAGTGTGCGGCATCTTGGAACTGTTAACTGCTAT
TAGAGGCAGGTCAGATCCAACCAAAAGAGATAAAAAAGGGTCGTACCGCTTTGTACTATG
CCAAAAACAGCATAATGGGAATAACAAACAGTGAAGAAATTCAATTGATTGAAAATGCTA
TAAATAACTATTGGAAGAAGCACTCTGAAGATAATAATGATGATGATGATGATGATGATA
ATAATAATGAAAATATATAAATGAAAAAAGAGAGAGAAAACGCAATCACCCTATTTAG
CAAGCCGAAGAAGTGCCACTCCTAGAATTGAAGACGAAGAGGACGATACGAGGATGCTCA
ATCTGGCAGACGATGACTTTAATAACGATCGTGATGTCAAGGAATCTACAAC'TTCGGATT
CGCGCAAGAGATTGGATGACAATGAAAATGTTGGTACTCAATACTCATTTGGACTGGA AAA
AACGTAAAACAAATGCCTTGCAAGATGAAGAAAAATTAAAAAGTATCTCACCCTCTCTA
TGGAACCTCATTTCTCCAAAGAAGGCAAAATCTGTAGAGATAAGTAAAATACATGAAGAAA
CGGCTGCTGAAAGAGAAGCAAGACTCAAGGAAGAGGAAGAATACAGAAAGAAAAGATTAG
AAAAGAAAAAGAAAAAAGAACAGGAACACTACAAAAGCTGGCCGAAGATGAGAAAAAAA
GGATCGAAGAACAGGAGAGAGCAGAAAGTCTTAGAAATGGAAAGATTGGAAAAAGCTACTT
TAGAGAAAGCAAGAAAAATGGAAAGGGAAAAAGAAATGGAAGAAATCTCTTATAGAAGGG
CAGTAAGGGACTTTATATCCGTTAGGACTGAAGATTATTAAC'TTCAACGATAAACTTGATT
ACAAAAGATTTTTCGCCGTATATTATTTGTAGACGAAAAAACGATAAAATTTGTGCTCG
ACTTGCAAGTAAATGATATTGTTGAAGGATATCGACTTGCTCTCAAAGGACAACCAACCA
CTTCTGAGAAGATTCCCGTCGATCCCTCGCACCTGACTCCATTGTGGAATATGTTGAAAT
TCATTTTCTGTATGGAGGTAGTTATGATGATAAAAAAGAACATGGAAAATAAAAGAT
ATGTTGTAACCTTTGATGGGGTTGATTTGGACACAAAGATTGGGTATGAGCTTTTGGAGT
ACAAAAAATTTGTTAGTTTGCCCATGGCGTGGATTAAATGGGATAACGTTGTTATTGAAA
ACCACGCAAAAAGAAAAAGAAATTGAAGGAAATATGATTCAAATATCAATAAACGAATTTG
CAGCATGGAGAAAACGATAAGCTGAACAAAGCGCAGCAGCCGACGCGCAACAGCGTTCTC
TAAAAATACCTCGAGAGTTACCGGTTAAATTTCAACACCGTATGAGCATATCTCTCGTCC
TCCAGCAGACATCCAAAGAACCATTTTGTTAA

YIL112W, 1083 aa (SEQ ID NO 134)

MNETTTKQPLKKRSLSSYLSNVSTRREELEKISKQETSEEDTAGKHEQRETLSEEVSDK
FPENVASFRSQTTSVHQATQNNLNAKESDLAHKNDASSHEGEVNGDSRPDDVPETNEKI
SQAIRAKISSSSSPNVRNVDIQNHQPF SRDQLRAMLKPKRKTVD DFI EEGLGAVEEE
DLSDDEVLEKNTEPENVEKDIEYSDSKD TDDVGSDDPTAPNSPIKLGRRKLV RGDQLDA
TTSSMFN NESDSELS DIDD SKNIALSSSLFRGGSSPVKETNNLSNMNSSPAQNPKRGSV
SRSDNSNKSSHIAVSKRPKQKKGIYRDSGGRTRLQIACDKGYDVVKMIEEGGYDINDQ
DNAGNTLVHEALQGHIEIVELLIENGADVNIKS IEMFGDTP LIDASANGHLDVVKYLLK
NGADPTIRNAKGLTAFESVDDESEFDDEEDQKILREIKRSLIAAKKWTNRAGIHNKSK
NGNNAHTIDQPPFDNTTKAKNEKAADSPSMASNIDEKAPEEEFYWTDVTSRAGKEKLFKA
SKEGHL PYVGTYVENGGKIDLRSSFESVKCGHEDITSIFLAFGF PVNQTSRDNKT SALMV
AVGRGHLGTVKLLLEAGADPTKRDKKGR TALYAKNSIMGITNSEEIQLIENAINNYLKK
HSEDNDDDDDDNNNETYKHEKKREKTQSPILASRRSATPRIEDEEDDTRMLNLADDDF
NNDNRVKESTTSDSRKRLDDNENVGTQYSLDWKKRKTNALQDEEKLKSI SPLSMEPHSPK
KAKSVEISKIHEETAAREARLKEEEYRKKRLEKKRKEQELLQKLADEKKRIEEQEK

QKVMERLEKATLEKARKMEREKEMEEISYRRAVRDLYPLGLKIINFNDKLDYKRFLPL
YFVDEKNDKFVLDLQVMILLKDIDLLSKDNQPTSEKIPVDPShLTPLWNMLKFIFLYGG
SYDDKKNMKNRYVNFDFGVDLDTKIGYELLEYKKFVSLPMAWIKWDNVVIENHAKRKE
IEGNMIQISINEFARWRNDKLNKAQQPTRKQSLKIPREL PVKFQHRMSISSVLQOTSKE
PFW

YIL115C, 4883 bp, CDS: 501-4883 (SEQ ID NO 135)

TTTCAATGCGCTACAACCTGACTGAACCAGTCCACAAATTTGGCTGGTCTCTATCGTTCTC
GCCCTGAGAGATTTTATTTTCTTATAAATTTTACTAAATAAGGATTTGTACTTTTGATAG
AGTTTTTTTTTTTTCTGACGTTTGTATTAGTTAATATTATATAATAGTATTTAGGAACTA
GGTGGGAGGGGACATCGCAACTTTTATCGTGACCTACGACCAGTGTTTTTCAATTGTTT
GATCAAAAGAGAAAAAAGACAAAGGACCGAAGGATAGTTGCACGCATAAACTGGAGAAA
AAATTGTGTTTGACATCGGCGTTTAGGCTTGTTTGTCTGTCTACACATACGCTGCTTCAC
ACCAATTCATATTTCTCAGGTTAATTTGTCTCCTCTCCAACCTCAATAACGATTTTGGCT
GAAGGTTTAATTTTATTATTGCAATTTTAGCAGAGAAACGCACATAAATATATATATT
GATTACAGAACCATTATAACATGTCTTCTTTGAAGGATGAAGTACCCACTGAGACTTCCG
AAGACTTCGGTTTTAAGTTTTTAGGTCAAAAACAAATTTCTACCTTCTTCAATGAAAAAC
TGCCATTTGCATCTCTACAAATCTCGATATTTCAAACAGTAAGTCTTTATTCTGTTGCTG
CCTCTGGTAGAAGCGGTGGTGGCGAATTACAATTACTGAGAGATCATATCACCTCCG
ACTCTACTCCGTTAACGTTCAAGTGGGAGAAAGAAATCCAGATGTAATATTGTGTGCT
TTCATGGTGATCAGGTTTTGGTTTCAACCAGAAATGCATTATATTCTGTTAGACTTGGAGG
AATTGAGTGAATTTGAAACGGTCACTTCTTTTGAGAAGCCAGTTTTCCAATTGAAGAACG
TTAATAACACTTTAGTAATTTTAAATTCAGTCAATGATTTATCAGCACTGGATTTAAGAA
CAAAATCGACTAAGCAACTGGCACAAAACGTTACCTCTTTTGATGTCAAAATTCGCAGT
TAGCAGTTCTACTAAAAGATAGAAGTTTTCAAAGTTTTCATGGCGAAATGGCGAAATGG
AAAAACAATTTGAGTTCTCTCTACCGTCAGAAATAGAAGAGCTTCCAGTAGAAGAATATT
CCCCTTTGAGTGTTACCATCTCTCTCCACAGGATTTTTTGGCGGTTTTCGGTAATGTTA
TATCAGAGACCGATGACGAAGTTTCATACGATCAAAAATGTACATTATAAAGCACATAG
ACGGCAGCGCCTCATTTCAAGAACTTTTGATATTACACCTCCATTCCGGGCAAAATAGTAA
GGTTCCTCATATATGTACAAAGTTACCTTGCTGGTTTAATTGAACCTGATGCAACGTAA
ATGTGCTAGCATCATGTTCAGTGAAGTAAGTATATGGGACTCGAAACAAGTTATTG
AACCTTCCCAGGATTCTGAACGAGCAGTATTGCCCATCAGTGAGGAAACAGATAAGGACA
CAAAATCCAATAGGTGTGGCAGTTGACGTCGTTACTTCAGGCACTATTCTAGAACCTTGTT
CCGGTGTGATACGATAGAGCGATTGCCGCTCGTTTACATATTGAATAACGAAGGTAGCT
TACAGATAGTCCGGTTGTTTCATGTGGCAGCAATCAAAAGCGGCCATTATAGCATAAATC
TGAATCTTTTAGAACATGAGAAATCTCTCTCTCTACATCAGAAAAAATTCCTATTGCTG
GACAGGAGCAGGAAGAAAAAAGAAAAATAATGAATCAAGTAAGGCTTTATCAGAGAATC
CTTTACATCAGCAAAATACATCAGGCTTCACTTTTCTTAAACACAACCAGCCGCTGCCA
ATAGCCTGCAGTCTCAAAGTTCTTCAACCTTTGGTGCTCCCTCATTTGGATCATCCGCAT
TTAAATTTGACTTGCCATCAGTCTCATCTACCAGTACTGGTGATGCGTCCAGTGAACAAG
ACGCAACAGATCCTGCTTCTGCTAAGCCAGTATTTCGGCAAAACCCGCGTTCCGAGCTATTG
CCAAAGAACCCTCAACATCAGAATATGCCTTTGGCAAGCCATCTTTGGTGCTCCCTCCT
TTGGCTCTGGAAAGTCATCTGTTGAATCGCCTGCCCTCCGGATCTGCCTTTGGTAAGCCCT
CTTTTGGTACTCCTTCCCTTTGGCTCTGGAAATTCATCTGTTGAGCCGCTGCCTCCGGAT
CTGCATTTGGTAAGCCCTCTTTTGGTACTCCTTCCCTTTGGCTCTGGAAATTCATCTGCTG
AGCCGCTGCTTCCGGATCTGCCTTTGGTAAGCCCTCTTTTGGTACATCTGCATTCCGAA
CTGCATCAAGTAACGAACTAATCTGGATCCATATTGGAAAGGCTGCATTTGGTTTAT
CATCTTTTGCACCCGCCAACAATGAACCTTTTCGGATCAAACTTTACTATTTCAAAACCTA
CAGTTGACAGCCCAAAGGAGGTAGATTCAACGTCACCTTTCCCATCTTCTGGCGATCAAA
GTGAAGATGAGTCTAAGAGTGATGTAGACTCTTCTTCGACACCTTTTGGTACGAAACCTA
ACACCTCTACGAAACCAAGACCAATGCCCTTTGATTTTGGGAGTTCTTCTTTGGATCTG
GATTGTTCAAAGGCTCTGGAATCTGTTGGTTCCGATACAACCTTTTAAATTCGGTACTCAGG
CTTACCTTTCTCTTACAGTTAGGAAACAAATCACCATTAGTTCTTTCACAAAAGATG
ATACTGAAAATGGATCTTTAAGTAAGGGCTCTACCAGTGAAATCAATGACGATAATGAAG
AACACGAAAGCAATGGTCCCAACGTAAGCGGTAATGATTTGACAGATTCTACGGTTGAGC
AAACATCTTCTACTAGATTACCGGAACTCCCTCCGGATGAAGATGGTGAAGTTGTGAGG
AGGAATCCGCAAAAATCCCCATAGGCAAGCTAACTGAACTATAAAAAAAGTGCCAATA
TTGACATGGCTGGTTTAAAAAATCCTGTATTGGAATCATGTCAAAGCAAAATCCGAAT
CGCCGTTTTTCAGCATTTGCAACAAATATTACCAAAACCAAGCTCTACAACACCTGCTTTTT
CGTTTGGTAACCTCCACAATGAATAAAAGTAATACATCTACGGTTTCACCAATGAAGAAG

CTGATACTAAAGAACTAGTGAAAAGGGCCCCATAACCTTGAAGAGTGTGGAGAATCCGT
TTCTACCAGCGAAAGAAGAAAGAACTGGAGAAAGTTCTAAAAAGGATCATAACGATGACC
CAAAAGATGGTTATGTATCAGGAAGTGAATATCTGTAAGGACTTCTGAAAGTGCCTTTTG
ATACCACAGCAAAACGAAGAAATTCCAAAGTCACAGGACGTGAACAATCATGAAAAAGCG
AAACAGACCCAAAATATAGTCAACATGCTGTGGTTGATCACGATAACAAGTCTAAAGAAA
TGAATGAACTTTCGAAGAATAATGAAAGGAGCGGTCAACCAAATCATGGTGTCCAAGGAG
ATGGAATAGCATTGAAAAAGACAATGAAAAAGAGAATTTTGATTCAAATATGGCAATAA
AGCAATTCGAAGACCACCAATCTTCAGAAGAGGACGCGAGCGAAAAAGACAGTAGACAAA
GCAGTGAAGTTAAAGAATCAGATGATAACATGTCACTCAACAGTGACCGGGATGAAAGTA
TATCTGAGTCCCTACGATAAACTGGAAGATATTAATACTGATGAGCTACCTCATGGTGGAG
AAGCTTTTTAAAGCACGTGAAGTGAGCGCTTCCGCTGATTTTGATGTACAACTTCATTAG
AAGCAATATATGCTGAATCTGGCATACAGACAGACCTTTCAGAAAGTTCCAAGGAAAATG
AAGTTCAAACGGATGCCATACCCGTGAAACACAACAGTACACAACTGTTAAGAAGGAAG
CAGTCGACATGGTCTGCAAACTGAGCCTGTTGAAACATGTAATTTTCTGTTCAAACAT
TTGAAAGTGACGAAAAATTTATTTAGCAGAGCAATGCAAAACCAAAGCAATTGAAAGAAATATT
ACACAAGTGCAAAAGTATCAAATATTCCTTTTCGTTTCAAAAATTCACGTTAAGGTTGA
TTGAGAGTACATTTTCAAGCGTCAAGCTGAGTTTACTGTTCTGATGGAAAACATCCGGA
ATATGGATACTTTTTTTTACTGATCAATCGAGCATCCCTTTGGTGAAGCGTACAGTGCAGT
CTATCAATAATCTGTATACTTGGAGAATACCAAGGCTGAAATTCATTAATATTTGAGA
ATAATATCAAGTGTGAACAAATGCAAAATAACAAATGCTAACATTCAAGACCTGAAGGAAA
AAGTTACAGATTATGTCAGGAAAGATATTGCACAAATAACTGAAGATGTAGCCAATGCAA
AAGAGGAGTATCTGTTTTTAATGCATTTTGATGATGCTTCGAGTGGATACGTTAAAGATC
TCAGCACGATCAATTTAGAATGCAAAAGACATTACGTCAAAGCTATTTCGATGTGTCCG
CCAAAATTAATCATACTGAAGAGTTGCTGAACATTTTAAAATTGTTTCACTGTAAAGAATA
AGAGATTGGACGATAATCCATTAGTGGCAAACTAGCTAAAGAATCTCTTGCACGTGACG
GTTTACTAAAAGAAATCAAATTTATTCGCTGAGCAAGTGAGTAGGTTACAATTGGAGGAGA
AAGGTA AAAAGGCTTCGTCGTTTCGATGCATCTCTTCAATAACAAAGGACATGAAAGGAT
TTAAAGTAGTAGAAGTTGGGTTGGCCATGAATACGAAAAAGCAAATTGGTGATTTCTTCA
AAAATTTGAACATGGCAAAATAG

YIL115C, 1460 aa (SEQ ID NO 136)

MSSLKDEVPTETSEDFGFKFLGQKQILPSFNEKLPPASLQNLDISNSKSLFVAASGSKAV
VGELQLLRDHITS DSTPLTFKWEKEIPDVIFVCFHGDQVLVSTRNALYSLDLEELSEFRT
VTSFEKPVFQLKNVNNLTVILNSVNDLSALDLRTKSTKQLAQNVTSFDVTNSQLAVLLKD
RSFQSFARNGEMEKQFEFSLPSELEELPVEEYSPLSVTILSPQDFLAVFGNVISETDDE
VSYDQKMYIIKHIDGSASFQETFDITPPFGQIVRFPYMYKVTLSGLIEPDANVNVLASSC
SSEVSIWDSKVIEPSQDSERAVLPISEETDKDTPNIGVAVDVVTSGTILEPCSGVDITIE
RLPLVYILNNEGSLQIVGLFHVAAIKSGHYSINLESLEHEKSLSPTSEKIPIAGQEQUEEK
KKNNESSKALSENPTTSANTSGFTFLKTQPAANSLQSQSSSTFGAPSFSGSSAFKIDLPS
VSSTSTGVASSEQDATDPASAKPVFGKPAFGAIAKEPSTSEYAFGKPSFGAPSFSGSKSS
VESPASGSFAGKPSFGTPSFSGSGNSSVEPPASGSFAGKPSFGTPSFSGSGNSSAEPASGS
AFGKPSFGTSAFGTASSNETNSGSI FGKAAGSSSFAPANNELFGSNFTISKPTVDSPE
VDSTSPFPSSGDSQSEDESKSDVDSSSTPFGTKPNTSTPKPTNAFDGSSSFSGSFKALE
SVGSDTTFKFGTQASPFSSQLGNKSPFSSFTKDDTENGSLSKGSTSEINDDNEEHESNGP
NVSGNDLTDSTVEQTSSTRLPETPSDEDEGEVVEEAAQKSPIGKLTETIKKSANIDMAGLK
NPVFGNHVKAKSESPPSAFATNITKPSSTTPAFSFGNSTMNKSNTSTVSPMEEADTKETS
EKGPITLKSVENPFLPAKEERTGESSKDHNDPKDGYVSGSEISVRTSESADFDTTANEE
IPKSQDVNNHEKSETDPKYSQHAVVDHDKSKEMNETSKNNERSGQPNHGVQGDGIALKK
DNEKENFDSNMAIKQFEDHQSSSEDASEKDSRQSSSEVKESDDNMSLNSDRDESISESYDK
LEDINTDELPHGGEAFKAREVSASADFDVQTSLEDNYAESGIQTDLSESSKENEVQTDAL
PVKHNSTQTVKKEAVDNLQTEPVETCNFSVQTFEGDENYLAEQCKPKQLKEYYTSKVS
NIPFVSQNSTLRLESTFQTVAEFTVLMENIRNMDTFFTDQSSIPLVKRTVRSINNLYT
WRIPEAEILLNIQNNIKCEQMQITNANIQDLKEKVTDYVRKDIAQITEDVANAKEEYFLF
MHFDDASSGYVKDLSTHQFRMQKTLRQKLFDVSAKINHTEELNLILKLFVKNKRLDDNP
LVAKLAKESLARDGLLKEIKLLREQVSRQLLEEKGKKASSFDASSSITKDMKGFKVVEVG
LAMNTKKQIGDFPKNLNMAK

YIL148W, 1321 bp, exon1: 501-508, intron1: 509-942, exon2:
943-1321 (SEQ ID NO 137)

TCGATCAACTCTATCCAACAATTCTATAATATCCACTGTTTCATTAAACGAATATTGGTCTT

TTTCCCTTATGGTGAAGTAAATTTTCCATGCAATATCCGGGTAAGCTATCGACAAGTTTA
TTGACTGCAATTTGAGTTTATTACATCCGTACATTACTAAGATGTATGGTTTTCTATTT
TTGTGCTCCGTGTCGATATTTTCGTGGAGCAAACAGAAAAGATGCGGAACCTCTTAGCAC
TCCGCCTGGACATAGGCGGAGCATATTCCTCCTATGGGATGGGTTTTGTGTACTCTTTT
CTCTCTAGACAGGACCTCCGATTGCCTCCCTGAGGGTGAGATGGTTTTCCGGCCTCAGGAC
GGCCTTCTCCAGTTTCTAGCGAGGCATACATTCCAACCAAAGGTGTATCAAGAATATCTG
AAATTAAAGGTAGTTGAATCTCTATTTGTTGTTGTTATTACCGCTTATATCCCATAGTT
GAGACGACCAAGATTCAAACATGCAAATGTATGCACCATATCCATTCTAAACATAGTTTT
TCGAACGTTTCAGAGCTTAAAGGGACAATTATTTTAGAAACTGAATTTTTACCCAGTGGAA
TAACATCGTATCTGTAAAGTCTACAAAATTTTTATCCATCAAAAATTAACAAAGAAA
ACTGCCAAACTGAATATGAGGAACCTTCTCTCTAGGAATGACTTAGTGAATGTACAGTG
ACTTGTGGAAAATATGATTAGATTTTGTAGCGGGTGATGCGACTTAACAGTCTCATTGCCCT
AAGAAATATCCAAATTTGTGGTTTCATGCTCTCCCCAAGATATGACGATGAGAGCTCGTT
TAAATTTTTGTCTTCTTCCGAACAGTTATGAAAAAATATTACGTGTTTTATGATATCC
TTACTAACTTGTCAATTTTTTATAAAATTTATTTTAAACAGTTTGTCAAGACTTTGAC
TGGTAAGACCATCACTTTGGAAGTTGAATCTTCTGACACTATTGACAATGTCAAGTCAAA
GATTCAAGACAAGGAAGGTATCCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCA
ATTGGAAGACGGTAGAACCTTGTCTGACTACAACATTCAAAAAGAATCCACTTTGCACTT
AGTCTTGAGATTGAGAGGTGGTATCATTTGAACCATCTTTGAAAGCTTTGGCTTCCAAGTA
CAACTGTGACAAATCTGTTTGCCGTAAGTGTATGCTAGATTGCCACCAAGAGCTACCAA
CTGTAGAAAGAGAAAGTGTGGTCAACCAACCAATTGCGTCCAAAGAAGAAGTTAAATG
A

YIL148W, 128 aa (SEQ ID NO 138)

MQIFVKLTGKTTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRTLSDYN
IQKESTLHLVRLRGGIIIEPSLKALASKYNCDKSVCRKCYARLPPRATNCRKRKCGHTNQ
LRPKKKLK

YIL150C, 2216 bp, CDS: 501-2216 (SEQ ID NO 139)

AATATTCAACCTGAAGTTGCAGTCAAAGCGCGATTAACTTTTCCAACGTAACCGATCTA
ACTAACAATAGCACCGGATGGAGCAAAAATAACAGAAATTGGAAGTACATCTAAACGGCCA
ATTGAGAGCGGTACATCTTCTGATCCAGACACCAAAAAGGTTAAAGAGAGTCCAGCAAAAT
GATCAAGCTTCCAACGAGTGATGTAATATTAACAATGTAATTATATAAAATATGAAACAT
CTACATATTTTAAATGTCACTAATGTCAATTACAGAGGACATAAAGTGATTTATGACACAT
CCGTACTAGTAGTTAAGTATGAACAAATTTTGGGTTTATTTGCCATTTTTTTTCCACGCGG
GTTTCTTGGATGCGCAAAACCCACCTTTTCTAACACCACTAAGAAATATCAACTTTATAGG
CCATCGAAGATAAAGGAACGTAAGTTTGTCAATTCAACCTCACATTTTCAACGCACATTA
AGCACTTGGTTTCGTGGAGAAATGAATGATCCTCGTGAAATTTTAGCGGTTGATCCGTACA
ATAATATTACTTCTGATGAAGAGGATGAGCAAGCCATCGCGAGAGAACTTGAAATTATGG
AACGAAAGAGGCAGGCCTTAGTGGAACGATTAAAAAGAAAGCAAGAAATTTAAGAAACCCC
AGGATCCTAATTTTGAAGCCATCGAGGTACCTCAATCTCCTACCACCAACCGTGTGAAAG
TGGGGTCTCATAATGCTACACAACAAGGCACAAAATTCGAAGGTTGCAATATTTAATGAAG
TAAGGTTATCTCAATTACAGCAGCAACCAAAACCACAGCTAGTACAACCACATACTTTA
TGGAGAAATTTCAAACGCAAGAAGAAGCAAGATAAACAATTGCCAAGTTTGAAGCA
TGATGAATGCAAGAGTACATACGTTTCAGTACCGATGAGAAGAAATATGTGCCGATAATCA
CAAACGAATTAGAAAGCTTTTCAAATCTTTGGGTTAAAAAGAGGTACATACCTGAAGATG
ACTTAAAACGGGCTTTGCATGAGATCAAAATCCTTCGGTTGGGCAAACTTTTTTGCTAAAA
TTCGCCCACCTAAATTTCAAGAGCCTGAATACGCCAACTGGGGCCACCGTAGGCCCATTA
GCCACAAATCGGACATCAAATTTACATCATCTGAAAAGCCAGTCAAATTTCTTCATGTTCA
CCATAACGGACTTTTCAGCATACACTAGATGTTTATATCTTCGGGAAAAAGGGTGTAGAAA
GATATTATAATCTTCGCCTGGGTGATGTGATAGCAATATTAACCCAGAAGTACTACCAT
GGAGACCCTCAGGGCGAGGAAATTTATCAAATCCTTCAACCTTCGAATTAGTCATGACT
TCAAATGTATCCTGGAGATAGGTTCAAGTAGAGATTTAGGTTGGTGTCCCATAGTGAATA
AAAAGACTCACAAAAATGTGGCTCTCCCATTAACATATCTCTTCATAAGTGTGCGGATT
ACCATAGAGAAGTGCAATTTTCGTGGAACAAGTGCTAAAAGAATTGAATTAAATGGTGGGT
ACGCCTTGGGCGCGCTACGAAAGTGGAATCTCAACCAAGCCTATATAAGGCCAAAGGGG
AAAACGGGTTTAATATAATCAAAGGTACTCGTAAGCGCCTGTCAGAAGAGGAGGAAAGAC
TTAAAAAGAGCTCTCACAATTTTACGAATAGTAATTTCTGCCAAAGCATTTTTTCGACGAGA
AATTTTCAGAAATCCAGATATGCTGGCAAACTTAGACAATAAAGAAGGAAAAATAGAAA
CTAAGAAATCGACAGCACTGAGCCGCGAACTAGGCAAAATTTATGAGAAGGAGGGAATCCA

CGCGATTAGAAGATAAGAGCGTCGGAGAGCGACAGAAAATGAAACGAACACAGAAAGTG
CCCTCCAGACAGGGCTTATCCAACGCCTAGGATTCGATCCCACTCATGGAAAAATTTCCC
AAGTACTCAAGTCTTCTGTATCAGGGAGCGAACCTAAGAACAACCTTACTCGGTAAAAAAA
AAACTGTTATAAACGATCTCTTGCATTACAAGAAGGAAAAAGTCATTCTCGCACCTTCAA
AGAACGAATGGTTCAAGAAAAGAAGCCATCGCGAAGAAGTTTGGCAAAAACATTTCCGAT
CCAAGGAACTAAAGAACTTCTGACGGTAGTGCCAGCGATCTTGAGATAATATAA

YIL150C, 571 aa (SEQ ID NO 140)

MNDPREILAVDPYNNITSDEEDEQAIARELEFMERKRQALVERLKRKQEFKKPQDPNFEA
IEVPQSPTKNRVKVGSHNATQQGTFEGSNINEVRLSQLQQPKPPASTTTYFMEKFQNA
KKNEDKQIAKFESMMNARVHTFSTDEKKYVPIITNELESFNLWVKRYIPEDDLKRALH
EIKILRLGKLFKIRPPKFQEPEYANWATVGLISHKSDIKFTSSEKPVKFFMFTITDFQH
TLDVYIFGKKGVERYYNLRGLDVIAILNPEVLPWRPSGRGNFIKSFNLRI SHDFKCI LEI
GSSRDLGWCPVNVKTHKKCGSPINISLHKCCDYHREVQFRGTSAKRIELNGGYALGAPT
KVDSPSLYKAKGENGFNIIKGTTRKRLSEEEERLKKSSHFTNSNSAKAFFDEKFNPD
LANLDNKRRIIETKKSTALSRELKIMRRRESSGLEDKSVGERQKMKRTTESALQTGLI
QRLGFDPTHGKISQVLKSSVSGSEPKNNLLGKKKTVINDLLHYKKEKVILAPSKNEWFKK
RSHREEVWQKHFGSKETKETS DGSASDLEII

YIL167W, 1133 bp, CDS: 501-1133 (SEQ ID NO 141)

GACATTTTGA AAAAATTACATTTATAGAAGTTTATTATAACGTAACAGTTAACAACAAAG
GCTCATAGTCCGAGATCAATATAATAAATTATTCAAGGTTTAAGGAAGAAGTTACCATGG
AAATGACTTACTATGAAAAGACACCTTTGATTTCGTCAATTTTTGAACAATGGTAAGACAA
ATTTCGTGGTTTTACGTTAAGCATGAGATGTTACAACCAGGTGGAAGTTTCAAATCGAGAG
GAATCGGGCATTGATAAGGAAGAGTAATGAAGAAGCGCTAAGCGAGGGTTCTGGGAAGC
TTGCTGTATTTTCTAGCTCTGGGGGAAATGCTGGTTTAGCAGCAGCAACTGCCTGCAGAT
CGATGGCACTTAATTGCACTGTAGTGGTTTCTAAAACTACAAAACCTAGAATGGTAAAGA
AAATTCAAAGTGCAGGAGCCAAAGTCATTATCCATGGTGATCATTGGGGGGAAGCAGATG
AATACTTGAGGCACGAATGAATGGCGCAAGAAAGCCAACATGGTTTCAAGACACTATATG
TGCACCCGTTTGATAACGAGACAATTTGGGAAGGTCAATTCTACGATTGTGGATGAAATCA
TAGAACAATTGAAGGAAAAATGATATCCTTACCTAGGGTGAAAGCTTTGGTTTGTAGTG
TTGGTGGTGGTGGCTATTTAGTGGCATAAATTAAAGGCCTAGATAGGAATCAGCTTGCTG
AAAAAATTCGGTCTGCTGTAGAACTGCCGGTTGTGACGTATTGAATAAGTCTCTCA
AAAAAGGTAGTCCAGTTACTCTTGAAAAATTGACAAGTGTTGCAACTTCTTTGGCCTCCC
CATACATAGCATCATTCGCGTTTGAGAGTTTAAACAAGTATGGATGTAAGTCTGTAGTTT
TATCAGATCAAGACGTTCTGGCAACATGCTTGAGATATGCCGATGACTACAATTTTATAG
TGGAACCAGCCTGTGGAGCATCCTTACATTTATGTTATCATCCAGAGATTCTTGAAGACA
TTCTGGAACAAAAATATATGAGGATGATATCGTTATTATAATCGCATGCGGTGGATCAT
GTATGACGTATGAAGACTTGGTGAAAGCGTGCAGCACATTAAACGTATCATAA

YIL167W, 210 aa (SEQ ID NO 142)

MAQESQHGSKTLVHPFDNETIWEHSTIVDEIIIEQLKENDISLPRVKALVCSVGGGLF
SGIIKGLDRNLAEKIPVVAVETAGCDVLNKSLLKKGSPVTTLEKLT SVATSLASPIASF
FESFNKYGCKSVVLSQDVLATCLRYADDYNFIVEPACGASLHLCYHPEILEDILEQKIY
EDDIVIIIACGGSCMTYEDLVKASSTLNVS

YJL034W, 2549 bp, CDS: 501-2549 (SEQ ID NO 143)

CCATGAACTCAGCATGTGCTACTCCAGTTAATGACTTGTTTCGTATCGTTTCATGCCATAAG
CCATCACCTGGCCAGTTGGCGTATGTACAAAGATGCAAGCTACCGGTGTCTCATCGTGGT
CAAGAGCGTATCTAGCCAAACGGACAGCTGTCTCATATGTTTAAATATGCTGCATAGTGT
GAGTCCCTCTAGTTTTTACCAGCAGCCACCAGCCGCTTCTCGAGCAAAGTGATAGATCCCAT
AGGACTCATCATCTAATTTTGCTATGTTAGCTGCAACTTTCTATTTTAAATAGAACC
TTCTGGAATTTTACCCGGCGCGGCACCCGAGGAAGTGGACAGCGTGTGAAAAAGTTGC
TTTTTTATATAAAGGACACGAAAAGGGTTCTCTGGAAGATATAAATATGGCTATGTAATT
CTAAAGATTAAACGTGTTACTGTTTTACTTTTTTAAAGTCCCCAAGAGTAGTCTCAAGGGA
AAAAGCGTATCAAACATACCATGTTTTTCAACAGACTAAGCGCTGGCAAGCTGCTGGTAC
CACTCTCCGTGGTCCCTGTACGCCCTTTTCGTGGTAATATTACCTTTACAGAATCTTTCC
ACTCTTCCAATGTTTTAGTTAGAGGTGCCGATGATGTAGAAAACTACGGAAGCTGTTATCG
GTATTGACTTAGTACTACTTATTCTGTGTTGCTGTGATGAAAAATGGTAAGACTGAAA
TTCTTGCTAATGAGCAAGGTAACAGAATCACCCCATCTTACGTGGCATTACCGATGATG

AAAGATTGATTGGTGTATGCTGCAAAGAACCAAGTTGCTGCCAATCCTCAAAACACCATCT
TCGACATTAAAGAGATTGATCGGTTTGAAATATAACGACAGATCTGTTTCAAGGATATCA
AGCACTTGCCATTTAATGTGGTTAATAAAGATGGGAAGCCCGCTGTAGAAGTAAGTGTC
AAGGAGAAAAGAAGGTTTCTACTCCAGAAGAAATTTCTGGTATGATCTTGGGTAAGATGA
AACAAATTGCCGAAGATTATTTAGGCACTAAGGTTACCCATGCTGTCTGTTACTGTTCCCTG
CTTATTTCAATGACGCGCAAAGACAAGCCACCAAGGATGCTGGTACCATCGCTGGTTTGA
ACGTTTGTGAGAAATTGTTAATGAACCAACCGCAGCCGCCATTGCCTACGGTTTGGATAAAT
CTGATAAGGAACATCAAAATTATTTGTTTATGATTTGGGTGGTGGTACTTTTCGATGTCTCTC
TATTTGTCTATTGAAAACGGTGTCTTTCGAAGTCCAAGCCACTTCTGGTGATACTCATTTAG
GTGGTGAAGATTTTGACTATAAGATCGTTTCGTCAATTGATAAAAGCTTTCAAGAAGAAGC
ATGGTATTGATGTGTCTGACAACAACAAGGCCCTAGCTAAATTGAAGAGAGAAGCTGAAA
AGGCTAAACGTGCCTTGTCCAGCCAAATGTCCACCCGTATTGAAATTGACTCCTTCGTTG
ATGGTATCGACTTAAGTGAAACCTTGACCAGAGCTAAGTTTGAGGAATTAAACCTAGATC
TATTCAGAAGACCTTGAAGCCTGTGCGAGAAGGTTTTGCAAGATTCTGGTTTGGAAAAGA
AGGATGTTGATGATATCGTTTGGTTGGTGGTTCTACTAGAATTCCAAGGTCCAACAAT
TGTTAGAAATCATACTTTGATGCGTAAGAAGGCCCTCCAAGGGTATTAACCCAGATGAAGCTG
TTGCATACGGTGCAGCCGTTCAAGCTGGTGTCTTATCCGGTGAAGAAGGTGTGCAAGATA
TTGTTTATTGATGTCAACGCTTTGACTCTTGGTATTGAAACCACTGGTGGTGTCTATGA
CTCCATTAATTAAGAGAAATACTGCTATTCTTACAAAGAAATCCCAAATTTTCTCTACTG
CCGTTGACAACCAACCAACCGTTATGATCAAGGTATACGAGGGTGAAAGAGCCATGTCTA
AGGACAACAACTTATTAGGTAAAGTTGAATTAAACCGCACTTCCACCAGCACCAGAGGTG
TACCTCAAATTGAAGTCACATTTGCACTTGACGCTAATGGTATTCTGAAGGTGTCTGCCA
CAGATAAGGGAACTGGTAAATCCGAATCTATCACCATCACTAACGATAAAGGTAGATTAA
CCCAAGAAGAGATTGATAGAATGGTTGAAGAGGCTGAAAAATTTCGCTTCTGAAGACGCTT
CTATCAAGGCCAAGGTTGAATCTAGAAACAAATTAGAAAACTACGCTCACTCTTTGAAAA
ACCAAGTTAATGGTGACCTAGGTGAAAAATTGGAAGAAGAAGACAAGGAAACCTTATTAG
ATGCTGCTTAACGATGTTTGAATGGTTAGATGATAACTTTGAAACCGCCATTGCTGAAG
ACTTTGATGAAAAGTTGGAATCTTTGTCCAAGGTCGCTTATCCAATTACTTCTAAGTTGT
ACGGAGGTGCTGATGGTTCTGGTGCCGCTGATTATGACGACGAAGATGAAGATGACGATG
GTGATTATTTCGAACACGACGAATTGTAG

YJL034W, 682 aa (SEQ ID NO 144)

MFFNRLSAGKLLVPLSVVLYALFVVILPLQNSFHSSNVLVRGADDVENYGTVIGIDLGT
YSCVAVMKNGKTEILANEQGNRITPSYVAFTDDERLIGDAKNQVAANPQNTIFDIKRLLI
GLKYNDRSVQKDIKHLFPNVVNKDGKPAVEVSVKGEKKVFTPEEISGMILGKMKQIAEDY
LGTVKTHAVVTVPAYFNDAQRQATKDAGTIAGLNLVRIVNEPTAAAIAYGLDKSDKEHQI
IVYDLGGTTFDVSLLSIENGVFVQATSGDTHLGGEDFDYKIVRQLIKAFKKKHGIDVSD
NNKALAKLKREAEKAKRALSSQMSTRIEIDSFVDGIDLSETLTRAKEELNLDLFKKTLK
PVEKVLQDSGLEKKDVIDVLVGGSTRIPKVQQLLESYFDGKKASKGINPDEAVAYGA
QAGVLSGEEGVEDIVLLDVNALTGLIETTGGVMTPLIKRNTAIPTKKSQIFSTAVDNQPT
VMIKVYEGERAMSKDNLLGKFELTGIPAPRGVPQIEVTFALDANGILKVSATDKGTGK
SESITITNDKGRLTQEEIDRMVEAEKFASEDASIKAKVESRNKLENYAHSLNQVNGDL
GEKLEEDKETLLDAANDVLEWLDNDFETAIAEDFDEKFESLSKVAYPITSKLYGGADGS
GAADYDDEDEDDGDYFEHDEL

YJL035C, 1253 bp, CDS: 501-1253 (SEQ ID NO 145)

TACCTAAGTCAATACCGATAACAGTTCGGTAGTTTCTACATCATCGGCACCTCTAACTA
AAACATTGGAGGAGTGGAAAGAATTCTGTAAAGGTAATATTACCACGAAAAGGGCGTACA
GGACCACGGAGAGTGGTACCAGCAGCTTGCCAGCGCTTAGTCTGTTGAAAAACATGGTAT
GTTTGATACGCTTTTCCCTTGAGACTACTCTTGGGGACTTTAAAAAAGTAAACAGTAA
CACGTTAATCTTTAGAATTACATAGCCATATTTATATCTTCCAGAGAACCCTTTTCGTGT
CCTTTATATAAAAAAGCAACTTTTTCGACACGCTGTCCAGTTCTTCGGGTGCCGCGCCGG
GTGAAATTTCCAGAAGGTTCTATTAATAAGAAAGTTGCAGCTAACATAGCAAAATTAGA
TGAAATGATGAGTCTTAATGGGATCTACACTTTGCTCGAGAAGCGGCTGGTGGCTCGGTA
AAAAGTAGAGGACTCACACTATGCAGCATATTAAACATATGAGGACAGCTGTCCGTTTGG
CTAGATACGCTCTTGACCACGATGAGACACCGGTAGCTTGCATCTTTGTACATACGCCAA
CTGGCCAGGTGATGGCTTATGGCATGAACGATACGAACAAGTCATTAACCTGGAGTAGCAC
ATGCTGAGTTTCATGGGGATCGATCAGATCAAGCGCATGTTGGGCTCCCGAGGAGTTGTTG
ACGTGTTCAAAGACATTACTCTATATGTTACTGTAGAACCCTGTATAATGTGTGCATCTG
CTCTCAAGCAATTAGACATTGGAAGGTGGTGTTCGGTTGTGGCAACGAGAGATTGAGAG

GCAACGGTACTGTCCTTGTACAGTAAATCATGATACGTGTACATTAGTGCCCAAGAACAATA
GTGCGGCAGGGTACGAGAGTATACCGGGGATCTTGAGGAAAGAAGCAATAATGCTGCTGA
GATACTTTTATGTAAAGACAAAATGAAAGGGCGCCAAAGCCACGGTCCAAGAGTGACAGAG
TGTTGGATAAAAACACGTTTCCGCCTATGGAATGGTCAAAGTATCTTAATGAAGAAGCAT
TCATTGAGACTTTTGGTGATGATTACAGGACTTGTTTTGCGAATAAAGTTGACTTGTCCA
GTAATAGCGTCGATTGGGATTTGATTGACTCCACCAAGATAATATAATCCAAGAAGCTGG
AAGAACAATGCAAAATGTTTAAGTTTAATGTACATAAGAAATCTAAGGTTTGA

YJL035C, 250 aa (SEQ ID NO 146)

MQHIKHMRTAVRLARYALDHDETPVACIFVHTPTGQVMAYGMNDTNKSLTGVAHAEFMGI
DQIKAMLGSRGVVDVFKDITLYVTVEPCIMCASALKQLDIGKVVFGCGNERFGGNGTVLS
VNHDCTCLVPKNNSAAGYESIPGILRKEAIMLLRYFYVRQNERAPKPRSKSDRVLDKNTF
PPMEWSKYLNEEAFIETFGDDYRTCFANKVDLSSNSVDWDLIDSHQDNIIQELEEQCKMF
KFNVHKSKV

YJL070C, 3167 bp, CDS: 501-3167 (SEQ ID NO 147)

TCCCTGATGGTCAAATACTGTGCATGGCATCCCGTGCAGTCAAGGATGCTTTGAGACTA
GTTTCATCTGCCCTTCTTGTAGCGTGTTCAGCAACTGGCCTACCAGCGGGACGCCCTTTGGGT
AAAGTTACCAGTGTTCGCATTTTCGCCATCTGGTGGGCTACTGGCCGTGGGTAACGAACAA
GGTAAAGTGAGGCTCTGGAAATTAACCCTACTAAATTTCCATTTATAGACAACTTAG
ATATTAAGCAATGTACAAATACATACAAAAATATCACTGTAAAAAATGCGAAGAA
ACTTGAATTTGAATATGATTCTGCCCACTTTTCTTGCTGCTCATTATAGTCAGAAATG
AAAAATGTCCGAGAAATTAATATAATATATGAAAAAAGGGGACATTGAGTTTAAAG
AATTTGATTAAATGTCTCTCAATATCCTCTGTAAGAGTTATCTAAATCTCACTTTACT
TATTCATCTCGCTGGGAATTATGCAGCGGTAGAGAGAAGGCCCTCGTTACTCTTTGACG
AATATCAAAATTCGTACTAAGCCTAATGAGACGAAGAATAAAGAAGCCAGGGTCTTGT
CAGAGAAATGACGGTGATGTCTCCCATCTGTTTGAACACAGAAGAAATATCAGTCGATG
ATATGGATATGATTCTTTGCCACCGAATTTGACAGGCAATGGTTTTAGGTTACCTA
TGTTTTTCGATCTTGAAGACGAAGAAAACAAATTTGATCCACTTCCTTCAGTTTCCCATC
ATTATGGAATGGAGAAAGTGACAGCTTTGTCTCATCGTACACGCCCTCAAATCTGAAAA
CGGGTGAAGAACTAAAGATCTTTTCATTAATCCGTTTGAATTTGGTTTTCTCAAATGAGAA
AAGATACATTTGCTGCTTCCAAACAAGATGGCATTTCAAACATAAAAAATGACACTGAAA
AGTGGTTTTTATACCCAAAACCACTGCCAAAGTTTGGAGATTGAAGACGATAAACGAT
TCCAAGATCCCTCTGACTCTGACTTAAATGACGATGGAGACAGTACTGGGACCGGAGCCG
CTACACCGCACCGCCATGGCTACTATTACCCAAGTTACTTTACCGATCACTACTACT
ACACAAAATCTGGTTTGAAGGAAAAGGAAATATAAAAGTACCATACACCGGTGAATATT
TCGATTTAGAGGATTACAAAAACAATACATTTACCATTAAAGTAATCAGGAAAATACGC
AAAACCCACTTTACCTTATTCTAGTAAGGAGGAGTCACTAGAGGAAGAATTTTACAG
ATGTGCCCTACGTTTCAAGAATTTAGGGATGATTTTGATACATAATAGAGTTAATCCAAT
CTCATAAATTCACGAGGTTTACGAAAGCGATTATCTTATTTATTAGATAAATTTGAAT
TGTTTCAGTACCTAACTCTAAGAAAGAAATTTAGCTAATAAAATGTTCCCTACAGAG
ATTTTTATAATCTCGTAAGGTAGATCGAGACTTGTCTTTAAGTGGTTGTATTTCTCAAC
GTCAATTGAGTGAATATATATGGGAGAAAATAAATTTAGAACCTGAAAGGATAGTTTATC
AAGACCCGGAACGTCAAGGAACTCAGTTTGAGAGACATTTTTCAGTTTGGTTGTCTCT
CTAATGACCAACCCATTGCGATTGGGTTGAAATTTGATTGATGATGAATTTTGGATTGGT
ATAGAAATATTTACCTAATAGATTACCATCTAACTCCTAACAAAGTAGCAAAGTTGGTCG
GCAAAGAAATGAGGTTTTACCTATTAGCCAAAGTGTTTCTGGAGTTTGATAATTTTCATTG
AAGGTGAGTACCTAGCAGAAATTTTCAAAAATACGTTATTTCATATCCTCGAAAAATCAA
AGTACCAATTTGGCCCAAGTATCAGTTAATTTTCAATTTCTATTCCAGTGGTGAAGACTGGT
ACAAGAAATTTTCTCAATGGTTGCTACGATGGAAGCTAGTATCGTATAATATCCGCTGGA
ATATACAAATTTGCCAGGATTTTTCCCAAACTATTCAAGGAAAATGTCTGTCAAATTTCC
AGGAGTTTTTGGATCTTATCTTCAATCCTTTATTCACTCTGGAAGAGGAGCAGTTACCAA
TAGATTCATCTGTAAATACTGATATCATTTGGTCTGCAGTTTTTTTATCAAATGTGTGTT
CTATGGATCTGGTCATTAAAGAGTCGATGAATATTACTGGAAGAATTTTACTGATATGA
ATTGTAAGCCAAAATTTTGGACAGCACAGGGTGACAATCCAAGTGTGCGCATTACATGT
ATTATATTTATAAAAGTTTAGCGAAAGTTAATTTCTGCGGTCACAAAATCTTCAAATA
CAATCACCTTAAGAAATTTATGTTCTCACTATCCAGCAGAACTTCCAATTTGGAGTGG
ATTTATATTTTACAGATCAAGTTGAATCGTTAGTGTGCAACTTACTGCTTTGTAATGGTG
GTCTGTACAGGTAGAACCCTTTGGGATACTGCAACAATGATTCAATATTTATTTTATC
TCTTTCAAATACCCATTTTAGCTGCGCCATTATCATCTGTTTCATTACTGAATTCGCAA

AATCGACCTTTTGAAGAATAAAAAACGTGCTTCTAGAACATGATTATTTGAAAGACCAGG
AAACAGCCAAAATCAATCCTTCTAGAGATATCACTGTGGGCGAACAAAGATCATATGAGA
CAAATCCTTTTCATGAAAATGTTTAAGATGGGACTAAAAATTTCTTTATCATCAAAATCGA
TTCCTTTACAATAGTTCATACACGCTAGAACCTCTCATTGAAGAATACAGTGTAGCAGCAA
GTATTTACTTGCTGAACCCAACAGATTGTGTGCGAGTTGTGCGAGAACAAGTGTGCTATCTA
GTGGCTATGAAGGTTGGTACAAGGCTCATTGGATTGGCGTTGGAGTTAAAAAGGCGCCTT
ACTTTGAGGAGAACGTGGGTGGGATAGATAATTGGTACGATACAGCGAAAGATACCTCGA
TAAAGCACACGTTCCGATGATTAGAAGAAGATATAGAAAGGAGACATTGGATCAAGAGT
GGAACCTTCGTTCCGGATCACTTTGGAGTAATTAACCTCCATTTGGTAG

YJL070C, 888 aa (SEQ ID NO 148)

MQAVERRRPSLLFDEYQNSVTKPNETKNKEARVLSNDGDVSPSVLKQKEISVDDMDMISL
PTEFDRQMVLSGPMFFDLEDEENKIDPLPSVSHHYNGESDSFVSSYTPSNLKTGEETKD
LFINPFELVSQMRKRYIAASKQDGISNIKNDEKWFLYPKPLPKFWRFEDDKRFQDPDS
DLNDDGSDSTGGAATPHRHGYYPYFTDHYHYTKSGLKKGKNIKVPYTGFEYDLEDYK
KQYIYHLSNQENTQNPSPYSSKEESLEEEFLTDVPTTFQEFRDDFAYIIELIQSHKFNEV
SRKRLSYLLDKFELFQYLSKKEILANKNVPYRDFYNSRKVDRDLSLGCISQRQLSEYI
WEKINLEPERIVYQDPETSRKLSLRDIFQFGCSSNDQPIAIGLKLIDDEFDLDWYRNIYLI
DYHLTPNKVAKLVGKEMRFYLLAKVFLEFDNFIEGEYLAEIFIKYVIHILEKSKYQLAQV
SVNFQFYSSGEDWYKFSQWLLRWKLVSYNIRWNIQIARIFPKLFKENVVSNFQEFDLI
FNFLTKEQLPIDSSVNTDIIGLQFFLSNVCSMDLVIKESDEYWKFEFTDMNCKPKFW
TAQGDNPVVAHYMYIYKSLAKVNFLRSQNLQNTITLRNYCSPLSSRTSQFGVDLYFTDQ
VESLVCNLLLCNGGLLQVEPLWDATMIQYLYLFQIPILAAPLSSVSLNSQKSTFLKN
KNVLEHDYLDQETAKINPSRDIIVGEQRSYETNPFMKFMGLKISLSSKSILYNSSY
TLEPLIEEYSVAASIYLLNPTDLCELSRTSVLSSGYEGWYKAHWIGVGKAPYFEENVG
GIDNWYDTAKDTSIKHNVPIMRRRYRKETLDQEWNFVRDHFVINSIW

YJL078C, 3146 bp, CDS: 501-3146 (SEQ ID NO 149)

TTTTTCTTCGCACATGGCTGGTTCCTGCTGGAGGCGGCTGGGTGTTTATAGTTACCGCAAT
GCAGGTCGCTTCGTTTACTTTTCTCTGCGTGCTCGAGAACTGATAAAATACTGGTTTAGGA
AAACCGTCCACTTATGGATTTAACAAGGAGGTGAAAGGTAGGTACCATGGCAATATAGCT
AGCAACGCTACGCACTAGCTGTGTGCTTGCTCTCTTGTTGTTTCGTCTTTTCGTATATTCG
GGGTTCGCCGCGTTAATTCAACAACAAATATGGTATCTAGGCAGGACCCAGCAACGGAA
GGATGTAATTGCTATATAGGGCCGATGAAACAGTTCTCATGTTTCAACTCGGTGCAAGAA
TTCTCTAAAACATATTTCTATACTTCAAAGTTTCTAGCTTCTTGCTTTTCGGTAGTTGCCA
AACCAATATCGGCATAAAATTATAATTGCTGCACCCCTGCAACTCCAAACAACCTAAAAC
AACTTAAAACGAAAACGCTTATGCTGGAGTTTCCAATATCAGTTCTGCTAGGATGCCCTAG
TAGCCGTCAAGGCACAAACCACGTTTCCAAACTTCGAGAGCGATGTGCTGAACGAGCATA
ACAAGTTCAGAGCGCTACATGTTGACACAGCGCGCTCACCTGGTCCGACACTCTGGCCA
CCTATGCGCAGAACTACGCCGACCAATATGATTGTTTCGGGTGTCTTAACGCATTCCGATG
GCCCATATGGTGAGAACCTTGCCCTTGGTTACACAGACACGGGAGCGGTGGACGCCCTGGT
ACGGGGAGATAAGCAAGTATAATTATCAAATCCCGGATTTCTGAATCCACGGGTCACT
TCACACAGGTGGTTTGAAGTCAACCGCCGAGATTGGATGTGGTTATAAATATTGTGGTA
CGACATGGAACAATTATATTGTGTGCTCCTACAACCCTCCTGGAACTACCTGGGTGAGT
TTGCAGAGGAAGTGAACCACTTATAAGCACTGTTTCTCTGCTCCTCATCCTCGTCTCTT
CTACCTCAACTACATCAGACACAGTCTCCACCATCTCATCCAGTATTATGCCCGCTGTAG
CGCAAGGGTATACAACAACGGTATCGTCTGCGGCTAGCAGCAGTTCTTTAAATCGACGA
CCATAAACCTGCCAAGACCGCTACCCTCACTGCGTCTCTTCTACCGTAATTACTAGTA
GCACAGAATCAGTTGGATCCTCCACTGTCTCATCAGCCTCAAGCTCTTCTGTCACTACTT
CCTATGCTACCTCCTCGAGTACCGTCTGCTCTAGTGATGCTACTTCACTCACTACCACCA
CCTCATCGGTTGCTACATCGTCCAGTACCACCTTCTCCGACCCTACCTCGAGCACTGCTG
CTGCTTCTTCTTCTGATCCTGCCTCAAGTTCGGCTGCCGCTTCTTCCAGCGCGAGTACCG
AGAACGCCGCTTCTTCTAGCAGCGCCATCTCGAGCTCTTCAATCAATGGTTTCTGCTCCTT
TGAGTAGTACTTCTACTACTTCCACCGCAAGCTCCAGAAGTGAACCTTCAATTCAGTTA
ATTCTGTTAAGTTTGCAAACACAACCTGTGTTTTCTGCTCAAACAACCTCTTCTGTAAGCG
CCTCATTATCATCATCTGTAGCTGCTGACGATATTCAGGGTAGCACTTCCAAGGAGGCCA
CAAGCTCAGTTTCCGAACATACTAGTATAGTAACTAGTGCAACTAATGCTGCCAATATG
CAACGAGACTTGGGTCACTTCCAGAAGTCTTCCGGGGCCGCTCTTCTCCTCAGCTGTGT
CGAATCTGTTCTGAATTCCGTTATAGCCGTCAACACCGACGTATCTGTAACTCAGTTA
GTAGCACAGCCCATACCACAAAGGACACCGCCACCCTCAGTAACCGCTCAGAAAGTA

TCAC TTCG GAAACTGCTCAGGCTTCAAGTTCAACAGAGAAGAATATTAGTAACAGTGCCG
CCACATCGAGTAGCATTTACTCCAACAGTGCTTCTGTGTCAGGACACGGTGTAACATACG
CTGCCGAATACGCCATTACATCCGAGCAATCCTCTGCGCTTGCCACATCTGTGCCTGCTA
CAAATTGCTCTAGTATCGTGAAGACCACAACCTTAGAAAATTCGAGTACCACAACCATCA
CAGCCATTACTAAGAGTACTACAACCTTGGCCACTACTGCTAACAACCTCCACAAGGGCAG
CTACCGCAGTAACCATAGATCCCACATTGGACCCTACCGACAACCTCAGCTAGTCCAACCG
ACAATGCTAAACACACCTCTACATATGGATCTTCTTCCACAGGCGCATCTTTAGATAGCT
TACGCACAACCACCAGTATTAGTGTCTCAAGCAACACCACACAGTTAGTCTCTACCTGCA
CTTCCGAGAGCGATTATTCCGATAGTCTAGCTTTCGCCATCTCCACTGCCACCACCACCTG
AAAGCAATCTGATCACAACACCATCACAGCTTCTTG TAGTACGGATAGTAATTTCCCTA
CCTCCGCTGCTTCTTCTACAGATGAGACGGCTTCACTAGAACAATCTCGACATCTTGTA
GCAC TTTGAACGGCGCTCAACCCAAACAGTGAGCTAACCACATCGCCTATGAAAACCA
ACACGGTGGTTCCAGCTTCTTCTTCCCTTCAACTACAACCACTTGTCTAGAAAATGATG
ACACTGCC TTTTCTAGTATCTACACTGAAGTCAACGCCGCAACTATCATTAAACCCGGAG
AAACATCTTCTCTGCTAGCGATTTCGCCACATCTGAAAAGCCAAACGAGCCCACTTCTG
TCAAATCCACCTCAAACGAAGGCACCTCTTCCACAACAACAACCTACCAACAGACTGTTG
CTACACTGTATGCCAAGCCCTCCAGCACAAGCCTAGGTGCAAGAACAACCTACTGGTAGCA
ACGGTCGTTCAACTACCAGCCAACAGACGGGTCTGCCATGCATCAGCCAACCTTCTCCTGA
TCTACACTCAACTAAAAGAAGGCACATCAACCACCGCAAACTTTCTGCATACGAAGGTG
CTGCAACACCTCTTTCATTTTCCAGTGCAATAGTCTAGCTGGAACGATTGCCGCTTTTG
TCGTAGCTGTTCTGTTCCGCTTCTAG

YJL078C, 881 aa (SEQ ID NO 150)

MLEFPISVLLGCLVAVKAQTTFPNFESDVLNEHNKFRALHVDAPLTWSDTLATYAQNYA
DQYDCSGVLTHSDGPYGENLALGYTDGAVDAWYGEISKYNYSNPGFSESTGHFTQVVK
STAEIGCGYKCGTTWNNYIVCSYNPPGNYLGEFAEEVEPLISTVSSSSSSSSSTSTSD
TVSTISSSIMPAVAQGYTTTVSSAASSSSSLKSTTINPAKTATLTASSSTVITSSTESVGS
STVSSASSSSVTTSYATSSSTVSSDATSSTTTSSVATSSSTSSDPTSSTAASSSDP
ASSSAAASSSASTENAASSSSAISSSSMVSAPLSSTLTSTASSRSVTSNSVNSVKFAN
TTVFSAQTTSSVSASLSSSVAADDIQGSTSKEATSSVSEHTSIVTSATNAAQYATIRLGS
SRSSSGAVSSSAVSQSVLNSVIAVNTDVSSTSVSSSTAHTTKDTATTSVTASESITSETAQ
ASSSTEKNISNSAATSSSIYSNSASVSGHGVTYAAEYAITSEQSSALATSVPATNCSSIV
KTTTLENSSTTTITAITKSTTTLATTANNSTRAATAVTIDPTLDPTDNSASPTDNAKHTS
TYGSSSTGASLDSLRTTTSISVSSNTQLVSTCTSESDYSDSPSFAISTATTTESNLITN
TITASCSSTDSNFTSAASSTDETAFTRTISTSCSTLNGASTQTSSELTTSPMKTNTVVPAS
SFPSTTTTCLENDDTAFSSIIYTEVNAATIINPGETSSLASDFATSEKPNEPTSVKSTSN
GTSSTTTTYQTVATLYAKPSSTSLGARTTTGSGNRSTTSQQDGSAMHQPTSSIIYTLKE
GTSTTAKLSAYEGAATPLSIFQCNSLAGTIAAFVAVLFAF

YJL179W, 830 bp, CDS: 501-830 (SEQ ID NO 151)

TTGCATTATCAACTATAATTCCATTTCCTAGAGGAGTTTTTATAGTCCTGCCATCTAATT
GTAGAGCAATCTTTCCCTTTCTCAACATCCCTATTAGTGACACCTTTCCCAAACTTCT
GTGAAGTTTTGCTCAATCTATTGTTTCCGCTAGGAGTGTTATTCTCAATCGTGTTGTCTG
TCCCCAGTGGCTGGGCATTTAATGAGTAGAATCGGGCAGTTTCAATCTTATGGAATTCA
CAATGAAGCATCCCTTCCTTAATGATGGCAGCATTCCTGATTCTCTTTGTAGGGTTTTCG
TTTGCCTTCAAGTGTTTTGTTCTTATTTAGCCTTTTCTTTACCTTAATTTTTTTCTTTT
CTCTGAAGAAAATGAATGAGTTTAAAGATATAGCAATTAAAAAGTAACAGTGAAGAAATT
TCTCAGATGAGCAGATGGGAATTAAAGAACTATCTACAGAGCTCTTTACTAAATTGAATC
AATAATACATACTTACAAACATGTCACAGATAGCACAAGAAATGACAGTGAGCTTAAGAA
ACGCCAGGACACAATTGGATATGGTCAATCAGCAGCTAGCATATTTGGACAGACAAGAAA
AGCTTGCTGAATTGACAAAGAAAGAACTAGAGTCTTATCCAACGGACAAAGTATGGAGAT
CTTGCGGTAATCGTTTATCTTACAGGATAAATCCAAATACGTTAATGATTTATCACATG
CCGAAACTGTTCTTCTGGATCAAAGAAAAACATTAAGATAAAGAAAGAACTATTTAGAAA
CTACTGTTGAAAAACAATAGACAATCTAAAGGCATTGATGAAGAATTAA

YJL179W, 109 aa (SEQ ID NO 152)

MSQIAQEMTVSLRNARTQLDMVNQQLAYLDRQEKLAELTKKELESYPTDKVWRSCGKSFI
LQDKSKYVNDLSHAETVLLDQRKTLKIKKNYLETTVEKTIDNLKALMKN

YJL180C, 1478 bp, CDS: 501-1478 (SEQ ID NO 153)

AATAGTTCCTTCTTTATCTTTAATGTTTTCTTTGATCCAGAAGAACAGTTTCGGCATGTG
ATAAATCATTAACTGATTTGGATTTATCCTGTAAGATAAACGATTTACCGCAAGATCTCC
ATACTTTGTCCGTTGGATAAGACTCTAGTTCTTTCTTTGTCAATTCAGCAAGCTTTTCTT
GTCTGTCCAAATATGCTAGCTGCTGATTGACCATATCCAATTGTGTCTGGCGTTTCTTA
AGCTCACTGTCTATTTCTTGTGCTATCTGTGACATGTTTGTAAAGTATGTATTATTGATTCA
ATTTAGTAAAGAGCTCTGTAGATAGTTCTTTAATTCCCATCTGCTCATCTGAGAAATTTTC
TTCAGTGTACTTTTTAATGCTATATCTTTAAACTCATTCAATTTTCTTCAGAGAAAAGA
AAAAAATTAAGGTAAAGGAAAAGGCTAAATAAGAACAAAACACTTGAAGGCAAACGAAAC
CCTACAAAAGAGAATACGGAATGCTGCCATCATTAAAGGAAGGGATGCTTCATTGTGAATT
CCATAAGATTGAACTGCCCCGATTCTACTCATTAAATGCCAGCCACTGGGGACAGACA
ACACGATTGAGAATAACACTCCTACGGAACAAATAGATTGAGCAAAAC'TTCACAGAAGT
TTTGGGAAAAGGTGCTACTAAATAGGGATGTTGAGAAAGGAAAGATTGCTCTACAATTAG
ATGGCAGGACTATAAAACTCCTCTAGGAAATGGAATTATAGTTGATAATGCAAAGTCTC
TCTTAGCATACCTATTAAAACTGGAGTGGTCTGCTCCCTATCCAGTCTTTCCATCAAACTC
ACTCTTTGCCACTAACTTCATTAGTGGCAAGATGCATAGATTTACAAATGACAAATGAGC
CTGGCTGTGACCCCTCAATTAGTTGCAAAAGATTGGAGGCAACAGTGATGTTATAAAAAATC
AGTTGTTAAGATATTTAGATACCGATACTTTATTGGTCTTTTCCCCTATGAATGAGTTTG
AAGGAAGATTACGCAATGCGCAAAATGAGTTATATATACCCATCATCAAAGGAATGGAAG
AGTTTTTACGCAACTTTTCATCCGAGTCTAATATTGCACTACAAATTTTAGATGCCGACA
TCCATGGGTTACGAGGCAATCAGCAGTCCGATATCGTTAAGAATGCAGCAAAAAAATATA
TGACAGCTTTATCACCATGGGATCTTGCAATTCTTGAAAAAACTGTATTAAACCAAGAT
CCTTCATTGTGCGCGTGCTATTATTAGAAAATAAAAAAGATACTGCGAACTTAAT'TCCCG
CCTTGAAAACGTATATGGATAATATTGTACGTGCCGCCACCTTAGAAACAATCTTCCAAG
TTGAAAAGTGGGGAGAGGTTGAAGATACTCATGACGTTGACAAAAGAGACATCAGAAGAA
AAATTCATACTGCTGCGATTGCTGCTTTTAAGCAATAA

YJL180C, 325 aa (SEQ ID NO 154)

MLPSLRKGCFFIVNSIRLKLPRFYSLNAQPLGTDNTIENNTPTETNRLSKTSQKFWKVS
NRDVEKGKIALQLDGRITIKTPLNGIIVDNAKSLLAYLLKLEWSSLSLSIKTHSLPLTS
LVARCIDLQMTNEPGCDPQLVAKIGGNSDVIKQLLRDLDLTLVFSMNEFEGRRLNA
QNELYIPIIKGMEFLRNFSSSNIRLQILDADIHGLRGNQSDIVKNAKKYSSLS
DLAILEKTVLTKSFICGVLLLENKKDTANLIPALKTMDNIVRAATLETIFQVEKWGEV
EDTHDVKRDIRRKIHTAAIAAFKQ

YJL181W, 2336 bp, CDS: 501-2336 (SEQ ID NO 155)

GCAAGTCAGTACGATGCATCCTTGGATCAAGAAGGTGAGTCTGGAACGGTGCTTCTAAT
GGCGATGTTTACCATTATAATGAAGGGGACTTGGCTGCCTCCTTCAAGGGATGTAGATCA
AGAGGTACGTGTGCTAGTGAAATAGGTACATGTACCAGAAAATCAAGAAATCTTAGATG
TGTGTAATCTTGCAATTTAGTTTCAAACAAGATCCTTGTATTTATATAAACAAGATATA
ATTTTTAAAAAATTTAGAAAAAGCAAATATAATTCAGGTCCCACTTGAATAATGGCA
CTGTATTGATGCATTTTCTTATGCTTAGTGACGCGTTTTTCGCGCGTCAGTTTCAAGTTT
TCTTTGGCTTTTTTTTTTTTCATTTTCGTAAAGGTCTTAAAGGATTAAAAATGCAGTA
TTGAAATAAAGAACAATTACGAACGGTGAAGCTGCTATTTTGGTTATTATACCCCTCCAG
GACAGTACGCGCAAACATTTATGGAGATATTCAAGGAAGAAGAAGAAGCTTTTTCCG
CGATAGAAGGTATAATATATGCTGTGAGGTGTATGACCCTGTACCCCGTCATTTACATA
AAAGCAAAACAAAGATCATCAATGCTGTCTAAATTAATTATAGAAACGCATCTTTTCATATT
ATACAATACTCAATAACATTTTCAGATATACAAGCCTATCTTTCTACTTGGCTTAGGGATC
TTGGAACGCAGGTCCATACCAAACAATTCTTTTCAGAAAGTATTTCTCTCATGTTTGACC
GCACTGTATCTATCTTTCAGGAAATGTACGATAGAGGGAGGTTTTCCACATTTGATCGCAC
GTC'TTTATCTCAGATTGAAAAGCTACCAGAAGCTCTTAAACGATGCAGGATTAAAGAATT
TTTTTTCAAGCTACGATTATGCTTTTCGGGGTTGCATACAACCTTGTAATTTGCTCTGAAT
ACAGGTATGACGAAGTTCATTACATATCGAACGGCACTTACTCATTAGTTGCATCGATGA
AGATAGATCCTGTGAAGTCATTAAAAGGGAACATTTTAGGCTTACAATTCGGAATTTA
ACATATCTAATATATTAATTGAAATTTTTCATTTGCTCGATGGATTAGCATTTTTTAAGG
TGAACCCGTAGATTATCTATATCTACAGCTTCAGCAGAAAACAATCTTTTCGAGTATCT
CCGAAGGTAATCATCAGGTCTAGAAATTGGGGAGAAGTTTAATGTTTCCATTGTTGAGGA
CTGGAGATTTTGAAATCTGCTGATTGACGACGCGGGAGCTGTCATAACATTTACAGAAG
CGAAGGATGTAAAACTAGAAATAATCAGTCTGGATGAAGTTTCTGGGTAATGCAGTGGA
AATCTGTCTTCAAAATTTAGAGAGAAGGGCAGCAAAATGACAGTTTATTATCAAAACAC
ACCTACAATTTAAGAAGGCCAACAAATTTCAATGAAGATAATAATGGGCTAGGACTAATTG

TAGACAGAAATATTCCAACAGATGATTTTACGCTAGCTTCTACAAACCGTCAAAGTCCCC
CGCCTTCAAATACTGGTTGTTTCATTACACAGGTCTAAACCCTTGCATATCCCCTTTATCAT
CTGTTATTTCGTGAAGACTTTTATGATAGCTCTCTAAATGAGCGTATATCTAAAGACGGAG
ATAGCAGTTTGTGAATCCTTCAGTGGCGCCGAAAGTATCTTATCAGACTACGATTTTTCATG
ATAATGAATTTTTTAACAACCAAGTCACCTCATTATTTTTTCAGAACACATAGACAATAACT
CGAGAGAGGTGGTAATAACAGATGAAAATACGATAATATCTTTGGAAAATACCCAAGTAA
GTCCGTGGTCAAATTACTCATGGCAAAAAATTTACCCGCATCAATTACAGGTCTCTATTA
TCCAAC TGCGCATGGGAACTTCATTGTGGCTTATGATTCTGATTATAACCTTCATCAGT
TCAAAATTCGTTTGTGTGACGATATAAAATGTATACAATCCACAGAGCAAGACATACAAA
TACGTGTCCCGCTCGGCGCAATAATGTGCAGCGTCACTGGTATCTTGAATATTAGGACGA
AGGACGCTGACAAGTTGCTTCGGGTATTAAGCTTTTATACCACTGACCACACGGAAGCTG
TATCGCACTCAAACAATCAAGATGCTACTGCAAGTCCACTTTCGTCAAGTTTCATCAGCAA
TGGATCTCAAGCATTCATTACAGAAATGTTCTCTACAATAATGCCCAAGAGTTGACGC
AGGACGTCATCGGTTCAAATCAGACCTAATCAGTAATATTTCGTCAAAAAATATAA

YJL181W, 611 aa (SEQ ID NO 156)

MEIFKEEEEEAFSAIEGIIYACEVYDPVPRHLHKSSTKIINAAKLIIETHLSYYTILNNI
SDIQAYLSTWLRDLGTTGPYQITLSEISLIMFDRTVSIFRKCTIEGGFPHLIARLYRLK
SYQKLLNDAGLKNFFSSDYAFGVAYNLVNCSEYRYDEVHYISNGTYSLVASMKIDPAEV
IKREHFRLTIPKFNISNILEIFHLDDGLAFFKVNPDLSISTASAETIFRSISEGNHGV
LELAGSCLMFPLRTGDFEICRIDDAGAVITTFEAKDKVLEIISLDEVSWVMQWKSCLQNY
ERRAANDSSFIKTHLQFKANNFNEDNGLGLIVDRNIPTDDFTLASTNRQSPPPSNTGC
SLHRSKPLHIPLSSVIREDFYDSSLNERISKDGDSSCESFSGAESILSDYDFHDNEFFNN
QSPHYFSEHIDNNSREVVTIDENTIISLENTQVSRWSNYSWQKISPHQLQVSI IQLRMGN
FIVAYDSYDNLHQFKIRLCDDIKCIQSTEQDIQIRVPLGAIMCSVTGILNIRT KDADKLL
RVLSEFYTTDHTAEVSHSNNQDATASPLSSVSSAMDLKHS LQKCSSTIMPQELTQDVIGSK
SDLISNIRQKI

YJL187C, 2960 bp, CDS: 501-2960 (SEQ ID NO 157)

TCTTGCAACCATCGTCCCTCTAAGGAAAGAAATGTGGCACCTTTAAATAGGTTCCACCTCA
CAGATGCCAACATGTGGGAGATAGGGGGCTATTGCGAATTTATTAACGTCTCTAGTACTG
GTAAGCCTTTTCLTAACATTTCTGTGGTCACGTGATGTATGTTTCTTTTTTTTATTCTCTC
CGGGTGATAACGACGCGGAAAAATATTTTTTTCATTTTTCTTTTAACCATCACAATTTGCGA
CGCGACGCGGAAAAAATGCAGAGAAGTAAAAGAATGCTGGATAAGAAATCAACAACACAG
TTGAACATTTGGCGTGCCTCTGTGTATTAAGTAAAGGTTGTCCAAGAGGCTCTTTTTTGTA
TGTATGCGTGTGTTAACTATCCTGCACATCATCTTGCGCAGTTAGTCCAATAAAAAAGGA
TTACTACTGAACAGGTCTTACTATTTTGATTGCGTAGTGCTGGGGAAAAAGTAAACACAC
ACAGGCGCACACGAGAACAGATGAGTTCTTTGGACGAGGATGAAGAGGACTTCGAAATGC
TGGACACGGAGAACCCTCCAGTTTATGGGGAAGAAGATGTTTGGCAAACAGGCCGCGGAAG
ACGAGAGTGATGATTTTGCTATAGGGGGTAGCACCCCGACCAATAAACTGAAATTTTATC
CATATTCGAACAACAAATTGACAAGAAGTACGGGGACCTTGAACCTGTCTATTAAGTAATA
CAGCTTTTGTAGAGGCTAACTCCAAATTTCTTGGGAAAAATTGAAGAAGAGGAAGAAGAG
AGGAAGAAGGCAAGGATGAGGAAAGCGTGGATTCTCGTATTAAAGGTTGGTCTCCGTTCC
ATGAAATGAAAGTGTACTACTCCTATTACAAAAAGATCTGCGGAAAAAACGAACAGTC
CTATTTCTCTCAAACAATGGAACACGATGGTTTCCGAAAAATGATGCTCGCACTGAAA
ATACATCCTCATCCTCTTCATATAGCGTCGCTAAACCTAACCAATCAGCCTTTACGTCTT
CGGGCCTCGTATCTAAATGTCTATGGACACTTCGTTATACCCTGCGAAATTGAGGATAC
CAGAAACACCAAGTGAATAATCAACCCTTAGTGGAGGGAAGAGACCATAAGCATGTCCACC
TTTCGAGTTTCGAAAAATGCATCGTCTTCTCTAAGTGTTCCTCTTAAATTTTGTGTAAG
ACAATAATTTACAAGAAGACCTTTTATTTTCAGATTCTCCGTCTTCGAAAGCTTTACCTT
CCATCCATGTACCAACCATAGACTCATCCCCACTGAGCGAGGCAAAATATCATGCACATG
ATCGTCACAATAACCAGACAAACATCCTGTCTCCCACTAATAGCTTGGTTACCAACAGCT
CTCCACAAACATTCGATTCTAACAAAGTTCAAAAAATCAAAAGAGCAAGGAATTCGGTTA
TTTTGAAAAATAGAGAGCTAACAAACAGTTTACAACAATTCAAAGATGATTTATACGGCA
CGGACGAGAATTTCCACCTCCAATCATAATATCAAGTCATCATTCAACTAGAAAGAACC
CTCAACCTTATCAATTTCTGGACGCTATGACAATGACACTGACGAAGAGATCTCCACTC
CAACAAGACGAAAAATCTATTATGGGGCAACATCTCAAACACATAGAGAAAGCAGACCAT
TGTCACTCTCCTCTGCCATCGTGACAAACACAACAAGTGCAGAGACGCATTCCATATCTT
CCACCGATTCTTCGCCGTTAAATTTCAAAGCGCTCTAATCTCTTCAAATAAGTTATCAG
CAAATCCAGATTCCCCTCTTTTCGAAAAATTTACGAATGTGCATTCCATTGGTAAAGGCC

AGTTTTCACGGTCTACCAGGTTACGTTTGCCCAAACAAACAAAAAGTATGCAATCAAAG
CCATTAAACCAAACAAATATAATTCTTTGAAACGCATATTACTGGAAATTAATACTAA
ACGAGGTAACAAACAAATTACAATGGATCAAGAAGGGAAGGAATACATCATCGATTACA
TCAGTTCTCTGGAAGTTTCAAAATTCATACTATATTATGACAGAATTGTGCGAAAATGGTA
ATTTGGATGGATTTTACAAGAGCAAGTTATCGCAAAGAAAAAAGGTTGGGAAGATTGGA
GAATTTGGAAAATCATCGTGAATTAAGCCTGGCTTTACGATTTCATCCATGATTCTTGTC
ACATTGTGCATCTGGACTTGAAACCCGCAAACGTCATGATCACATTTGAAGGTAACCTAA
AACTAGGTGACTTTGGAATGGCTACTCATTTACCGTTGGAGGATAAAAGTTTTGAAAATG
AAGGTGACAGAGAATATATTGCACCAGAAATCATTTCTGATTGTACGTACGATTACAAGG
CAGATATTTTCCCTGGGTCTGATGATTGTTGAAATTGCAGCGAACGTTGTGTTACCTG
ACAAATGCCAACGCATGGCATAAGTTGAGATCGGGTGATTATCGGATGCAGGAAGATTAA
GTTCCACAGATATTCATTCTGAATCATTATTTTCAGACATTACGAAAGTAGATACAAATG
ATTTATTTGATTTTGAAAGAGACAATATCAGTGGTAATAGTAACAACGCTGGCACCTCCA
CTGTTCAATAACAATAGTAATATCAACAACCCTAATATGAATAATGGCAACGATAATAATA
ATGTCAATACTGCCGCTACCAAGAATCGTCTTATTTTGCATAAAAGTTCTAAAATCCCCG
CATGGGTACCGAAATTTCTTATTGATGGTGAATCACTTGAGAGAATAGTACGATGGATGA
TAGAGCCCAATTATGAGAGAAGGCCACGGCAAATCAAATCTTACAACTGAGGAATGCC
TGTATGTAGAAATGACACGCAATGCAGGTGCTATTATCCAGGAAGACGACTTTGGACCTA
AGCCAAAATTTTTTATATGA

YJL187C, 819 aa (SEQ ID NO 158)

MSSLDEEEDFEMLDTENLQFMGKKMFGKQAGEDESDDFAIGGSTPTNKLKFPYSNNKL
TRSTGTNLNLSLNTALSEANSKFLGKIEEEEEEEEGKDEESVDSRIKRWSPFHENESVT
TPITKRSAEKTNSPI SLKQOWNQRF PKNDARTENTSSSSSYVAKPNQSAFTSSGLVSKM
SMDTSLYPAKLRIPETPVKKSPLVEGRDHKHVHLSSSKNASSLSVSPLN FVEDNNLQED
LLFSDSPSSKALPSIHVPTIDSSPLSEAKYHAHRHNNQTNILSPTNSLVTNSSPQTLHS
NKFKKIKRARN SVILKNREL TNSLQQFKDDL YGTDENFPPII ISHHSTRKNPQPYQFR
GRYDNDTDEEISTPTRRKSIIIGATSQTHRESRPLSLSSAIVTNTTSAETHSISSTDSSPL
NSKRRLISSNKL SANPD SHLF EKFTNVHSIGKQGFSTVYQVTF AQTNKKYAIKAIKPNKY
NSLKRILLEIKILNEVTNQITMDQEGKEYIIDYISSWKFNQSYIIMTELCENGLDGFLO
EQVIAKKRLEDWRIWKIIVELSLALRFIHDSCHIVHLDLKPANVMITFEGNLKLGDFGM
ATHLPLEDKSFENEGDREYIAPEIISDCTYDYKADIFSLGLMIVEIAANVVL PDNGNAWH
KLRSGLSDAGRLSSTD IHSESLFSDITKVD TNDFDFERDNISGNSNNAGTSTVHNN SN
INNPNMNGNDNNVNNTAATKNRLILHKSSKIPAWVPKFLIDGESLERIVRWMIEPNYER
RPTANQILQTEECLYVEMTRNAGAI IQEDDFGPKPKFFI

YJL188C, 809 bp, CDS: 501-809 (SEQ ID NO 159)

AATTCCCGCATGGGTACCGAAATTTCTTATTGATGGTGAATCACTTGAGAGAATAGTACG
ATGGATGATAGAGCCCAATTATGAGAGAAGGCCACGGCAAATCAAATCTTACAACTGA
GGAAATGCCCTGTATGTAGAAATGACACGCAATGCAGGTGCTATTATCCAGGAAGACGACTT
TGGACCTAAGCCAAAATTTTTATATGATAAATGGAACAAAAACCTTGTTTTATTATACA
TACTTTTTTCCACACGTGCTTATGGGCCGATTGTATAAATAATCCAATAACGAAAAAG
AGTGTAATTGCAGTCCGGTAGTAATACCATGTAAACCTTAGATGAGTTTATTTTAAAGTA
CAGCCGCTTCAAGCATTTTTATTTTTATTTTACAGATGTAGCAGATAACAACCGTTAAAT
TATATTATATATATATATATATATATATCAAAATACGACGTATTACATATATATTGAGAAT
AAGGGAAGGATGGAAGACAAATGACAAAAAGTTTGAAGCATAAATATGTTCTTCGCTTAG
ATGTTTCATCTTGGTTCTTCTCCAGTTTCTTCTCTTAGCGTTGTAACGGATAGTGTGTTG
GTTCTCAATCTGATCCATTGTGGCAATGGTCTGTTTTGCTTCTTAGCCTTAGCCATTTTT
TGCTTGATTCTGAAAGACTTTTGAGCCTAATTAAAAGGGAAACATATCGTGCACATACGA
AGTGTACAATTGTAAAAAATGTTAGTAACAATGTTCAAACCTCATCAATATGATGCATTCA
CGGATCCAAGCAATACCACCTGACATAA

YJL188C, 102 aa (SEQ ID NO 160)

MTKSLKHKYLRLDVLHGLSSPVSSLSVVTDSVVGSDPLWQWSVLLLSLHFLDLSERL
LSLIKRETYRAHTKCTIVKNVSNNVQTHQYDAFTDPRQYHLT

YJL189W, 1042 bp, exon1: 501-506, intron1: 507-892, exon2:
893-1042 (SEQ ID NO 161)

TATTCAAGAAATTATTTACATCTTCCAGCGAGTAAACATGCCGCTGGTAATCGCGCGTCC
TCAATATTTGAGTTTTTCAAATAGTGAGGTGTGGATGTATAGAGGAATTACACACTTTTA

AGTATGTGATGTATGGGCGCACAGTACCAATTTAACTTTTTTTTTTTTTCATTTTTTAGC
TTGATTTTCAAAAACTTATGGGCGTTTATAGGCTCCGGCTCAAACTACCACCACCGCG
GCAGGCCGAGGCAACAGTACGCTTGGCGGGGACGCCGAAGCGACTCCTTCTGTTCCAA
GCTCAATGGTCCCTTGCCTTACGCTCGCGCTGGGCTAACTAACGCAATTCGGCTTTTGG
GCTGTGAGAGAACCAGAAATTATCTTCGCTTGATAGATACTTTAAACTTCTACTTAAT
ATACTTTCTACAATTTTTTGGTACATTCATATTATACTGAAAATTGAAAAAGACAAGCAA
ATAAACACAGATAGATCAACATGGCTGTATGTTAGAAAGATATTATAAATCCAGTTAGA
TGCTGAACGTGATCAATAGCAAAATATAAACCACATCCATCTAAATGACCTTACCACCTAC
AATTTGGATTTGAAATAGAAGCAATGTGTAAATATAGGGAAGGATTAGGAGTGTAAAC
CATACTAAAAATTTTTCTTATCCGAAACAGAAATCTAAAGTCGCCACTACGCAGATTAAAA
TATGGTCATAAACTGCTTATCTGAGAACTTTTGGTGGTCCAGCGTGGTTTATGTCAGGT
GGTATTGCCCTTGGATCCGTGAATGCATCATATTGATGAGTTTGAACATTGTTACTAACAT
TTTTTACAATTGTACACTTCGTATGTGCACGATATGTTCCCTTTTAATTAGGCTCAAAA
GTCTTTCAGAATCAAGCAAAAAATGGCTAAGGCTAAGAAGCAAAACAGACCATTGCCACA
ATGGATCAGATTGAGAACCAACACTATCCGTTACAACGCTAAGAGAAGAACTGGAG
AAGAACCAAGATGAACATCTAA

YJL189W, 51 aa (SEQ ID NO 162)

MAAQKSFRIKQKMAKAKQNRPLPQWIRLRNMTIRYNAKRRNWRRTKMNI

YJL190C, 893 bp, CDS: 501-893 (SEQ ID NO 163)

TCTCGACAGCCCAAAGCCGAATTGCGTTAGTTAGCCACGCGCGAGCGTAAACGCAAGG
ACCATTGAGCTTGGAACAGAAGGAGTCGCTTCGGCGTCCCGCCAAGGCGTACTGTTTGC
CTCGGCCGTGCCGCGTGGTGGTGGTAGTTTGGAGCCGGAGCCTAAAACGCCCATAGTTTTT
TGAAAATCAAGCTAAAAAATGAAAAAAAAAAAAAGTTAAATTGGTACTGTGCGCCCATAC
ATCACATACTTAAAAGTGTGTAATTCCTCTATACATCCACACCTCACTATTTGAAAACT
CAATATTGAGGACGCGCGATTACCAGCGCATGTTTACTCGCTGGAAGATGTGAAATAA
TTCTTGAATATGGGTTTGCAGTTAGTCAATTTCAATCTAAATAATCTTAATCGACTATTC
AATCTTAAATTTGTAAGGTTTTTAAATGGCCTTTCAGTTCTAGTATTTTTTATAAAACAA
GACCAACATACATATCCAAGATGACCAGATCTTCCGTTTTAGCTGATGCTTTGAATGCCA
TTAACAACGCTGAAAAGACCGGTAAGCGTCAAGTTTTAATCAGACCATCCTCCAAGGTCA
TTATCAAGTTTTTTGCAAGTTATGCAAAAAGCACGGTTACATTGGTGAATTTGAATACATCG
ATGACCACAGATCTGGTAAGATTGTTGTTCAATTGAACGGTAGATTGAACAAGTGTGGTG
TTATTTCCCAAGATTCAACGTTAAGATTGGTGACATTGAAAAATGGACTGCCAATTGT
TGCCAGCCAGACAATTTCGTTACGTCATCTTGACCACCTCTGCTGGTATCATGGACCATG
AAGAAGCCAGAAGAAAGCACGTTTCTGGTAAGATTTTGGGTTTCGTTTACTAA

YJL190C, 130 aa (SEQ ID NO 164)

MTRSSVLADALNAINNAEKTGKRQVLIRPSSKVIKFLQVMQKHGYIGEFYIDHRSKG
IVVQLNGLRLNKGVISPRFNVKIGDIEKWTANLLPARQFGYVILTTSAGIMDHEEARRKH
VSGKILGFVY

YJL197W, 4265 bp, CDS: 501-4265 (SEQ ID NO 165)

CTTCTTCGGGGTCCCCAATGTCACTGCCATCTCTAAAGTAGATAGAAAGGGCGATCGCT
ATTTAAGTGTACATGACTTTCTTAAACGAGAGGTGTTCAGCTTCTATTTTGGCTTTCCTAT
GTGTCATTACTCTAGGTTATGGTATCATGGCATCTGTTGTCAAGGGTAACGCAACCTCTG
CGTAAGAGATACGCTACGATAGCATGTAACAGCGTATATATAATCTATATGTATTTCGAT
TAATCCAACACTTCTGTTGTGTAGTCTAATGTTTCGAAAAAAGGTACGCTTCCCTGTTAT
AATCAGGTATATTTTCGTTATTTCTTATAAGCTAAAAGATTAAAAATTTTCCACTTTCCTT
GAAATTTGGTTCGTTTCGTTGAAAAATATTATTACGTATTGAAGAAGTGCATGAAGATAAA
AGATGGGATTACTGGAATAAAGGGAGGAAAAATCCTGCAGAACGTTGTTGTTTCAATC
GAAGGTTTCTTCATTCGAAAATGGGTTCTTCAGATGTTTCAAGTCGTGAATGTTTCATTGG
TTTATAATGAAGATCCCGATTTCACCGATGGCACAACACCATGTGATCGGTTGGGATGG
ACTTGATGAATGTTCTAGATGACAAGGATGAAATAAAGCAAGAGTCTGTCCCAGTCTCAG
ATCGTGAAATTGAGGATACGGAATCCGATGCTTCCGCTGTTTCTTCATTTGCTAGCGCTA
ATGAGTTAATAGCTGAGCCACACGCTGCAAGTGAAACTAATCTTGGAACATAATGGTCAAG
ATGGAAGAAATGCTTTAGAACAACAAGAGACGTGGTTGCTAGACTAATAGAAGAAAACA
AGGAAACGCAAAAAGAGGGTGATAAGTCTGTATTGTCCCCAAGGTTTGGTACGATAAAT
TTTTCCAGCCCGATGTTACCGATCCTGAAGATATAGGCCCTATTAATACACGCATGATTT
GCAGAGACTTTGAAAATTTTGTGCTTGAGGATTACAATAGATGTCCGATCTGTCTATTG

CAGAGCCTGTTTTCAATTTTCTATCAGAAATTTACGGCATGACAAGTGGCTCTTACCCAG
TGGTAACTAATTTGGTTATCAACCAAACACAGGGGAGTTAGAGACAGAATACAATAAAT
GGTTTTTTCAGACTACATTACCTGACCGAAAAACAAGACGGGAGGAAAAAGGAGGCATGGCC
AGGACGATTTCAATAATGTACCTCTCGATGTCTGCGTTGAATTTAGTACGTGATTTGGTTG
AAAAAGATATGAATCTGTTTTTTGAGAAAGCTGATCATCTAGACGTGAATGCGGTGGATT
TTAAATTTGGTTTGTGTGTCAGAGGGATCTGATATTGCCACAGATAGCAATGTTAGTACTT
TTTTGAATTTCTTCATATGAAATAACTCCGCTTCAATTTCTCGAATACCGATAAAGAAAC
TACTAATACCAGACATGTTTGAAAACCGTTTAGACAAGATAAATTCAAATCCGAGTGACC
TTGTCATAGAAATTAACCTATAGAAGGGAATCACCATTGGCCTTCAAACATTTTTGCTT
ATAATAAACTCGAACCAGCATCAGGTACTACTGGTTTGGTCAATTTGGGAAATACATGTT
ACATGAATTTCTGCGTTGCAATGCCTGGTACACATTCCGCAGTTGCGTGATTATTTCCCTT
ATGATGGTTATGAAGACGAAATCAATGAAGAAAATCCTCTTGGGTACCACGGCTATGTGG
CTAGGGCATTTAGTGACTTGGTTTCAAGATTTGTTTCAAACAGGATGAGCATAATGCAAA
GAAATGCTGCTTTCCCCCTTCAATGTTCAAATCCACTATCGGGCACTTTAATTCGATGT
TTTCTGGTTATATGCAACAGGATTCTCAAGAATTTTTAGCCTTCTGTTAGACAGTTTAC
ATGAAGATTTGAACAGGATAATAAAGAAAGAATACACAGAAAAACCATCATTTATCTCCTG
GTGATGACGTGAATGATTGGAATGTAGTCAAGAACTGGCAGACGATACCTGGGAGATGC
ATTTAAAGAGAAATTTGTTCCGTTATAACGGATTTATTTGTGCGGGATGTACAAATCAACGC
TATATTGTCCCGAATGTCAAAATGTTTCTATAACGTTTGACCCGTATAATGATGTTACAT
TGCCGCTTCCGGTTGATACAGTGTGGGATAAACTATAAAAATTTTTCCCATGAACCTCTC
CACCATTCTTCTTGAAGTTGAGTTAAGCAAATCGTCCACTTATATGGACTTGAAGAAAT
ATGTTGGTAAATGTCGGCCTAGATCCAAATACACTATTTGGCTGTGAGATTTTCAGTA
ATCAAATCTATGTTAACTATGAGTCAACAGAGTCAATGCTCAATTTTTAACCTTGCAGG
AATTGATCAAACTGCTGATGACGTTATTTTTATGAATTACCAGTAACAAATGACAATG
AAGTAATTTCCCGTATTGAATACTAGAATTGAAAAAGGCTACAAAAATGCAATGTTAT
TTGGAGTCCCTTCTTTATTACGTTAAAGAAAGATGAATTGAATAATCCAGGTGCAATAA
GAATGAAATTGCAAAACAGGTTTGTCCATTTAAGTGGTGGGTATATCCCATTTCTGAAAC
CTGTAGGAAATCGAACCGATTTTGTCTGATGCTTTTCCATTATTAGTAGAAAAATATCCAG
ATGTTGAATTTGAACAATATAAAGATATACTACAGTATACGCTTATTAAGGTGACTGACA
AGGATAAATCCTTTTTTCCATCAAGATTCTGTCTGTAGAAAAAGAGCAGCAATTTGCTA
GTAATAACCGAACAGGGCCTAATTTCTGGACCCCTATCTCCAGTTAAACCTTGACAAAG
CTACAGATATAGCAGATAAACTTGAAGATGTGGTGAAGGATATCTACAATTATTCTCCT
TAGTAGATTGTGCTGAAGGGTCTTATGCAAGTGGATGATGAGGGAGATACCGAGGGTA
GTGAAGCAAAGAATTTTCCAAGCCCTTCCAATCGGGAGATGATGAAGAAAATAAAGAAA
CTGTAACAAATAATGAAAAATGAAATAATACTAATGATCGGGATGAAGATATGGAACATA
CAGATGATGTTGAAGAAGATGCAAGTACAGAGCCAGAATTAACAGATAAGCCAGAGGCGT
TAGATAAAATTAAGGATAGCTTGACTTCCACTCCGTTTGGCGATTCTTTCTATGAATGATA
TTATTGTTTGTGAGTGGAGCGAATTGGGTTCAAATGAGGCATTTTCCGATGATAAAATAT
ATAACTGGGAAAATCCAGCTACTTTGCCTAACAAAGAGTTGGAGAACGCTAAGTTGGAAA
GATCTAACGCTAAGGAAAGAACCATAACCTTGGACGATTGTCTCCAATTATTTTCCAAAC
CAGAAATACTAGGATTAACCGATTTCGTGGTACTGCCCTACATGCAAGGAACATCGTCAGG
CTACCAAAACAAATACAACCTTTGGAATACACCAGATATTCTGCTAATTCACCTTAAAGGT
TTGAAAGTCAAAGGTCTTTTAGCGATAAAATGATGCCACGGTTAATTTCCCATTTACAG
ATTTGGATCTGTGAGGTACGTTGTCTATAAAGATGATCCAGAGGTTTAAATCTATGACC
TGTATGCAGTAGATAACCACTATGGTGGTTTGGGTGGTGGGCATATACCGCGTACGTAA
AGAATTTTGCCGACAATAAATGGTACTATTTTGATGATTCTCGAGTAACGAACTGCGC
CAGAAAATAGTATAGCTGGATCGGCTTATTTGCTATTTTACATTTCGCGTCATAAAGATG
GCAATGGATTAGGCAGCTCTAAACTACAGGAAATAATCCAAAAGTCACGCCACGGATATG
ATGAGCGTATCAAAAAGATATACGATGAACAGATGAAGTTGTATGAATTTAATAAGACTG
ACGAGGAGGAAGATGTTTCTGATGATATGATAGAATGTAATGAAGATGTGCAGGCCCTG
AATATAGTAATCGTAGTTTGGAGGTGGGCATATTGAACTCAGGACTGCAACGACGAAG
ATGACAATGATGATGGTGAGAGGACAAATTCAGGTAGGAGAAAGTTAAGATTGTTGAAAA
AAGCTACAAGAATAATTCAGGCTTGGGTTTCATCGAGTACGCTCTGAAATATCTGAGGAT
GCCAGAAAACGAAGTCGCTGATTTGAATTTAAAAAATGGTGTGACACTAGAATCGCCAG
AATAA

YJL197W, 1254 aa (SEQ ID NO 166)

MGSSDVSSRECSLVNEDPDFDTGTTPCDRLGVLDLMNVLDKDEIKQESVPVSDREIEDT
ESDASAVSSFASANELIAEPHAASETNLGTNGQDGRNVLEQQRDVVARLIEENKETQKEG
DKVCIVPKVWYDKFFDPDVTDPEDIGPINTRMICRDFENFVLEDYNRCPYLSIAEPVFNF

LSEIYGMTSGSYPVVTNLVINQTTGELETEYNKWFRLHYLTKQDGRKRRHGQDDSIMY
LSMSALNLVRDLVEKSMNLFFEKADHLVDNAVDFKIWFVSEGSDIATDSNVSTFLNSSYE
ITPLQFLLELPKLLIPDMFENRLDKITSNPSDLVIEIKPIEGNHHWPSNYFAYNKLEPA
SGTTGLVNLGNTCYMNSALQCLVHIPQLRDYFLYDGYEDEINEENPLGYHGYVARAFSDL
VQKLFQNRMSIMQRNAAFPSPMFKSTIGHFNSMFSGYMQQDSQEFLLDLSLHEDLNRI
IKKEYTEKPSLSPGDDVDNWNVVKLADDTWEMHLKRNC SVITDLFVGMKSTLYCPECQ
NVSITFPDYNVDVTLPLPVDTVWDKTIKIFPMNSPPLLELEVELSKSSTYMDLKNYVGKMSG
LDPNTLFGCEIFSNQIYVNYESTESNAQFLTQELIKPADDVIFYELPVTNDNEVIVPVL
NTRIEKGYKNAMLFVGPFFITLKEDELNNPGAIRMKLQNRVHLSGGYIPFPEPVGNRTD
FADAFPLLVEKYPDVEFEQYKDILQYTSIKVTDKDKSFFSIKILSVEKEQQFASNNRTGP
NFWTPISQLNLDKATDIDDKLEDVVKDIYNYSSLVDCAEGVLMQVDEGDTGEGSEAKNFS
KPFQSGDDEENKETVTNNENVMNTNDRDEDMELTDDVEEDASTEPELTDKPEALDKIKDS
LTSTPFAILSMNDIIVCEWSELGSNEAFSDDKIYNWENPATLPNKELENAKLERSNAKER
TITLDDCLQLFSKPEILGLTDSWYCPTCKEHRQATKQIQLWNTPDILLIHLKRFESQRSF
SDKIDATVNFPIITDLDSRYVVYKDDPRGLIYDLYAVDNHYGGLGGGHYAYVKNFADNK
WYFFDDSRVTETAPENSIAGSAYLLFYIRRHKDGNGLGSSKLQEI IQSRHGYDERIKKI
YDEQMKLYEFNKTDEEDVSDDMI ECNEDVQAPEYSNRSLEVGH IETQDCNDEDDNDGGE
RTNSGRRKRLRLKKVYKNNSGLSSSTSEI SEGCPENEVADLNLKNGVTLESPE

YJL198W, 3149 bp, CDS: 501-3149 (SEQ ID NO 167)

TGTCGATTTTCCACTGATTTGGATGTATGTTGCATGGTGCTAGATTGTGAATAAATCATTT
TCCACTGGTTTCTAGCAGAGGTAAGAAAATCAGTAGTAGCGGCAGCAGCCAAGAAAATG
GCAGCCTGGCAAGCAGCGAAGGCCATCTGTGCTGCATTTCCACACTCCTTGTATGACTGC
ATACGCATAAAGAGGTGCCTTGCTGTAGGCGTATATGATCCTAAGCAACAGAGAAACCAC
GGTTCTCTTCTCTTCTTATTTTCGTTATTGTCTTCCCTTTTTACTATGGGTAAAGTCGCCC
TAAAGCGGGCGCTCACAAATATCGCCGAGCTACAGCCGTTTTTTTTTTTTTTTTTTTTT
TTTTCGCTGCTTCTCGAAGAATGAATGGCTCACTGAAAAATTTTGATTCATCGATATAAA
GAACACTGTTCACTTCGATGTCATCCGCCAATAAAGTTGTTTTTAGGATAAACGAGTAA
GTGGTAGCTGGTACAGGATCATGAGATTTTCACACTTCTTGAAGTACAATGCTGTCCCAG
AATGGCAAAACCATTATATGGACTACAGCGAGCTGAAAAATCTTATTTACACGCTACAAA
CAGATGAACCTTCAGGTTGGTGATAACGAAGAAGATTGGCGCAGGAAAGAGCTCTTAACA
TTACATAGATTGTTCAAAAAACAAGTTTCTTTTTTAAAAATGCGAAGGAAGATACGCTCTCCG
GTATGAACAAAGATGCAGGCATCGTTGAGGAAACCATCGAGTTGCGAGAGTTGCCTACTG
CTCAGACGGTCGCTGCCAAACCTTCTCCTTTTCAAGAATGAAGGAAAAGATATTTTACA
AAAGAAGGTGCTCTTCCGCATCGTCCGTCTCTCCACGGCCAACGAAAATCTGCAATTAG
ACACTTATGATACGTTTGTGGTGATTTAACAGCTGAAAAACAGAAAGTAGATGATTTTTT
ATAAGAGGACAGAAGCGAAGTTCTACGACAAAATTTGACGCGCTGGTGAAGGACCTGAAGA
AAATCGGAGTTATAGAATACGATATCGACGATGATACTCTGTTTAACGAACCGATTGCCA
GCACAAATGACGAAGTTCCCCACTAGACTTGGATGATGACGAAGACGACGACGAATTTT
ACGATGATCAATCTAATATTGAAGATAATACTGCTTTGCTGCATCATTCGCAGTATAACA
TTAAGTCTCAGAAAAAATCGCTGTTGAAGAAGTCGATCGTAAACCTATATATCGATCTTT
GCCAGTTGAAGTCGTTTCATCGAATTGAACCGCATTGGGTTTGCAAAAATTACAAAGAAAT
CAGACAAAGTTCTTCACTTGAATACAAGAACCGAACTGATCGAATCGGAGCAGTTTTC
AAGACACATATGCATTCAGGCAGAAACGATCGAATTGCTAAATTCCAAAATTTCCAGC
TAGTCACATTTTATGCGCGCATCACTGACCGGCCTCATAATATCTCGCATAGCAAGCAAG
AGTTGAAATCCTACCTGCATGACCACATTGTTTGGGAAAGAAGTAACACTTGGAAAGACA
TGTTGGGACTGCTATCGCAAGCTGACGAGTTGACACCAAGGAAACAGAATATAATGCAA
ATAAGCTGGTAGGCAAGTTAGATTGGGAATACTACAGATGGCCACTACCCAGACCGATAA
ACTTAAAAATTCAGTAGTATAAAACAAGTTGCACTACCGAAATTAATTTTACCAAGAAAG
CATACAAGATTTACTTTATTATTCTAGTCACTGGACTCTTGTAGGAATAAAGACCTTCA
ACGACGCTGCTCAGCACCGCTGCATGGCCCTTGTGCGAGTGTGTCGCCTTTTTGTGGGCTA
GTGAGGCCATCCCATACACATTACAGCATTCTTGTACCACTACTTGTAGTCTTTTCA
AAGTCTTAAAAACCTCCGACGGGCTATAATGAGTGTGCAAGCGCTTCATCAGAAATTT
TGGCCGATGTGGTCTTCTACAATTATGATTCTGCTGGCAGGTTTTACTTTGGGTGAAG
TACTTGCACAAATATAACATCGCCAAAGTTCTTGCCTCGTGGTTGTTGGCCTTCGCTGGTT
GTAAACCCAGAAACGTTCTTTAATGGCAATGTGTGTGCTGTTCTTCTTATCAATGTGGA
TTTCCAATGTGCGCAGCACCTGTTCTAACATATTGCTTGTATCTCCCTATTGGATGCCA
TGGATGCAGATAGCCCATTTGCGCAAGCATTGGTGTAGGTGTAGCGTTGGCTGCAATA
TCGGTGGTATGTCTTCAACCAATCTCTTACCTCAAAACATCATTTCCATGTGCTGTA
AACCTATGGTATTGGCTGGGGCAATTCTTTGCTGTTGCATTGCCATCTGGTATCTGG

CCATGCTTTTGGTTTGGATTATTGTTCACTACTTTCAAGATGAATAAGACCAAATTGG
AAAAATTTAAGCCTATTAAAGACGAAATTCACAGTTAAGCAGTATTATATCATTACTGTCA
CTGTGGCCACTATTTGTGTGGTGTGTGGAAAGCCAGATTGAAGGTGCTTTTGGGTGAT
CAGGTCAAATGCAATCATTCATCCATCGTTTGTGTTTGGTACCGGATTACTATCAACAC
AAGATTTAAATGCCTTTCCGTGGTCAATCGTTATTTGGCAATGGGAGGTATTGCTTTGG
GGAAGGCCGTCTCATCCTCGGGTTTGCATCAACCATTGCAAAGCATTACAAAAGAAAA
TTGAGAATGATGGTGTGTTTGGCATTCTATGTATTTCCGTATCCTGATGTTGGTTGTGG
GTACTTTCGTCTCGCATACAGTATCCGTATTTATCATCATTCCTTGGTGCAAGAAGTTG
GTGACAAGCTTGGCAACCCCAAAGCTGCTCCTATCCTTGTGTTTCCGGTTGTGCATTATTGT
CATCCTGTGGTATGGGACTAGCTTCTTCGGGGTTCCCAATGTCACTGCCATCTCTAAAG
TAGATAGAAAGGGCGATCGCTATTTAAGTGTGTCATGACTTTCTTAACGAGAGGTGTTCCAG
CTTCTATTTTGGCTTTCCCTATGTGTCACTACTCTAGGTTATGGTATCATGGCATCTGTTG
TCAAGGGTAACGCAACCTCTGCGTAA

YJL198W, 881 aa (SEQ ID NO 168)

MRFSHFLKYNAVPEWQNHVMDYSELKNLIYTLQTDDELQVGDNEEGFGAGKSSNITDRFKN
KFSFKNKEDTSSGMNKDAGIVEETIELRELPTAQTVAAPSPFRMKEKIFYKRRSSSA
SSVSSTANENLQLDYDTFVGDLTAEKQKVDDFYKRTEAKFYDKFDALVKDLKKIGVIEY
DIDDDTLFNEPIASTNDEVPLDLDDDEDDDEFYDDQSNIEDNTALLHHSQYNIKSQKKS
LLKKSIVNLYIDLCLQKSFIELNRIGFAKITKKSCLKVHLNTRTELIESEQFFKDYAFQ
AETIELLNSKISQLVTFYARITDRPHNISHSKQELKSYLHDHIVWERSNTWKDMLGLLSQ
ADELTPKETEYNANKLVGKLDLEYRWPLPRPINLKFTSINNVALPKLFFTKKAYKIYFI
ILVTGLLLGIKTFNDAAQHRCMALVECVAFWASEAIPHLHITAFVPLLVVLFVKVLTSD
GAIMSAASASSEILAMWSSTIMILLAGFTLGEVLAQYNIKVLASWLLAFAGCKPRNVL
LMAMCVVFFLSMWISNVAAPVLTYSLLSPLLDAMDADSPFAQALVLGVALAANIGGMSSP
ISSPQNIISMSYLPYGIGWGQFFAVALPSGILAMLLVWILLFTTFKMNKTKLEKFKPIK
TKFTVKQYIIITVTATILLWCVESQIEGAFGSSGQIAIPIVLFFGTGLLSTQDLNAFP
WSIVILAMGGIALGKAVSSSGLLSTIAKALQKKIENDGVFAILCIFGILMLVVGTFSHT
VSAIIIIPLVQEVGDKLGNPKAAPILVFGCALLSSCGMGLASSGFPNVTAIKSVDRKGR
YLSVMTFLTRGVPASILAFLCVITLGYGIMASVVKGNATSA

YJR049C, 2093 bp, CDS: 501-2093 (SEQ ID NO 169)

ACTGCCATCTCTTCCATCTTTGAAAAGATTATTAAGTTCGTCGTTAAGTTCCGCAATCT
GCATTTTCATTTAAAGACGGATCATATATCTTGTGCTTTTTTGTGTTTATCTCTTTACTTA
CTTGTGCGCTTCCATTCGTTGGCCTCTTTTATGGATTTTACCTTAGACACGTTCCCTGGGCC
TCTGGTAACGTGAATAATCCTTGTATCCACCTGCCGACTCTGCTTGCTGCTCTTGAAATC
GTACCAGAATGAGTTGGCCTTATCTACATTTCTACTCATTTGAATGCACAGGTATCTG
ATTACTGATGTGGTGCCTTGGCATATAACGGTGTGTCATTTTATTGCTCTTTTCATG
CATCCTGAAATTATTTACCCGCACTACGCAAAGAGAACGGAGAAAAAGGTATAATAGGGC
AAATGATCATTGACATCGTGATCGTAAGCCAAAAAATAACAATAGGCTCCCTAAATAA
GTAGAGTAAAGCTCTTGAGATGAAGGAGAAATGACATGAATAATGGCGTAGATAAATGGG
TAAATGAGGAAGATGGTCGAAATGATCATCATAACAACAATAAATACTTGATGAAGAAGG
CCATGATGAACAATGAGCAAAATTGATAGAACTCAGGATATCGACAACGCCAAAGAAATGT
TGAGGAAAATATCAAGTGAAAGCAGCTCGCGCAGAAGCTCCCTGTTGAATAAAGATTAT
CTCTCGTGAACGGCAATGCAAACAGTGGCGGTGTTACGAGCATTACGGAACAAGAGGAA
GTTCTAAGAGTAGTAATACACACTTTCAGTATGCCTCCACGGCGTATGGTGTAAGAATGT
TGAGTAAAGATATATCTAATACCAAAGTGGAAGTGGATGTGGAATTTGATGATTGTTA
CGAAACTCAACGATGCTCAGTGTATTTCTTAACAAGAGAGTTGGTAGAATGGGTTTTGG
TACATTTTCCACGTGTGACTGTTTATGTGGATTCCGAATTGAAAAACAGCAAAAAATTTG
CCGCTGGCGAGTTATGTGAAGATAGTAAATGTAGAGAATCAAGGATCAAGTATTGGACAA
AGGATTTTCATCAGGGAACATGATGTTTTCTTCGATTGGTAGTGACTTTGGGTGGCGACG
GTACTGTTCTTTTGTAAAGTTCCATTTTCAGAGACATGTACCACCCGTTATGTCGTTTT
CATTAGGGTCTCTAGGATTTTTAACAAATTTAAGTTTGAACATTTTCAGGGAGGATTTAC
CTCGGATTGTAATCATAAATCAAGACAAATTTACGGTTGAGGTTGGAGTGACAAATTT
ATCGTAGACACCGCCCTGAAGTAGACCCAAACACGGGGAAGAAAAATATGTGTGGTGGAAA
AACTAAGCACACACCACATTTTGAACGAAGTGACCATCGATCGTGGTCCAAGTCCTTTTC
TATCCATGTTAGAATTGTATGGTGACGGCTCATTAATGACCGTTGCGCAGGCGGACGGAC
TGATTGCTGCTACTCCGACTGGGTCCACGGCTATTCTTTGAGTGCAGGTGGGTCAATTGG
TATGCCCAACCGTCAATGCAATCGCTTTAACACCCATTTGTCCACATGCATTGAGTTTCA
GACCCATCATCTTACCAGAAAGTATAAATTTAAAGTGAAAGTCTCGATGAAGTCAAGGG

CTCCAGCATGGGCGGCTTTTGATGGGAAAGATAGAATTGAATTGCAAAAAGGTGATTTTA
TAACCATATGCGCCAGCCCATATGCTTTTCCAACCGTGGAAGCCTCGCCCGATGAGTTTA
TTAACAGTATCAGTCGACAACCTAACTGGAATGTGAGGGAACAACAAAAGTCCTTTACGC
ATATTTTGTCCCAAAAGAACCAGAAAAATATGCACATGAGGCGAACAAAGTCAGAAATC
AAGCAGAACCTTTAGAGGTAATAAGAGATAAATACTCTCTGGAAGCAGACGCTACTAAGG
AAAACAACAACGGAAGCGATGATGAGAGCGACGATGAGAGTGTAACTGCGAAGCTTGCA
AATTAAGCCTTCGAGCGTCCCAAAACCTTCTCAAGCAAGGTTTTAGTATAA

YJR049C, 530 aa (SEQ ID NO 170)

MKENDMNINGVDKWVNEEDGRNDHNNNNNLMKKAMMNEQIDRTQDIDNAKEMLRKISSE
SSSRSSLLNKDSSLVNGNANSGGTSINGTRGSSKSSNTHFQYASTAYGVRMLSKDISN
TKVELDVENLMIVTKLNDVSLYFLTRELVEWVLVHFPRVTVYVDSELKNSKKFAAGELCE
DSKCRRESRIKYWTKDFIREHVDVFDLVVTLGGDGTVLVFSIFQRHVPPVMSFSLGSLGF
LTNFKFEHFREDLPRIMNHKIKTNLRLLECTIYRRHRPEVDPTGKKICVVEKLSTHHI
LNEVTIDRGPSPFLSMLLEYGDGSLMTVAQADGLIAATPTGSTAYSLSAGGSLVCPTVNA
IALTPICPHALSFRPIILPESINLKVKVSMKSRAPAWAAFDGKDRIELQKGFITICASP
YAFPTVEASPDEFINSISRQLNWNVREQQSFTHILSQKNQEKYAHEANKVRNQAEPLEV
IRDKYSLEADATKENNNGSDDESDESVDNCEACKLPSSVPKPSQARFSV

YKR094C, 1255 bp, exon1: 501-508, intron1: 509-876, exon2:
877-1255 (SEQ ID NO 171)

AGGTTGTGTTCTTCAATGATGGGCAATGCAATTTGGCGTTAAGCGCCTGAGCAATAAGGT
AACAGCGAAATTTATGACATATTATTTGCAACCTTTTACAACTAGTAGATTTAGTGATT
TATTACCTATTTGGCATTCAATTTGTGTTCTATATGTGGATGAGGATAGCCGCCTTTCTTCT
CATCGGAGGCCATATCATCTTTTCGACAATCCTTTTTAAATACTATTTCCATCCGTGCCTC
TAATGATTTTGTGTAGTTGTCTGGGTGCAATCTTTCCATTTTGTGTAACCTTTTTTTTTT
TTTTTCATGTTTTTTCAGATTCTGAAGTACCGCAATAGGATATGGCGGATAATCCGCCATAT
GATCCGCCTCATACTAGCCATTACCCATCTATCCAGGCATTATGGGTATGCAACTCATA
ATCTCAAATACACAAATAAGAGCAACCTTATATATCACTTTTTCCCGTTTCAGCAAGAGGT
AAAGCCACCAAAGGTTCAAATGCAAATGTATGTTACGGCGAATACAGAATACTATGTTT
GAAATAATATGAGGATTATACGATAGCAAAAAAGCCATAAACGAAAGACATAAATGGAAA
ATGATTGACAAGCTCACAAATTTATTAACAAGTAGCAATTGAGAAAAACTATTACTCGCG
GCAAGCTTCTGAGTTTACATTAATCTGTAGAGCAAATTGAAAATGTGCGCATATGTGCTG
AAGGGTTTGTGTTTCCATCTTATTTTGCAATAACATAGTTATATTTACTTGGTTCGCATAA
AAAATATTTTTTACTAACGTGAAGTTTCTTTCTTTATGATGTACGCACGCACGTCTGTGC
TTACTCCATAAATGAACCTTATTTCAATTTTGTACAGCTTCGTTAAGACTTTGACTGGTAA
GACCATCACTTTTGGGAAGTTGAATCTTCTGACACCATGACAATGTCAAGTCCAAGATCCA
AGACAAGGAAGGTATCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCAATTGGA
AGACGGTAGAAGCTTATCTGACTACAACATCCAAAAGGAATCCACTTTACATTTGGTCTT
GAGATTAAGAGGTGGTATCATTTGAACCATCTTTGAAAGCCTTGGCTTCCAAATACAACGT
TGACAAATCTGTTTGTCTGTAATGTTACGCCAGATTACCACCAAGAGCTACCAACTGTAG
AAAGAGAAAGTGTGGTCAACCAACCAATTGCGTCCAAAGAAGAAGTTGAAATAA

YKR094C, 128 aa (SEQ ID NO 172)

MQIFVKTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRTLSDYN
IQKESTLHLVLRRLRGGIIEPSLKLASKYNCDKSVCRKCYARLP PRATNCRKRKCGHTNQ
LRPKKKLK

YLR040C, 1175 bp, CDS: 501-1175 (SEQ ID NO 173)

AGCTCTCAAACAACCTAATACTATAAGTTCAGTACAAGCACAGGAGGTGTAGGTTTCAGTC
AAGCCATGTCTTTACTTCGTTTAAATGTTAGAAAACATCGCTTATTTGTTTTCTTAAACA
AATATATTAGGTTCAAGGCTTTCGAGGTGTAAGAAAACCCGTTGCTCCATATTCTTAA
GTATGATAAATAAAAAAACTTAATAAATTAATTAATGCTTCAAACCTTTTCTTTTTT
TAGTTTTTAAATATTTCAAACGTTATCTTCATTGAACGCCCAAATAGGGAAAAATCCTGGC
AAATTTTTTTATTGCTGTCATCCAAGGCTATGCTAGAAAATTCAAGAGCTTGGATGATTTA
AAAAGACACTCTCAATCGAGAAAGTTTATCTTTGTTATTTCTGCTTTACCTGATCATATT
CCGGCGTATTGTTTTCTAATCAAGTGATTTTCGATATCCAGTTACGAACCATTTACAACATT
CCTGAAATATTGCGTATCAATGATATTGCTCCTTCTTCTCCCTCATTAATAATATTCT
TCCTGGTAAGCTTTCTAATCAGCCACAGTTTTCGCTGCCAAAACCTTAACGCTCATGTTCCA
ATGACGATACACTTGCCAGGTCCGCAGCTGCAGATGCAGACATGGCATTCTTCATGGAGT

TTTAAACGATTTTCGACACCGCTTTTCCACAGTATACCTCATAACATGATGCAAAACCATTT
TAACCTACCTCAACCTGTTGCTGACTACTACTATCACATGGTTGATTTGGCCTCAACAG
CAGATTTACAATCTGATATTGCTCAGAGTTTCCGTTCACTCAATTCCAAACATTCATTA
CGGCCTTTCCATGGTATACCTCTTTGCTAAACAAAGCCTCCGCCACCACCATATACCTTC
CCCAACACTTCATAACAGGTGAGACAGAAGCTACCATGACTAATCATCTTATGCCAGCC
AAAAAACTCCGTTTCCAATTCTGTTCTTTCTCGACAGCGAACGCAGGCCAGTCCATGA
TTTCCATGGCTAATGAAGAAAACAGTACAACAGCACTTATATCCGCATCAAACCTCTTCTT
CAACATCCAGAACTAGTCAATCACAGAATGGTGCCCATGCCAAAAGCTTATATTTCCCCA
TGGCGTTGTTCCGAATCTTTGCAGTTGCCCTTTAA

YLR040C, 224 aa (SEQ ID NO 174)
MIFAPSFSLIKNILLVSFLISHSFAAKTLTSSSNDDTLARSAAADADMAFFMEFLNDFDT
AFPQYTSYMMQNHLTLPQPVADYYYHMYDLASTADLQSDIAQSFPFTQFQTFITAFPWYT
SLLNKASATTIYLPQHFITGETEATMTNSSYASQKNSVNSVFPSTANAGQSMISMANEE
NSTTALISASNSSSTSRSTSQSQNGAHAKSLYFPMALFGIFAVAL

YLR048W, 1618 bp, exon1: 501-590, intron1: 591-949, exon2:
950-1618 (SEQ ID NO 175)

GCACCCCTTTTCTTTTCAATAACAAAAAGAGCTTGGGCATTACGTTTTCAACACTTTT
AATATTTCCCTTTTTCATCCGTACATATAAAATGTAAACCCATGCATTCATGACAATTT
TACCTATTTCTTAAAGGCCTTTGTCACTTCTTTATGGGAATGGCGCTACTTTAATTTTCC
GCCTACTTTTGA AAAAATTTACCAAGGCGAAATTGAGTGCGCTAGGCGGAAGTTCCAGGGCA
CGGTCACCGAACCCTTTGTGCTGTTTGAACGAGGGTCCCGCTGGAGGTTGACGGACGCGG
GAGGAGCTGGAAGATGGAATGGAAGGACTGCAACACTCAGTAAGAAGGTTCTGTTGGTAGG
GAACATCACCTTCTCTAGTTCTGTAAAAATAATATGATCAAGTTTGAATCCTCGTATTG
AAAAATCGCGAGTTATTAAGTGTGAATTTAGAATACCGAAATAGCACAAGAAGAGATAA
GATAAGATACTGATAGGATAATGTCTTTACCAGCTACTTTTGATTGTGACTCCAGAGGATG
CCCAACTTTTGTGGCCGCTAACACCCATTTAGGTGCTAGAAACGTTCAAGTATGTACAC
ATATCCCATACGATTATGTTCTATAGATGATAATAGGTCTCGAAAAGAATATGTCCCCGA
TTTAATCATAATTTGGAGGTCAGAGGACCAAAGGTAATTTAGAGGAATTTTGAACACGCC
GGGTTTAGAAGAGTTAGAATTTCACTTCTTAGTGAGGGTAAGGAGAAGAACTCAATAAG
AATATACATCCTCGACTGTGTCAAAGATTATGAACCTCCGATGAAACAGTAAACAGTCAAA
AAATTCACGGGATATAATTCGGTACTTTTATTTGGATATGGAAGAAAACATTATATATGCA
CAAAATGAACGCTCTTACTAACATAATTTATCTTTCTCTCTTTTTTTTAGGTCCACCAAGA
ACCATACGTTTTCAATGCTAGACCAGATGGTGTTCACGTTATCAATGTTGGTAAGACCTG
GGAAAAGTTGGTTTTGGCTGCTAGAATTATTGCTGCCATTCCAAACCCAGAAGATGTTGT
TGCCATCTCTTCCAGAACCTACGGTCAAAGAGCTGTCTTGAATTTGCTGCTCACACTGG
TGCTACTCCAATCGCCGCTAGATTCACTCCAGGTTCTTTCACTAATTACATCACCCGTTT
TTTCAAGGAACCAAGATTGGTTATTGTTACCGACCCAAGATTAGACGCTCAGGCCATTAA
GGAAGCTTCTTACGTTAACATTCCAGTCATTGCTTTGACTGATTTGGACTCCCCATCTGA
ATTTGTTGATGTCGCCATCCCATGTAACAACAGAGGTAAGCACTCCATCGGTTTAATCTG
GTACTTGTGGCTAGAGAAGTTTGTAGACTAAGAGGTGCTTTGGTTCGACAGAAGTCAACC
ATGGTCCATCATGCCAGATTGTACTTCTACAGAAACCCAGAAGAAGTTGAGCAAGTTGC
TGAAGAAGCTGCTGCCGCTGAAGAAGGTGAAGAAGAAGAAGTTAAGGAAGAAGTCACTGA
AGGTCAAGCTGAAGCTACTGAATGGGCTGAAGAAAATGCAGACAACGTTGAATGGTAA

YLR048W, 252 aa (SEQ ID NO 176)
MSLPATFDLTPEDAQLLLAANTHLGARNVQVHQEPYVFNARPDGVHVINVGKTWEKLVLA
ARIIAAIIPNEDVVAISSRTYQRAVLKFAAHTGATPIAGRFTPGSFTNYITRSFKEPRL
VIVTDPRLDQAIKEASYVNIPVIALTDLDSPSEFVDVAIPCNNRGKHSIGLIWYLLARE
VLRLRGALVDRTQPWSIMPDLFYFRNPPEEVEQVAEEAAAAEEGEEEEVKEEVTEGQAEAT
EWAEENADNVEW

YLR088W, 2345 bp, CDS: 501-2345 (SEQ ID NO 177)
CTTCCCATGTAGAATATCATTGTCAAACATACTACTACCGTGAGAATCCAATCTACTAAA
AAGACCCAGCTAAAGTCCTTTTGGTGTGTCAATGGAACACCACGTAATTGTGAAATAGCT
TCCATGCTTGCTAACTTATTACCGTCAATAGAAGACTTGAGTCAGGTGGCTTTAATGAGT
ACTATTCCTTTTTTTTTTTTCCAAAGAGCACTATGTTGATAATACCGCAGTAATTTTTTTTG
AGTATCCTGTAGCCTAGAAAGGTTGAAGCTTATAAAACCGTGCCAACAGCTTTATAGTGG

GGAGTTTGGCTTCCCTCTATTTGTATATTGATCGCCATCCCACGAAGTTATTGGGAACG
CATCGTGAACCTCTCACTTTAATGCCAGCGGTAGAAAAAAGTCATAAACAAATACACGC
CGGCTACACTTAGAAAGAAATGACATTTGCTGTCTTATAAAGGACTTGACAGACCAAAG
ACGCGTATAATACACCAAGAATGGCCTTATTGGAGAAGTTGCATCGAAGGATTGTTGATA
TGGGGCTTGTCCCGGTATAATCGCCTTATTACCAGTTATTTCCATGCTATGCGCTCTAT
TTGGGTTTATTTCTATAGCTATTCTGCCTATGGATGGACAGTACAGAAGAACATACATTT
CTGAGAATGCATTGATGCCTTCACAAGCGTATAGTTACTTTAGAGAATCTGAATGGAACA
TTTTGAGGGGCTATCGATCTCAAATTAAGAAATGGTAAACATGACTTCTATGGAAAGAA
ACAAATTTGATGGGTTCTTGGTTACAAGAATTTGGTACTAAGACTGCTATTTACGAAAATG
AACAAATATGGAGAAACATTTGTACGGTGTAAATGCACGCTCCTAGGGGTGATGGAACAGAAG
CGATGGTGCTTGGCGTTCCATGGTTTAAATTCAGATGATGAATTCAATATTTGGCGGCGCAG
CTTTGGGTGTATCTTTAGCAAGATTTTCTCACGTTGGCCAGTATGGTCCAAGAATATAA
TTGTTGCTTTACGCGAAAATCCTCGTGCAGCATTAAAGATCATGGGTTGAGGCATACCATA
CTTCTTAGATTTGACTGGTGGTTCCATTGAAGCTGCTGTTGTTGTTGGATTATTCGAGTA
CGGAAGATTTCTTCGAGTATGTAGAAATCTCATACGACGGTCTGAATGGTGAGCTGCCCA
ATTTGGATCTTGTCAACATCGCTATATCCATTACGGAACATGAAGGTATGAAAGTTCTTT
TGCACGGTCTACCCAGTGATCAGTTAACTAATAATAATTTCTGGTCAAGATTAATAATAT
TATGCTTGGGAATAAGGGATTGGGCGTTGTCCGGTGTAAAAAGCCCCATGGTAACGAGG
CATTTAGCGGCTGGAGGATTCAATCTGTAACATTGAAAGCACATGGAACAGTGGTCATG
ATATTACTACATTTGGACGTATACCCGAAGCAATGTTTCGCTCTATTAATAACCTTTTGG
AAAAATTTTCAACCAATCGTTCTTCTTTTATTGTTATTAGCACCACGTCAGTTTCGTATCCA
TTAGTAGTTATTTGCCAAGCGCTGTGGCTTTATCTATAGCATTGCCATAAGTTCAATTAA
ATGCATTTATAAACAATGCTTATGCAAATATATCCTTATTTTCCGAGTATAATTTGGTAG
CGTTGTTGGTTTGGTTTCGTGTCATTGGTGATATCATTTGTTGTTTACAAGCGTTTCTTC
TAATACCTTCATCGGGATTATTGATGACAATTAGCATGGCATCTTGTTTTTTACCTTTGA
TACTTTCCAGAAAAATTCACATCTCAGAACCTATCATAACAGGTTGAAAAATGTTGCTTT
TTTTATATTTTCACTTTGGTTTCAACATCTTTGCTAATGATAAACTTTGCAATGGCTTTAC
TGATCGGCACATTGGCATTTCTTATGACATTTGTGAAGACCATTGTTGAAAGTTCTAGCG
AACATGAGGTGACAACTCAATCCTCTAACCCAATAAAAACTGAGCCGAAAGATGAGATAG
AGCTCGTCGAGAATCACATGGATACAACGCCAGCAACCCCCCAACAACAGAAACAAAAAC
TAAAAAATTTAGTACTATTAATTTTGACAAATCCATTTATTTCAATAACCTTATTCGGAC
TATTTTTTTGATGAATTTTCATGGATTGATATAATAAACAACCTGGTTTCAGCATGGT
TGGATTTGAAATGTTGGAGTTGGTTTGTACTTTGTATAGGTTGGCTTCCATGTTGGCTAT
TGATATTAGCGTCATCGTTTGAATCTAAATCTGTCTAGTAAGGTGAAAGAAAAGCAAA
GTTAG

YLR088W, 614 aa (SEQ ID NO 178)

MALLEKLHRRIVDMGLVPRIIALLPVISMLCALFGFISIAILPMDGQYRRTYISENALMP
SQAYSYFRESEWNILRGYRSQIKEMVNMTSMERNNLMGSWLQEFGTKTAIYENEQYGETL
YGVMHAPRGDGTTEAMVLAVPWFNSDDEFNIGGAALGVSLARFFSRWPVWSKNIIVVFSN
PRAALRSWVEAYHTSLDLTGGSIEAAVLDYSSTEDFFEYVEISYDGLNGELPNLDLVNI
AISITEHEGMKVS LHGLPSDQLTNNFWSRLKILCLGIRDWALSGVKKPHGNEAFSGWRI
QSVTLKAHGNSGHDITTFGRIPeamFRSINNLEKFHQSFYLLAPRQFVSISSYLPS
AVALSIAFAISSLNAFINNAYANISLSEYNLVALLVFVSLVISFVVSQAFLIPSSGL
LMTISMASCFLPLILSRKIHISEPLSYRLKNVAFLYFSLVSTSLLMINFAMALLIGTLAF
PMTFVKTIIVESSSEHEVTTQSSNPIKTEPKDEIELVENHMDTTPATPQQQKQKLNVLVLL
ILTNPFIISITLFGLFDFDEFHGFDIINKLVSAWLDLKCWSWFVLCIGWLPCWLLILASSF
ESKSVVRSKEKQS

YLR159W, 845 bp, CDS: 501-845 (SEQ ID NO 179)

TCCGTCCCAAAGATAGCTTGATCATCCTAAGCGGGTTCGCATTTTACTATCCCCAGTTCCG
AAGAATAACAAGGCTCAATGCATATGCTGTTTATCGTGCTCACAAGCGGTATGACGTTT
TTAGCAATGTAATTATATTAAGAGATCTTCAGTCACTATGAGTGGTTGATTGCCCCATA
GAGAGCTATAAGCCGACGTGAAAGCTGCTGGTTCCAGCTTGGCTCATGTCGTCACCATG
ACTAGTCACTTGGTCGCATTCAATTGCTACTCATCTGCGAGTGAGCATATTTGAGATCTGA
CTTGCCAAGGGATTAGAAATCACGTAAGACTCTTGATCCTTAGAAGATATTTCTGACAAAG
AACCACCTAAGCCATGCAAGTTTTCATTTTTCATTTGGTGGCGAAACAAAGGTGATGAAAG
TTTCTTCTTGTACAAACGCCAAGCCCGATAGGTGAGACAATTCTTGAAGTAATGGACCTC
TGAGTAAGCATATCAGTCGAATGAAGTTCCAATATGCGTTGGCCAAGGAACAGCATGGCA
GCAACTCGCGCAGTGGCGTCAAAAACTAATAAGTAAACACCACTGGCTTCCGGAATACT

ATTTCTCTGATCTCTCATTTTCTGTTGTACAGCAGTGGGACAGTAGAGCCATTGAAAAA
CTACAATCATATCTTGATATGCGGCCCGCAAACCAAGAGATTTATCCTTTGAGACATTGTG
AGACCTCCGTTTCGCAACCGTGCTCTCTGTTTTCATCACTATATGCACGCTCTTTCCAAA
GCTCCTGCACTTTGCACGTGGCGGAGCCATCGCCCGGCTTCCATATGTACGGCTGCCACA
CCTAA

YLR159W, 114 aa (SEQ ID NO 180)

MKFQYALAKEQLGSNSRSGVKLISKHHWLP EYFSDLSFSVQWDSRAIEKTTIISCM
RPNQEIYPLRHCETLRSQLFSSLYARSFQSSCTLHVAEPPGFHMYGCHT

YLR167W, 959 bp, CDS: 501-959 (SEQ ID NO 181)

ATCAAAAGAGTGTTTCAAGTAAGTAAAAACATTTGAGCCTCCCCATTTGTTGAAAGGAGA
GAAATTTAACTTGGTTGGGGTTAATTATTTGATGGGTATATTAATTTGCAACCGCAAGGT
ATCGATAATAAATATTCTACAAAACCTTTATCAATAGTGGTGAAGTCTTTAGTGCGATCT
ACCTGGGGTTAATGAACGAGAAGTTCTTGAGATATCTTTCCTGTTTACCTCCGTGCATCC
TGTAAGGAAATTTGGGTTTATCATTTATCATTTATTTTAGTACAAAACCTTTTTTTTTGGCCC
GGGCGCACTTTTTCAAGCGGTGGGAACATCAAAAATGAAAAACTAGATACTTTTAGACT
TATTAAATGGTTTAAATATTTTGAGATGTTCTGTTATATCAGAACTTCCCTTACTTCTATC
TTTTATTCCAAATACAAAGAAGTCACAAGATTACTTGGTAAGAAAGAAGCAGTTAATTTTT
AATTTTGGCGACAAGCCAAGATGCAAAATTTTCGTCAGAACTTTAACCGGTAAGACTATTA
CCCTGGAAGTTGAATCTTCTGACACTATTGACAATGTCAAGTCCAAGATCCAAGACAAGG
AAGGTATTCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCAATTGGAAGATGGTA
GAACTTTGTCCGACTACAACATCCAAAAGGAATCTACTCTACACTTGGTCTTGAGATTGA
GAGGTGGTGGTAAGAAAGAGAAAGAAAGAGGTCTACACCACCCCAAGAAGATCAAGCACA
AGCACAAGAAGGTCAAGTTGGCTGTCTTGCTCTACTACAAGGTGATGCTGAAGGTAAGG
TTACCAAATTGAGAAGAGAATGTAGCAACCCAACCTTGTGGTGTGGTGTTTTCTTGGCTA
ACCACAAGGACAGATTGTACTGTGGTAAGTGTCAATCCGTCTACAAGGTTAACGCTTAA

YLR167W, 152 aa (SEQ ID NO 182)

MQIFVKTLTGKTTITLEVESDITIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRTLSDYN
IQKESTLHLVLRLRGGGKKRKKVYTPPKIKHKHKVKLAVLSYYKVDAEGKVTKLRRE
CSNPFCGAGVFLANHKDRLYCGKCHSVYKVNA

YLR232W, 848 bp, CDS: 501-848 (SEQ ID NO 183)

AGCCACCAATTTCCACCAAGGCCCGGCATTCAGTACTTGTAAGAACACCAACAGGCAAAGT
CAACACCCCAATCATGAAGTTGCAATGGGACGTTCCCTACAGCGTGTGCTAAATCCCATC
CAACCAATATGTTCGGGGAATTGGTGGGCAATGAGGTGATTCGGCCAATATCGAAATATT
GCCCCGTGTAATACTGAACACCTGACAAACAGACCAGCGCCAATTCATCTTGATTTACCT
CTATGGTATCCAGGATATCTTGAGTTCTGATATAAGTCTCTCCCTCGCGTGGCTCGATCT
GAATAAAAACATTTCTCAGGTTCCGAAATTCATGAATTTTGCAGTGGTTGTAGAAAGCAT
AATAGTCTGTATGGAAGGAGCCCTTTTCAAAAAGGATCTTGAATCTTTTCTCAGTAGGTT
TATAAAACGTAATTAACAATGAATTCAAATTTGCAGTGAGACTATTCACTACTGCAACTT
CATTTTCTTGAGCACCCACGATGGGGGCTAGTAGTGGAAGAATAGGTAAGTCAATGCTGA
CCCAAGGCACCTTTCCCTCTGGCTTCTTCAGGATGTTTGAAATGCGATTCCACAGCACAAT
CGCTCCACGCATCTAGCTCAGCATTAATTGAATTCCTAGTTGACTTCGGCATCAAACCTA
AAGAATTTCCCGCATAAGTACGTCACAGCCTTATCGTCGGACGATAGTCCCATGGATTTAA
ATGTAGGGATGTTGAATTCATCCCTCAGAGATTCCGGATATTCTCCGTCTAATTCCAAAG
CTTTCTCCATAAATTACCAGTTTGTCTTTTCTTTTCCACAGAATATTTAGGCTTAATATGTA
CGTATTGA

YLR232W, 115 aa (SEQ ID NO 184)

MGASSGRIGKSMLTQGTFFPLASSGCLKCDSTAQSLHASSSALIEFLVDFGIKPKEFPHKY
VTGLSSDDSPMDLNVGMLNSSLRDSGYSPSNSKAFSIITSLFLFSTEYLGICTY

YLR233C, 2600 bp, CDS: 501-2600 (SEQ ID NO 185)

GCGCATTTTCCCCACCCATGCGAATCATGGCTGAAATCAATGCCTGTTAGGTGCCCTGCA
ACACTAGTCATGGTAACCTTCGCAGTTAGCCCCATTTCTGGCAAACGGGAACCCACTAAAC
ATGAAATCATAGTTCTTTACATACATGTAGCCGGAATCCCTTGAAGTTGATCTGCCTCTT
CCTAGGATCTGTGAAACTGCCTTCGCTATAGAATTTTCTCTGCGACACATAGACCTTTC
ATTATTGTCTATAATACACCTTTACGTAGCTGAAGCGAGCGCACAGACGAAGGTGCTTTT

AAAAGCGATGCCCTCTTTATTGACAGTTACTAATTGCGCAAACCTGCTTTTTTTTATCAAT
GTGATTTTCGCGTTTCACGCCATTATCCAATGTCAAAAAGGATAATGGAAATGTTAACATG
CCTGTATGATCCGACCGTTTTTAGCAAACCTTATCAGGGGAAAAAGTATATTCCATTAAAT
GACACATGCCACCATAGATAATGGATAATGAAGAAGTTAACGAAGAATGTATGAGATTAT
TTTTCAAGAACGCTCGTGCGCATCTGGATAAACATCTAACATCAAGGTTGACATGCGATG
AAAAATGCATATATCACGTTTCAGATGCTTCTCGGATGGAATACATCGCAAATCTACTAGGT
TTCTCGAAGAGCTACTTTTGAAACAAGAAAATATGTACCATAATAACAATTACGAACGCA
TAAATGATTCGCGTATACCATTTGGTTCTGAAACTTTTATGGCTTCAAATTCACGAACCTA
CACTCCAATGGTTTGAGCACTGGTTCCATGATATCATGCGACTAAGTAACAGAAGAAAGT
TCAGAGTTTTTAGAATTTTTTCAAAAAAAAATGATTCAATTTTTTCAAAATTACACACAGGT
ATTACTATGACATCATCGAACACCTATGCGCAAAGTACGATATGAATTCGGTTATTTCAA
ATGCTCTCTTCGCGAAGTTGAATTTAATGCAATACACAGATGGACTTTCAACTCATGAGA
AAATTTATCTTAAACACGAGTAATCCACTGACGTTTTCCATTGTAATCTCATTACAAAGAT
GCGTGATTAATCTAGGTTCCACACATTTTTATAAAACACTACTAAACAAGCCGCTTAACA
AACCCAAGAGTGTGGAAGGTTTTGAGAAGTCTATTAGGTACTTGAATATTGCCCTCACTCT
ATCTCCACGCGTTGGAGATACTTATTTTCAACGAGCGAAAATTTACTTGATCACTGGGA
AATTCTCACTGTATTTCTTTGAATTAGTAAGAGGAGCATTGGTAAGGATTCGGTCTAAAT
GTGCGTTAAACAATTTGAAAGATTTCAATTTTGACTCCTGATTTTCCGGAAAGAAGACGTC
TGATGAAAAAATTTGGCAATTTCTTGTGTCAAAAGATCTCAAAGGTGAGAAATCATTCTTTG
AAGGTCAAATTTGTTTGAATTTCTATCGATAGTAGAACACACTTTGGTTCCACAGTCAT
GGAACGCATACGCTGCTTCTAATTTGTTGGTTATTGAAAGAGCATTACAAATGGCTGCAT
TAAAGTATCATTCAGGTAATATTAATGTTATATACTTGAAAACCTTGGCTGCCACAATGGGAA
GTTTCGATCTTATGTTTACAACCTCGAAAAAGTAAGGAACAAAAGAACAACTCAAATATG
CAGATTTGAGTGAGCGCCAGGTTTTTTTTTTAGACTTGAGCTTTGATTTTATTGCTAATA
TCATAGACGTCGTCATCAAACCTCCTGGCAAAAAAACATGGAAGACTTTTCGATATCTAG
CCATTTATCGTTTGTCTTATGTGCTGGATTAAAGTCATATAGATCTATTTTGCAGTACACT
ACAGACACAGGAAGTTTTCGACTTTCATTTCGCTTGTGCTGAACGACTTGATAAATAGTC
CACTGAATTTGTTCAAGAAATATATATAGCCACAGGCCGAAAAGAAGCTATCTTTTTAGAG
AAGATATTATTTTCAGGGAATTTTCTTGCATTAACTTTGCACTAACAGATTTTAAATGACG
ATTATGTGTATGATTCTCCCGACATGATTAATAATATAATTGGATGCCCTACATTGACTA
AAGTGCTTTCTCAAAGAAGAATGTGTTCTGCGAATTAGATCAATAATATTTCTGGCA
TGAAATTTTTAGAGAAAAATGACACCGCGCTCATATGGAATGCCAGCAAAATATAAGTTTG
ATTTAATAAGCCCAAATATTAATAAATAACGCCAAATAGCATTATCGGAAATTTCTCTCCA
AAATAAATGTAAAAACACAACAGGAAAGAGTAGTCTCTTCGAGAAAAGTTGAGGCCAAAA
GAGATGAACAACAGCGCAAAAGAGCCGGGAAAATAGCTGTGACAGAATCGGAAAAACAAT
TTGCAAAATGTCCGAGAACAAAAAATTTGTCTCCGCTCCCAGAAAAAGATGGCGTTTCTT
CTGAGTTGGTAAACATGCTGCTTCACGAGGGAGAAAACTATCACTGGCCCACTATCCT
CTGATTTTCTCTCATATCCAGACGAAGCAATTGATGCTGATGAGGACATCACCGTCCAAG
TGCCAGATACTCCTACTTGA

YLR233C, 699 aa (SEQ ID NO 186)

MDNEEVNEECMRLFFKNARAHLDKHLTSRLTCDENAYITFRCLDGIHRKSTRFLEELL
KQENMYHNNNYERINDSVIPLVLKLLWLQIHEPTLQWFEHWFHDIMRLSNRRKFRVFRIF
QKKMIQFFKITHRYYYDIEHLCAKYDMNSVISNALFAKLNLMQYTDGLSTHEKII LNTS
NPLTFSIVISLQRCVINLGSTHFYKTL LNKPSPKPKSVEGFESIRYLNIA SLYLPAVG
TYFQRAKIYLI TGKFSLYFFELVRGALVRIPSKCALNNLKDFILTPDFPERRRLMKKLAI
LVSKDLKGEKSFFEGQIVLQFLSIVEHTLVPSQSWNASRASNCWLLKEHLQMAALKYHSGN
INVILENLAATMGSDLMFTTRKSKEQKNKLKYADLSERQVFFLDLSFDFIANIIDVVIK
PSWQKNMEDFRYLAIIRLLMCWIKSYRSILQYTHRRKFCTSFALLNNDLINSPLNCSGN
IYSHRPKRSYLFREDIIFREFSCINFALTDFNDDYVYDSPDMINNIIGCPTLT KVLSPE
ECVLRIRSIIFSGMKFLEKNDTGVIWNASKYKFDLISPNIKIKRQIALSEISSKINVKTQ
QERVVSSRKVEAKRDEQQRKRAGKIAVTELEKQFANVRRTKKLSPLPEKDGVSSELVKHA
ASRGRKTTITGPLSSDFLSYPDEAIDADEDITVQVPDPT

YLR234W, 2471 bp, CDS: 501-2471 (SEQ ID NO 187)

AATGGTATCACGGAATCATTTATGCGTTTCGTAATTGTTATTATGGTACATATTTCTTGT
TTCAAAAAGTAGCTCTTCGAGAAACCTAGTAGATTTGCGATGTATTCCATCCAGGAAGCAT
CTGAACGTGATATATGCATTTTCATCGCATGTCAACCTTGATGTTAGATGTTTATCCAGA
TGCGCACGCGCTTCTTGAAAAATAATCTCATACATTCTTCGTTAACTTCTTCACTATCC
ATTATCTATGGTGGCATGTGTCAATTAATGGAATATACTTTTTCCCCTGATAAGTTTGCT

AAAAACGGTCGGATCATACAGGCATGTTAACATTTCCATTATCCTTTTTGACATTGGATA
ATGGCGTGAACGCGAAAAATCACATTGATAAAAAAAGCAGTTTGGCGAATTAGTAACGTG
CAATAAAGAGGGCATCGCTTTTGAAAGCACCTTCGTCTGTGCGCTCGCTTCAGCTACGTA
AAGGTGTATTATAGACAATAATGAAAGTGCTATGTGTCGAGAGAAAAATTCATAGCGA
AGGCAGTTTCACAGATCCTAGGAGGAGGCAGATCAACTTCAAGGGATTCCGGCTACATGT
ATGTAAAGAACTATGATTTTCATGTTTGTAGTGGGTTCCTGTTTGCCAGAAATGGGGCTAACT
GCGAAGTTACCATGACTAGTGTGTCAGGGCACCTAACAGGCATTGATTTTCAGCCATGATT
CGCATGGGTGGGAAAAATGCGCCATCCAAGAGTTATTTGATGCGCCACTGAACGAGATTA
TGAATAACAACCAAAAAAAGATAGCAAGCAACATCAAGCGAGAAGCGAGGAATGCAGACT
ATCTGATGATATGGACAGATTGCGACCGGGAAGGAGAGTACATCGGTTGGGAGATATGGC
AGGAGGCCAAGAGAGGCAACAGGCTCATACAAAATGATCAAGTATACCGGGCAGTCTTTT
CGCATCTCGAAAGACAACACATATTAAATGCAGCACGAAACCAAGTCGATTGGATATGA
AGAGTGTGCACGCTGTAGGCACGCGGATTGAAATCGATCTTCGAGCAGGTGTTACATTCA
CCAGACTCTTAAACAGAAACGCTACGAAATAAACTGAGAAACCAAGCCACCATGACCAAGG
ATGGTGCAAAAACACCGCGGTGGTAACAAGAAGCACTCACAAGTCGTATCGTATGGTACAT
GCCAGTTTCCAAACGCTCGGCTTTGTAGTAGACAGGTTTGAAAGAATACGAAATTTTGTTC
CCGAAGAGTTCTGGTATATCCAATTGGTAGTCGAAAACAAAGACAACGGCGGAACAACAA
CGTTCCAGTGGGACAGGGGCCACTTGTTCGACCGGCTGAGCGTGTAAACGTTTACGAGA
CATGCATCGAAACCGCCGCAATGTTGCTCAAGTAGTAGACTTGAAATCAAAGCCAACAA
CGAAATACAGACCTTTACCTCTGACCACAGTGGAGCTACAAAAAACTGCGCCCGGTACC
TGCGTCTGAACGCGCAACCAATCACTAGACGACGAGAAAGCTATACCAAAAGGGGTTCA
TATCGTATCCAAGAACAGAGACTGATACTTTCCACACGCAATGGACCTAAAATCCTTGG
TCGAAAAGCAAGCTCAATTGGACCAACTCGCTGCAGGCGGCAGAACCGCTGGGCATCGT
ACGCGGCATCGCTGCTCCAACCCGAAAACACAAGTAACAATAACAAGTTCAAGTTTCCAC
GAAGCGGCTCCCATGACGACAAAGCGCATCCACCAATCCACCCCATCGTAAGTCTGGGGC
CTGAAGCAAAATGTTTCGCCAGTGGAAAGAAGAGTATACGAGTACGTGGCCAGGCATTTT
TGGCATGCTGCTCAGAGGACGCCAAGGGCCAATCGATGACCCTTGTGTTGGACTGGGCCG
TTGAACGTTTCTCAGCTTCAGGTCTCGTAGTCCTAGAGAGAAATTTCTCGATGTTTACC
CTTGGGCCCCGATGGGAAACCACCAAGCAGTTACCGCGGCTTGAAATGAATGCCCTCGTAG
ACATCGCGAAGGCCGAAATGAAGGCGGGCACTACGGCGCCGCCAAGCCGATGACTGAGA
GTGAACCTATTCTCTCATGGATACAAACGGCATTGGCACAGACGCCACCATTCGGGAGC
ACATAGACAAGATCCAAGTACGTAATTACGTTAGGAGCGAGAAAGTAGGCAAGGAACCT
ACTTACAACCCACGACCCCTGGGTGTCTCACTAGTGCACGGCTTCGAGGCCATCGGCCTCG
AAGACTCCTTTGCAAAGCCCTTCCAGCGCAGAGAAATGGAGCAAGACCTCAAGAAAATCT
GCGAAGGTATGCCCTCAAGACTGATGTTGTAAAGGACATAGTCGAGAAGTATAGGAAGT
ACTGGCACAAGACGAATGCCTGCAAGAATACTCTCTTGCAAGTTTATGACCGTGTCAAGG
CATCCATGTAA

YLR234W, 656 aa (SEQ ID NO 188)

MKVLCAEAKNSIAKAVSQILGGGRSTSRDSGYMYVKNYDFMFSGFPFARNGANCEVTMTS
VAGHLTGIDFSDSHGWGKCAIQELFDAPLNEIMNNNQKKIASNIKREARNADYLMITWD
CDREGEYIGWEIWQEAQRGNRLIQNDQVYRAVFSHLERQHILNARNPSRLDMKSVHVG
TRIEIDLRAVTFTRLLTETLRNKLNRNQATMTKDGAKHRGGNKNDQVVSYGTCQFP TLG
FVVD RFERIRNFVPEEFWYIQLVVENKDNNGTTTFQWDRGHLFDRLSVLTFYETCIETAG
NVAQVVDLKS KPTTKYRPLPLTTVELQKNCA RYLRLNAKQSLDAAEKLYQKGFISYPRTE
TDTFFPHAMD LKSLVEKQAQLDQLAAGGR TAWASYAASLLQ PENTSNNNKFKFPRSGSHDD
KAHPPIHPIVSLGPEANVSPVERRVYEVARHFLACCEDAKGQSM TLVLDWAVERFSAS
GLVV LERNFLDVYPWARWETTKQLPRLEMNALVDIAKAEMKAGTTAPPKPMTESELILLM
DTNGIGTDTATIAEHIDKIQVRNYVRSEKVGKETYLQPTTLGVSLVHGFEAIGLEDSFAKP
FQRREMEQDLKKICEGHASKTDVVKDIVEKYRKYWHKTNACKNTLLQVYDRVKASM

YLR238W, 1937 bp, CDS: 501-1937 (SEQ ID NO 189)

CTTCGTTACACTTAATATTAAATAACAGCTCTTTCCCTAATAATAACATATACACTAGAT
ATATAATACCAAATAAATTAAAAAAGAAAAACAAAAATAACGTAGCTTTGTACAG
TCGTAAAAAAGAACATAAACCAATCTTATTGCCAGCGTCTAACTAGTCCTATTATAT
TCCAATATATTAAAGGGGTAAAGGACTACTATTATTCGCCCTGAATTGAAATCTTTTAGAAA
GCACCTGTTCTCTCTCTGGTGTCTCTTTTCTCATCTATTATCTAATTTCTTCAACCTT
CGTTATTGTTGTTATTCCGTAATCGTGGTGTCTCAACTTTTGAAATTTCACTTGTTTACC
ATAACGGAACATAATTAAAAATTTGTTCTTGAAAGTCACAAGCACTACGTGAACACAAAA
TTAAGGCAAGAGTGACAAAGTAACCCCTCACAAGGAGCCTGTCGTTGGTTATATTGGAAGC

TATAGATATAATCGAATCCAATGACTGGTCCTGGACCTGAAATAAATAAGGAGGAGCACC
CCAGTTCTCCGGGCAAGAAACAGATAACATATAATAGTATACCCAAGAATGCAAATCTAA
TTGATGGATCTACGAATTCATCGAAGAGGCCAATTGAAAAGTATGACAAGAGAATAGCCG
ACCCAACAAAAAGCTATTTTCCACATAGCATATCAAGAACACCAAGGAGAAAAATATACTT
ACATTCTAGTCCCTCACATCACTAAATGGAACCTTTTGAGAGCAAACATGTGGTGATACCAT
TTAAACCAGATGGTTTGAAATTGGGAAGGCCTGTTGCTAATAGTAATAGCAGCTCCAGTT
CATCGCTCAGGGGCGGTAAAAGAGTGGAATTCACACACTTTTTCCCAAGTAAGGTCCGATA
ATGGTAATTTTCGATTCAAGAGTACTCTCCAGGAATCATGCATTGTTAAGTTGCGACCCGC
TCACGGGTAAAGGTATATATACGAGACTTAAAAATCCAGTAATGGTACGTTTCAATACGGTC
AAAGAATTGGCTCAAATGACGTAGAAATCAAAGTTGGCGATGTGATAGACTTGGGAACAG
ATATAGATACGAAAATTGAGCATCGAAAAATAAGTGCCACAGTTGAAGAATATTTGTAC
AACCTTTATTAGAAATCACCGATTTTGAAGATGAAGATAGTGATGATTGCCATACAATTA
CAGAAAAAGAGGAGGCTGCTGCCATAACAAGTCACATATATGGTGATTCCAACAACCTAG
AATTGGAAGAAGTTATCCTGGGCTCTGATACAGAAATACTGAGTGGAATTTTATTATAA
ATTGTATTGGTACGAGCCCGACTTTATCTAATATCATCAAAACCCTGGCAATGGAAATTC
CATTTTCCAAATGCGATAATTTTAAATTACAGTCGATGGAGAATTTCTTAATTAATTATA
CGACACATCTAGAATACACGAACAACTTTTAGTGGAAGAAAAATGATCAGCAACTGGTAA
AGCTGCAAAATGGATTAAAGAAGGAACTGTCTGGGGAAATACGAAAAGATTATCGAACAAA
ACAGAAATCAAGTAAACAGTTGGAAGGGACCATATGTTTTTCAAAAAGTCATTTGAAG
TGAAGAAAAGAAAGAAATAATGAAAAGCAAAAAAGCATGGAAGGGAAATAGAAGACTTGA
AAACTAGGTTAGAAGTGAACGATATAAGAATTCACAAATGATGAAGAAGAACAACAGA
AAGAACAAGAACTCTCAACTGCATCTAAAAAAAAGACTACCGAACATGACACTAGAGGCG
TCCCGGGCATGAATCCTAAGGGTACTGACAAATTTAGCATCAAGAACACGCTATGTAATC
ATTTACACTATTAACATTTGGAATATTTCCATCGGGATTATAGCTATTGTCTTCAAGA
TCCTTTCCCCCAACTAG

YLR238W, 478 aa (SEQ ID NO 190)

MTGPGPEINKKEHPSSPGKKQITVNSIPKNANLIDGSTNSSKRPIEKYDKRIADPTKSYF
PHSISRTPRRKYTYILVLTSNLGTFESKHVVIPFKPDGLKLGRPVANSNSSSSSSSLRGGK
RVDSHTFQSQRSDNGNFDNRVLSRNHALLSCDPLTGKVYIRDLKSSNGTFINGQRIGSND
VEIKVGVDVIDLGTIDITKIEHRKISATVEELFVQPLLESPIFENEDSDDCHTITEKEEAA
AITSHIYGDSNNLEEEVILGSDTEILSGIFINNCIGTSPTLSNIIKTLAMEIPFSKCDN
FKLQSMENFLINYTHLEYTNKLLVEKNDQQLVKLQNLRRKLSGKYEKIIEQNRNQVKQ
LERDHMFKKSFVKKRRNNEKQKSMEREIEDLKTRLEVERYKNSQMMKKNKQKEQELST
ASKKKTTEHDTGRVPGMNPKGTDKFSIKNTLCNHFTLLTFGTISIGIIAIVFKILSPN

YLR241W, 2849 bp, CDS: 501-2849 (SEQ ID NO 191)

CGAACATACCTGATATCAGAATAGATCCCAATGGTGCTATATTACGTGTAAGAGAGAGAT
TTAATTTGAATATGTCCGAAGAGATGCCACAGTGCAATTTTTCAGAATCTAATCAATGATA
GTGTAAATGCTTTTGCTGCCATATCGTGATTGATCATTTACATAATCTGGCACAATACTGGC
GGACCTGATTGGTTGATAATTGGTGCTTCAAAATTTAAATTTTCGTCACTCTAATTATACT
TAACATATAAATGGTACCTTCAATATATCTTCTTAGTAAAAAGTAGCATGATTTTGTGTT
AATTTGCACTTTTTTTTATTTAAAAATAAAAAATCACAGTTAATTTTTCATGATCTTGCAA
GACACGCCTCCCCCTAATGTGGCATATATAACAATTGTGAATCAGAAAAACTCAACACTT
TAACATAATGGCGGGCACGAAGGCTAAACAAACAAGATTAGCATTGAATGCCTTTTTTGG
GTACAATAGAACAGTACTGAATGACATCATATATCGAAAGGCTCAAGTCGGCAGCATCGT
ATCTTGATACAGTTCCAGATGAGCATCATGATTTTCAGAAAACCCACCGCCAAGGTTGTAA
CGACGCAACTGACTATTGCTACTTCACTAGGTATTTTGCTTTGCTTTTCGTTCTCAATTC
TACTAAAAAAGTGGCCTAGATTATACGCAAGCAGACGATATAAAGATGACGGGAACCTTC
GCTTACCGTCCCTGGAATCAGTCAAGTTTATTCGGCTGGTTAACAGTGTTGTATAAGATAC
GGGACGAACAGATTCTGGAATATGCAGGTTTAGATGCGTATGTGTTTTTGAGTTTTTTCA
AAATGTGCATCAAATTACTTTCTATTTTGTCTTCTCTGTGTGCGTTATATCTCCAG
TAAGATATCATTTTACTGGAAAAATTGATGACGGCAACGATGATGATGACAGTGAAGTT
CTTTAATACATCTGGTAAAAAGAATTGTGGAGGGAAGTGGCGATGGTGACAATCATTACAG
CTCCCGAACGTACAAATGTGTACCTCTGGATGTATGTTCTCTTCACATATTTCTTCACCT
TCATAGCAATTAATAATGGCAGTTGCGGAAACAAAGCACGTCGTAAGTACTAGGCAAGCTT
ATCTTGGGAAGCAAAATACGATTACTGATAGAACGATAAGGCTCTCAGGCATCCCGATAG
AGCTTCGTGATTTCGGAAGCCTTAAAGACCAGAATTGAACAATTAATAATCGGCACCGTTT
CATCAATCACTATTTGTGCGAGAGTGGGGTCTTTGAACAAGCTATTTTATTGTGCGGAAGA
AAATACTCAAAAACCTGGAATTAATAATTCAGAATGTCCAAGGGAGCTCCGTACTCGAC

AACCATATTTCGGAGAACTATCATTTATTGGGAAACGAGCAATCAGGCGCAGTTACACATG
GAGAAAATGTTCCATCAAGCAATAATAATGACGAGGATACTATACTATATTCTCAAATTT
CTCTTGGAGAGAGACCAAAAATGAAAATTGGATATCGTGGTATCTTTGGGAAGGAAGTAG
ATGCCATAGAGTACCTGGAGCAGCAATTAAAATTTATTGATGCTGAAATTTATTGAAGCGA
GGAAACAACACTACTCCGCAACACCTACGGCATTCGTTACGATGGATTCTGTTGCTAATG
CGCAATGGCAGCTCAGGCGGTATTAGATCCTAGAGTACATTACTTCATAACCAGATTGG
CTCCTGCACCTCAGGATATCAAGTGGGATCATGTTTGTCTTTCTAGAAAGGACCGGTTAA
CAAAAGTTTATTCTACTACCGTATTTATAGGCCTTTCAAGTTTGTTTTATGTCATTCCCTG
TATCATACTTAGCCACATTTGCTAAATTTGAAAACACTTTTCGAAATTCGGCCAAGCGTAG
GGCAGCTACTAAAAGATCACCAGTGGGCGCTAACATTGTAACGGGGCTATTACCAACCT
ATCTCTTCACATTGCTTAACTTTGGAATCCCTATTTTTACGAGTATTTGACTTCTTATC
AAGGATTGGTATCATACAGCGAAGAGGAAATCTCACTTGTTCAAAAATTTCTTTTATA
TTTTTGTCAACCTTTTTCTTAGTTTTCACATTGGCAGGTACAGCATCTAATTACTGGGCGT
ACCTCAGCGATACCACCAAAATTTGCTTATCAACTTGCTACATCTGTGAAGGAGTTCTCCT
TATTCATAGTCGATTTGATTATATTGCAAGGTATTGGTATGTTCCCGTTTAAAGTTGTTAT
TAGTTGGTAGTTTGATCGGCTTTCTCTAGTGAAAATCAAGGCTAAGACACCTAGGCAAC
GGAATGAACCTTACAATCCACCGATATTTAACTTTGGACTACAATTACCACAGCCAATTC
TGATTTTGATTATAACGTTGATCTACAGTGTAATGAGCACGAAAATTTTGACTTCAGGGC
TGGCGTACTTTATTATTGGGTTTTACGTCTATAAATATCAATTGATTTTTGCCACAGATC
ATTTGCCCCATTCTACAGGAAAAGTATGGCCATTAAATTTTAGAAGAATCATCGTTGGAT
TGCTATTGTTTCAATTAAACAATGACAGGAACACTGGCAGGATTGCAAGGAGGATGGGTTT
TGTCATCTTGCTTTTCCCGCTTCCAGTAGTGACATTATGTTTCTATATGATTTCCGAGA
AGAACTATTTGCCGTTGTCAAATATATCGCATTGAGTTCAATTCGCGAGTACGAAAGAG
ACAAATCTACGGTGAATTCGCCAATGAGGAAGAGTCGTATGCATACCTTACGCTGTGA
GTGAATTAGAGGGTCCGATGTTGGATTGA

YLR241W, 782 aa (SEQ ID NO 192)

MTSYIERLKSAAASYLDTPDEHDFRKPTAKVVTTLTIATSLGIFALLSFSILLKKWPR
LYASRRYKDDGNLRLPSWNQSSLFGLWLTVLYKIRDEQILEYAGLDAYVFLSFFKMCIKLL
SIFCFFSVCVISPVRYHFTGKIDDDDDSESLIHLVKRIVEGSGDGDNHSAPERTNV
YLWMVLFYFFTFIAIKMAVAETKHVVSTRQAYLGKQNTITDRITRLSGIPIELRDSEA
LKTRIEQLKIGTVSSITICREWGPNLKLHFCRKKILKNLELKYSECPRRLTRQPYSENY
HLLGNEQSGAVTHGENVPSSNNDEDTILYSQISLGERPKMKIGYRGIFGKEVDAIEYLE
QQLFKIDAEIIEARKQHYSATPTAFVTMDSVANAQMAAQAVALDPRVHYFITRLAPAPHDI
KWDHVCLSRKDRLTKVYSTTVFIGLSSFLVPIVPSYLA TLNLKTLKFWPSVGLLKD
QWAANIVTGLLPTLYLFTLLNFGIPYFYEYLTYSQGLVSYSEEEISLVSKNFFYIFVNLFL
VFTLAGTANAYWAYLSDTTKIA YQLATSVKEFSLFYVDLIILQGIGMFPFKLLLVGSLIG
FPLVKIKAKTPRQRNELYNPPIFNFLQLPQILILITLIYSVMSTKILTSGLAYFIIG
FYVYKQLIFATDHLPHSTGKVWPLIFRRIIVGLLLFQLTMTGTLAGFEGGWVLSCLFP
LPVVTLCLFLYDFEKNYLP LSKYIALSSIREYERDNSTVNSANEESYAYPYAVSELEGPM
LD

YLR321C, 1781 bp, CDS: 501-1781 (SEQ ID NO 193)

TTCAAGTGCACCTTTGTAAAGGAAGATTACAAGTCTCCAGTGGTCACAACTGTGGCCAT
TATTTTTGTGGATCGTGTTTTGCCAAAGATATGAAAAGGGCACCAATGCTTTATATGC
CACAAGGAGACCCACGGCAGTGCAAAAGTAGCATCTGACTTACAGAAGATGCTAAATAAA
AGGAAAAGTTGATGGAGAATGCCATATACCCCCAAAATTACACGCACCCGATGCTAATG
TACAGGAATTATAGAGCACATGACCCATAGATTTATCGAGCATTGTTGCAATTTGCAAG
ACTCTTTCACATAATAAAGTATGTAACTATATAGATAGAAGATGTCCCGTGTCTTTTGT
TCTACTAAATGATGATCTGCTCATTTAAAGTCGCCGCGACTACTTTGACAAAAA
ACTTAGAAAAATACGACAAATAGAGATTATTGAATGAAGTACATTGAAAAAAGAAAGA
AAGGCACATAGCAGCACACAATGTTCGACCAAAACCAGCTTATCCACAAGCTTATATTT
CTAACTTTTCATAACAGATTGACAAACGAAGATGATGGTATCCCCATCTTTACAATGGCTC
AACAAACAAGGCAGCATAAAAGGGCTAAAGTGGTCAACTATGCGGAATATGACAACGATC
TCTTTGATGAATTCAATATGAACGGTTCTAATTTCAACAATGCTGATACACACTATAAAG
ATAATGCAGTGTCTCATGAAAATACTCCGGCACTTACAAATGGTGTACCATGGACGGTT
CCGAATACAATGTCTTAGAGAACATGAATGGAGCTGATAGTATTATCTTAACAACAAT
ACGATCGCGGTTCAAACATGGTTGTGGAATCTTTATCCGGTTTGAATAGCAATAACAACG
CCAGCAATGGTCCGAGCAACAAGCGCAGGCACAGGATATTGGAAACGCCGTTCTACCGG
ATCTGCAAGACCAACACCACAACCCCTTCAACATATTGAGATACCCTAAAATAAGAGATA

CTTTCATTAAACGGAAGTGGTGTCTCCATATAGACTCAACACTGATCAAGAAACGAAGG
CAAACGCCAATTCTGGAGAGGCAATCATGATACCAATTACTTTGGATATAGAACATATGG
GTCATACCATAAAAGACCAGTTTCTCTGGAACACAATGACGACTCCATATCTCCGGAGG
AATTTGCCCTCTATATACTGTAAAGATCTTGATATGACTTCCGCTACCTTACAAACTCAAA
TTGCGAATATAATAAAAGAGCAGTTGAAAGACCTCGAAAATATTGCAGCCACTGAGATAA
TGTCTGACCTCCACGTGATAATCAACCTAACCTGCAACTTACAAGACAGATTTTTTTGAAG
ATAACTTCCAGTGGAACTTGAACGACAAATCACTTACTCCAGAAAGATTTGCTACATCCA
TTGTACAGGACCTTGGCTTAACAAGAGAGTTTCATCCCCTTAATATCTCAATCGCTTCATG
AAACTATCTTGAAGATAAAGAAGGACTGGGTAGATGGCCACTTGATTGAGGACCATGTCC
CAAACGATGCCGATTTGGGTACTTATCTGGTATAAGGCTGGATATTGATGAACGGGCT
CCAATTTGGTGCCCAAGGGTGGAATATTAACAAAAGAAGAAATACAAAAGAGAGAAATTG
AAAAAGAAAGAACTTAAGAAGATTGAAAAGAGAACTGATAGATTATCTAGAAGGGGCA
GGAGAAGATTAGATGACTTAGAAACCACAATGAGAATGTAG

YLR321C, 426 aa (SEQ ID NO 194)

MSHQQLIPQAYISNFHNRLTNEDDGIPIFTMAQQTRQHKRAKVVNVAEYDNDLFDEFNM
NGSNFNNADTHYKONAVSHENTPALTNVTMDGSEYNVLENMNGADSIIISNNKYDAGSNM
VVESLSGLNSNNNASNGPSNKAQAQDIGNAVLPDLQDQHNPFNILRYPKIRDTFINGKV
VSPYRLNTDQETKANANSGEAIMIPITLDIEHMGHTIKDQFLWYNDDSIISPEEFASIYC
KOLDMTSATLQTQIANIKEQLKDLENIAATEIMSDLHVIINLTCLNLDQDRFFEDNFQWNL
NDKSLTPERFATSIVQDLGLTREFIPLISQSLHETILKIKDWDGHLIQDHVPNDAAF
YLSGIRLDIDELGSNWCPRVEILTKEEIQKREIEKERNLRLKRETDRLSRRGRRLDDL
ETTMRM

YLR322W, 815 bp, CDS: 501-815 (SEQ ID NO 195)

GTCATATCAAGATCTTACAGTATATAGAGGCAAATTCCTCCGGAGATATGGAGTCGTCA
TTGTAGTTCCAGAGAACTGGTCTTTTATGGTATGACCCATATGTTCTATATCCAAAGTA
ATTGGTATCATGATTGCCCTCTCCAGAATTGGCGTTTGCCTTCGTTCTTGATCAGTGTG
AGTCTATATGGAGACCACTTTTCCGTTAATGAAAGTATCTCTTATTTTAGGGTATCTC
AATATGTTGAAGGGGTGTGGTGTGGTCTTGCAGATCCGGTAGAACGGCGTTTCCAATA
TCCTGTGCCTGCGCTTTGTTGCTCGGACCATGCTGGCGTTGTTATTGCTATTCAAACCG
GATAAAGATTCCACAACCATGTTGAACCCGCATCGTATTGTTGTTAGAGATAATACTA
TCAGCTCCATTTCATGTTCTCTAGGACATTGTATTGGAACCGTCCATGGTAACACCATTT
GTAAGTGCCGGAGTATTTTCATGAGACACTGCATTATCTTTATAGTGTGTATCAGCATTTG
TTGAAATTAGAACCGTTCATATTGAATTCATCAAAGAGATCGTTGTCATATTCGCGCATAG
TTGACCACTTTAGCCCTTTTATGCTGCCTTGTGTTGTTGAGCCATTGTAAAGATGGGGATA
CCATCATCTTCGTTGTCAATCTGTTATGAAAGTTAGAAATATAAGCTTGTGGAATAAGC
TGGTTTTGGTGCGACATTGTGTGCTGCTATGTGCCTTTCTCTTTCTTTTCAATGTAC
TTCATTCAATAATCTCTATTGTGCGTATTTCTAA

YLR322W, 104 aa (SEQ ID NO 196)

MRHCIIFIVCISIVEIRTVHIEFIKEIVVIFRIVDHFSPFMLPCLLSHCKDGTIIIFVCQ
SVMKVRNISLWNKLVLRHCVLLCAFLLSFFNVLSHSIISICRIF

YLR325C, 737 bp, CDS: 501-737 (SEQ ID NO 197)

CCACATGTCACAACTACTTTGTGAAGTTGCAATGCGTGATTAGTATTATAAAACATCATA
GCCTTGCCAAATAAACTCGCTTCCCAGAAAAGACGCCAAATTAACGCGCGTGTATGTG
ACAAAACAGGGCATCTCACATATTGCGGTACTGGTGTTCTTTTAGCTCATTCCGATATTA
TTCCAAGACGGAATTTTCATCTAGAGAAAATGCATCCGTGCATTTTCATAAACCCACACA
ATTAAAATGCCTTGCGAAAAGGAGGACTCGTCCGTGCAACTGTTGAAAAAATAGACGGA
GCATCATACGTTTCGAGTGGAATAATATGGAGAGTTTTCCAAGCTCTATGGCATGTAGAGT
CGTGATTGCTGCTGTACGCTTTTGCACAATATTGAATCTTCAATCTAAAGAATTAAATTT
TCTAATTTCAATGTAGAAATATTTCAACTGTTAGTTTTTTTATTTTCAGGTTGAATATAGTA
CGACAAAATATCAAGGAAAAATGGCTAGAGAAATCACCGACATCAAACAATTTTGGAAAT
TGACCAGAAGAGCTGACGTTAAGACCGCCACTGTTAAGATTAACAAAAAATGAACAAGG
CCGTTAAGCCATTCAGACAAACCAAGTTCAAGGTTAGAGGCTCTTCTCTTTGTACACTT
TGGTTATCAACGATGCTGGTAAGGCTAAGAAATTGATCCAATCTTTGCCACCAACTTTGA
AGGTTAACAGATTATAA

YLR325C, 78 aa (SEQ ID NO 198)

MAREITDIKQFLELTRRADVKTATVKINKKLNKAGKPFRTQTKFKVRGSSSLYTLVINDAG
KAKKLIQSLPPTLKVNR

YLR344W, 1331 bp, exon1: 501-519, intron1: 520-966, exon2:
967-1331 (SEQ ID NO 199)

TAAGGGCTGTCAATTTTTCATTTCCCTCAAAGTTAATGCGCAAGAGTTAGGATGATCTTG
ATTATTAGTTATTTGTTTGTTCATCAATTATGCCGACGTCCATGAATGCTATTGAAGTA
TCGATTACTTATGCTATTCTATTGTATTGAGCCGGCGGCTAGTAAACAAGACAGCATAC
CTTTCCAACATCCGTACATATTGATTATTGTATCTATGATTTTCATGTAATGTATGGGTT
AACTAATCCTTTCTCTTCTTTTTTTTTTTTCTGAAAATCAGTAGCTAGAGGAACCTGTTT
GTGAAAGATATGGAATATTCCGTCTAGGGAAGAGCCGAGAGCTGAGAGCAGTATCCATCG
GATGGAATCTTGCTGGATGCGTAACGACGACAGCTTGTCTAGAAGGCCAAGTACAAGAT
ACTAAGAAGACTATAACAACAGAAGACAATTTGTAGTGCGATTCTATATTATTGACGTA
ACCAACAAAAAGTATCAGAATGGCTAAACAATCATTAGGTATGTGCACAAATGCTAAAT
CACTGAAACCTGTAGAGCTGGAATTGAAAATATAGTTTGTACCTTTTGCTGAGGGCAG
AATGACTCAATGTTATCTTAATTCGATTAGAAAAAGAAGGTGCGTTATCCAAGGTTGAAA
CTTGTAAACTATTTAGGTGATGTCTCATAACTGCAACCACTGGAAAATGACGCAAAATATC
AAAAATAATAGGGAGATAAAGTCTCAGGACATGAAAAATCATAGAATTATTGTTCAATTT
ATCTAGCCGTATCTTACCTTATGGAAAAAGTGTGAATATGTTTTCTAAATCGAGCTTCC
CGGAAATTACACTATATTATGCATCCGTGATACATCTGAAATTCAATACTTTCTCCAAGG
TCCTGCTTACTTAAGAGGGTAAGATTTGTTGAAACTCGAAATACTAACATTATTTTCATTA
TTTTAGACGTTTCTCCGACAGAAGAAAGGCTAGAAAGGCTTATTTACCGCCCCATCCT
CCCAACGTCGTGTTTGTCTATCTGCTCCATTATCTAAGGAGTTGAGAGCTCAATACGGTA
TCAAGGCCCTTGCCAATCAGAAGAGATGATGAAGTTTGGTTGTTTCGTGGTTCCAAGAAGG
GTCAAGAAGGTAAGATTTTCATCTGTTTACAGATTGAAATTTGCCGTTCAAGTTGACAAGG
TTACCAAGGAAAAGGTCAACGGTGCTTCCGTTCCAATTAACCTGCACCCATCCAAGCTTG
TCATTACTAAATTACATTTGGACAAGGACAGAAAAGCTTTGATCCAAGAAAGGGCGGTA
AGTTGGAATAA

YLR344W, 127 aa (SEQ ID NO 200)

MAKQSLDVSSDRRKARKAYFTAPSSQRRVLLSAPLSKELRAQYGIKALPIRRDDEVLVVR
GSKKGQEGKISSVYRLKFAVQVDKVTKEKVNAGASVPINLHPSKLVITKLHLDKDRKALIQ
RKGGKLE

YLR367W, 1376 bp, exon1: 501-633 intron1: 634-1116, exon2:
1117-1376 (SEQ ID NO 201)

ACTTTTTGCTGCTGCTGGTTCGTTTGTCTTTTCGTTTTTAAAATTGCGCTAGACAAGTAAAC
AGGGATTGCTTAAAGAAATCAAAGTAGCTTAACTCTAAAGTATTATTTTCCTCAGTTGTGGG
CCCATGTGTTGGAGGGAAGGAATATATTGAAATGTAAATGTTCTTAAGTTCCGTTGAACT
TGGATATTGTTACAAGAGTTCTAGTCTTTGATACCATTTTTACGCAATTACAACCGCATT
ATTTACCTTTTCATCTTCAGTTTTACGGTTCAGTTTATTCTGTTACGAAAGAACTATGGT
GATTCAAAGGCGAAGTCCGTAGGATTGTAACCTCTATATCTTTAGGATACTTACAATTTT
GTACTGTTTTCAAGACCACTGTAACCGATAATAAACCGGAGGACACATTTTAACCCACTA
TTTTTTTCAGAAGATCAGATGCGAGAGCTCGAAGCATAAGTATAATACTAACGTTTCAAA
ACATAGTAATTAGGTAAAAAATGACTCGCTCTTCCGTTTTAGCTGATGCTTTGAATGCCA
TTAATAACGCCGAAAAGACCGGTAAACGTCAGGTTCTATTGAGACCTTCTTCCAAGGTTA
TCATCAAGTTTTTACAAGTTATGCAAAAGCATGGTATGTTCCAATATTTTTCAATATTT
TCACATGTGTTTCAATTTCTGCTTATTTTTTAAATGTTACCACGAGGTTTGTCCAAGTTCA
ATGTTGCGCAACTCTAACGAAGAAATAATTATTGCCATTGTTTTTACTCCGGGCTGATA
ACTAGATGGTGTGATCGGGCAGTATACTAATTTATACTGGACAAAGACTCGTAAAAGATG
TTCTTTGTGCTTAGTCCCATACTGTTTTTAAAGTGTCGGGATATTTAATCCCATGTGGA
AATGCTTCTTACACGGTTATGGATTACACCTCATGTGTAGCTACTATATCCATTACCGTT
TACTTTTTCTCAAATCTCACTCTTAAATTTTCAATGGCAAAATCTTCCGCACAATTT
AGACAACATTTCTTGTTTTTTATGAAGTAAGCAAAAATTTTCAATCAACAACGCTCCAT
GAGATTCTTCAATACTAACATTTACTCCTTATTTAGGTTACATTGGCGAATTCGAATACA
TTGACGACCACAGATCTGGTAAGATTGTCGTCCAACGTAACGGTAGATTGAACAAATGTG
GTGTTATTTCCCCAAGATTTAACGTTAAGATTGGTGACATTGAAAAATGGACCGCCAAC
TATTGCCAGCCAGACAATTCGGTTACGTTATTTTGACTACTTCTGCGGGTATTATGGACC
ATGAGGAAGCTAGAAGAAAGCACGTTTCCGGTAAAATCTTGGGTTTTGTCTATTAA

YLR367W, 130 aa (SEQ ID NO 202)

MTRSSVLADALNAINNAEKTGKRQVLLRPSSKVIKFLQVMQKHGYIGEFYIDHRSGK
IVVQLNGLRNKCGVISPRFNVKIGDIEKWTANLLPARQFGYVILTTSAGIMDHEEARRH
VSGKILGFVY

YLR393W, 1340 bp, CDS: 501-1340 (SEQ ID NO 203)

CCCTCAACCCGCATTTTGCTGAGAATTTTCACCAAGGCCCTAGGTGATATTAGATTCCAC
CTGACTAATTGCATTACAGCCGACCCAAGGCAATATCAGTTTAATAAAAATATCATGTATC
TCACCCTCTTCTTGGTATTAGTAAAGAGACGCCCTGATCTTGTAAACAGTGGTGAAGATTGT
ACTAGAGCAGAATCAAGAATTTAAAAAGTGTAAGGCAAGGCAGAGGCGATGTACATAAA
ACTTCGAAGTAAGAAATATTTAATAGTTCCTCGCCACATCACTATGCAGCTATATAAAAAAC
TACTATAAACGTTTGTTCCTTACGCACAATATCCTTGCCCTAGAAATCGTTTTTGA
AATTTAAATTTTATTACCATTATTGATTTCGCCCTTCAGAAAAATATGGAAGAGTGCAT
ATTTAAAAAGGACTATTTTCAGCATATAGTAAAAGTCAGGTATTGTATTGCGATAT
CAGAGTAACTTAACTAATATGCAGGGCCTTTTAAAAGGTTTACCATCCCACGCTTA
CGCGGATGTCCTTCTTGGATAAATTCCTCAAGCCTATGATGGCAACGGCTTCCCCAAAGG
AATACCAGATCAAACAACTGGTCAAGCCAATAGGCTTAACACAAGCACCAAGGAAAAGCA
CCAAATAGCTCCCAGGGGAACCTTTGAGGGATATGTTTGATTTCGAAAAGACAAACCACA
GAGTTAAAGAGTTGGCCGTTGAATTCAGCAAAATCTGGACTTTATGACGTGCAAGCTTCC
AAAAGACAAAGGGGAAATGTTTATAGCTCCAGTTTCATATTGGAAAAGAAGATAAAGCTT
TGTTTTTCTCTCATTTGATAGGAACGGCAATGGATGGTACGAAACAACAGAATATCGAGG
ATATGTTAAGGGGTAAACCAGTATAGTGAGGTTATTTAGTACAGCATCTGGCGATAAGT
TGAGTAGTTCATACTTCCAAGGAATCGTAGACGATAACAAAAAACTGACTACTTGACTG
AAGCTGATGCGCGTTTAAAGTTTAAATGCAGTAACGTCCAAATCATCGAGGTCAATCTTG
TAGAAAACGCTGTGAAAAGTGCTCTAGTGAAAACGCTTGCTCGTTGGGCCAATCGCGTTC
CATCCTGGCGCCAGCCATTTTATTTTCAATGTTCTAGAGGCCAATGGCCATTTTCCGTCA
GGGAAGAGCTCTTTTGCAATAATGCTTTTCTGGATACGCTTTCTTGTGGACCAGCAGT
TAAAAATTAGGTGGGCAGCTTGCGGGGAGGCTACTCCATCTGAAAAGGAAGCATTTGTGGA
AGTTTGCCAAACGTCTGTGA

YLR393W, 279 aa (SEQ ID NO 204)

MQGTFKRFYHPTLTRMSFLDKFLKPMMATASPKYQIKQLVKPIGLTQAPRKSTKYSQGN
SLRDMFDSEKTNHRVKELAVEFSKSGLYDVQVQFKTKGLFIAPVSYWKEDKALFFPHLI
GTAMDGTKQONIEDMLRGKTSIVRLFSTASGDKLSSSYFQGI VDDNKKTDYLTADARLS
LNSNVQIIIEVNLVENAVKSALVKTLARWANRVPSWRQPFYFEC SRGQWPF SVREELFCN
NVFSGYVFLVDQQLKIRWAACGEATPSEKEALWKFAKRL

YLR423C, 1754 bp, CDS: 501-1754 (SEQ ID NO 205)

TTCTATTGGTGTAGTTATACCAGAACCATCCTTCCCAAGGCCTTTTCCCGCAACATATCC
CATACTCGAAAGTAACCTTCGCACCAATACCATATGTCCTCGTTAATTTTGAGATCGTTGG
GGCATTGCGCGCTACTAGTTTTCAAGGCATCATTAGTGATGTCATGTCATCTACTATTGCT
TGAATTATTATCTTCTCATCGCTATAATTATAGGAATCGATTCTTCTTTTTTTGAAAAA
GAACTTTTTATCTGTGTTGGAGTCCGAATCCTCCATGTTTGGCGTACTGAAGGCTTAAG
TTCTTCGACCTCTCTCGGTGTACTATTTTCAAATTTTGGATTMTTGTATTGTTTGAC
ATAATGTAAATACTAGATGCGCGCTCTAAGGCCTCAGTATTAATAAATTGCAAGATATCCC
TAACCTTGATAATTATTTGAAAGTCGCATAACGTACGATAAATTCGATACTGCCGAGGATAT
TATCAACGTATTTAACACCTATGAACGAAGCAGATGTTACAAAATTTGTTAATAATGCCA
GGAAAACGCTGACCGATGCTCAACTTTTATGTTCAAGTGCTAATTTAAGGATTGTAGATA
TTAAGAAAAAATTGTCATCTTGGCAGTTGAGTATTTCAAAACTCAATTTTCTAATAGTTG
GCTTGAGACAGCAAGGAAAGTTTCTTTTACACTATTTTAAAGGAAGGCATTGGGACAAAGC
TAATCCAGAAAACAATGGAATCAAGCTGTCTTAGTGGTCTTAGTTGATGAGATGAAGTACT
GGCAATATGAAATCACTTCTAAAGTACAAAGGTTGGATGGTATAGTAAATGAATTGAGCA
TATCAGAAAAAGATGATACCGATCCCTCTAAACTAGGAGATTACATCTCGAGAGACAACG
TTAACTTATTGAATGACAACTGAAAGAAAGTGCCAGTAATTGAGCGTCAAATTGAAAACA
TTAAGCTTCAATACGAAAATATGGTCAGAAAAGTTAACAAAGAACTGATTGATACCAAGT
TGACGGACGTAACCTCAAAAATTCCAAAGTAAATTTGGTATAGATAACCTGATGGAAACAA
ATGTTTGCAGAGCAGTTTAGCAGGGAACCTAACCGACCTTGAAAAAGATTAGCAGAGATAA
TGAATTCATTGACACAGCACTTTGATAAGACATTGCTGTTACAAGATAAAAAAATTGATA
ACGATGAACGTGAGGAGCTGTTTAAAGGTGGTACAAGGCGACGACAAAGAACTATACAACA
TTTTCAAACTCTGCATGAGGTAATTGATGACGTGGACAAAACAATTCTTAACTTGGGTC

AATTTTTGCAGGCAAAAATAAAGGAAAAGACAGAACTACACAGCGAAGTTTCTGAAATAA
TAAACGATTTCAATAGAAATTTGGAATATCTATTAATCTTTAAAGATATTTCCAATCTGA
TTGATAGCTTCAAAAATTCCTGTACACAAGATATTCAAACAACCTAAGGAACTTTGTGAAT
TTTATGATAATTTTGAAGAAAGCTACGGTAACTTAGTTCTAGAAGCAAAGAGGAGAAAGG
ATGTGGCAAACAGAATGAAAACCTATATTGAAAGATTGTGAAAAGCAGTTGCAGAATTTAG
ATGCTCAGGACCAGGAAGAACGTCAGAATTTTATAGCGGAAAATGGAACCTATCTTCCTG
AGACAATCTGGCCCCGTAAAATTGACGATTTTTCTTCCCTGTACACTTTAAATTACAACG
TGAAGAATCCTTAG

YLR423C, 417 aa (SEQ ID NO 206)
MNEADVTKFVNNARKTLTDAQLLCSSANLRIVDIKKLSSWQLSISKLNFLIVGLRQQGK
FLYTILKEGIGTKLIQKQWNQAVLVVLVDEMKYWQYEITSKVQRLDGIVNELSISEKDDT
DPSKLGDIYSRDNVNLNDKLKEVPVIERQIENIKLQYENMVRKVNKELIDTKLTDVTK
FQSKFGIDNLMETNVAEQFSRELTDLEKDLAEIMNSLTQHFDKTLQLQDKIDNDEREEL
FKVVQGGDKELYNIFKTLHEVIDDVDTILNLGQFLQAKIKEKTELHSEVSEI INDFNRN
LEYLLIFKDISNLDISFKNSCTQDIQTTKELCEFYDNFEESYGNLVLEAKRRKDVANRMK
TILKDCEKQLQNLDAQDQERQNFIAENGTYLPETIWPFGKIDDFSSLYTLNYNVKNP

YML026C, 1342 bp, exon1: 501-547, intron1: 548-948, exon2:
949-1342 (SEQ ID NO 207)
ATCTGTAAATAAAGCCCATGAAATATCAATCTCACAATGAAAGAATTGTATAATTCAG
AATGATTTGACGTAAAAGCAAGTCTCATTCAAGAACTGTAAAATCCGTACACACTACTG
AATTTTACATCCATACATTTTTTTTGAATTTTCATGTTTTTTTGAATAATTGGAAGGGC
TAAATTATCCGTCGGGGTGTCTCTAGCTCGGCTCAACCTAGGCAAATGCGTTTACTGG
GGCCATCCAAGCTCATCTTCCAGAGATTCCGCTTTCAGAGGCAAGAAGCTCGTCTCCGC
AGGCTCTTGTTCGGGAGGAGGAGAAATTTGCGCGGAAACTGGTTGATGCCTGGGCTA
TGGTAATTCTGACACCTTTGCTATCTAACTGGAAAAGGTCTTAGTAATAACAATATCA
GGTACTTTAATATTGTTAAAGATATACTATTAGTGAATAACCGATCTTACGAAAAGCCAA
TAGAGCAGAAAGTGGTAAAGATGTCTTTAGTTGTACAAGAACAAGGTTCTTCCAACACA
TTTTACGGTATGTTTTACGAGTACAGTGCAGATATGTTGAGAGAGTTTACATTACATGG
GATAATAGCTTAATATTGCGATTGAAAATATGTGAGTGCCTCCGATGGAATAATAACG
TCACGGGTTACCAAATACGAGGCCGAATTAACCTACGCTACTATAAAAAATTATCCTAG
ATTTTAAAGTAATACACAGTTTATTGGAATAACAATATATGACTCAATGCGAATTTAAA
AATTTACAGTCAATACAGCTTGACAAATTCATATTTATCGTCCCTCCATGTTCTGACGCCA
TTCCAAAATGATGCGCCATGTTGAAAATTTCTCGAAGAACCCTAGCAGTGGTGTGAAATAA
ATTATAACATAAGATGTACAATTTTTGTGCGCCCATTAACATCAGTTTGTGTAACAC
CAATGTGATGGTAACATTAAAAATTGTTTACGCTTTTGACCACTATTAAGGGTGTGGTTCG
TCGTTACTCCAACCTGGTCTGTGAAGAAGGCTGATGTTGATTGTCACAAGAGAGCTGGTGA
ATTGACCCAAGAAGAATTGGAAGAATTGTCCAAATCATGCAAAACCCAACCTCATTACAA
GATCCCAGCCTGGTTCTTAAACCGTCAAAACGACATTACTGATGGTAAGGACTACCACAC
TTTGGCTAACACGTCGAATCCAAGTTGAGAGATGACTTGGAAAGATTAAAGAAGATCAG
AGCCACCGTGGTATTAGACACTTCTGGGGTTTACGTGTTAGAGGTCAACACACCAAGAC
CACTGGTAGAAGAAGAGCTTAA

YML026C, 146 aa (SEQ ID NO 208)
MSLVVQEQGSFQHILRLNNTVDGNIKIVYALTTIKGVGRRYSNLVCKKADVDLHKRAGE
LTQEELEIRIVQIMQNPHTHYKIPAWFLNRQNDITDGKDYHTLANNVESKLRDDLERLKKIR
AHRGIRHFWGLRVRGQHTKTTGRRRA

YML063W, 1268 bp, CDS: 501-1268 (SEQ ID NO 209)
TATATTATTTTTTCCCTTCTGGGTTCTTTTCTTCTTTCTTGTGTTACCTTTTTTGCTTT
TTCATAAAATAATTTCTCTAGATTTGAAGACAGCATTTTTGTACATCCATACACCATACA
CCATACACCATAGCACCAGTACACTATATTTTTATGAATTTTACTAAGAATTTATCTCTGC
AGGAGCTCCACTGAAAAAAAAGAGCAGCATGGATGTCCGGTAGAAGTGCTACTGAGTAA
ATGGGAAGGACGCGGTAGATCCAGTGTGAATCAAGGTGGTGCCGGTGTGAAGCCGCTC
GGCCGGCTGGACTCTCCAGGCCGGAGTGATGATGCCACGCTGAACGTAACACAGTTTCA
CAATACCAGTGTCTCATTAGTGAGTTCCAATGTATAGTTAGTAGTGGTATTTTGATATA
TGTGAGTGGTAGCAGATTTGAACTTAGTTAGTTGATTTCGCCTTTGAGGAAACCAAGCAA
AAAACCGATCTAGACTAATCATGGCTGTTGGTAAGAATAAGAGACTATCCAGAGGTAAGA
AGGGTTTGAAGAAGAAGGTGCTTGACCCATTTACCAGAAAGGAATGGTTCGATATTAAAG

CCCCATCCACTTTTGGAAAACAGAAATGTTGGTAAGACTTTAGTTAACAAGTCCACTGGTT
TGAAGAATGCTTCCGATGCTTTGAAGGGTAGAGTTGTGCGAAGTTTGGTTGGCTGACTTGC
AAGGTTCTGAAGACCATTTCTTTCAGAAAGGTCAAGTTGAGAGTCGATGAAGTTCAAGGTA
AGAACTTGTTGACCAACTTCCACGGTATGGACTTCACTACCGACAAATTGAGATCAATGG
TCAGAAAATGGCAAACTTTGATCGAAGCTAATGTTACCGTTAAGACTTCCGATGATTACG
TTTTGAGAATCTTTGCTATTGCCCTTACCAGAAAGCAAGCTAACCAAGTTAAGAGACACT
CTTACGCTCAATCTTCCACATCAGAGCTATCAGAAAAGTTATTTCTGAAATCTTGACCA
GAGAAGTTCAAAACTCTACTTTGGCTCAATTGACCTCCAAATTGATTCCAGAAGTTATCA
ACAAGGAAATCGAAAATGCTACCAAGGACATCTTCCACTACAAAACATCCACGTTAGAA
AGGTTAAGTTATTGAAACAACCAAGTTCGACGTTGGTGCTTTGATGGCTTTGCATGGTG
AAGGTTCCGGTGAAGAAAAGGGTAAGAAGGTTTCTGGTTTCAAGGATGAAGTCTTGGA
CTGTGTAA

YML063W, 255 aa (SEQ ID NO 210)

MAVGKKNKRLSRGKKGLKKKVDPFTRKEWFDIKAPSTFENRNVGKTLVNKSTGLKNASDA
LKGRVVEVCLADLQGSSEHDFRKLVRVDEVQGNLLTNFHGMDFTTDKLRSMVRKWQTL
IEANVTVKTSDDYVLRIFAIAFTRKQANQVKRHSYAQSSHRAIRKVISEILTREVQNST
LAQLTSKLIPEVINKEIENATKDIFPLQNIHVRKVKLLKQPKFDVGALMALHGECSGEEK
GKKVSGFKDEVLETV

YML128C, 2042 bp, CDS: 501-2042 (SEQ ID NO 211)

TTAATAGGGTTAGCCACCATGTCTCGAACATGTTACAGGCTCGGAGCTTGTGGCGGGT
GCCTCGCTTACTGGAGTACCATTAGCGGTGTGTTGAAGCTAACGAGTTCATCTTCAAT
CTTTATTTCCACTTCTTTACAAGCTTCTGCCTTTCTCTATGACGTCTTTCCCAAACAC
TACCTCTTGACACGACTTGTGTTTTCGTTTCTCTAAGAATATCACTATTTTCACTTT
TTTACCTTTTCCACCATACGTGCGTAAGCAACAGCATTACGCCGGCCTCACCTTAGAG
GGGAAGAATAAGGGATCTTTGGAAGTGAAGGAAAATAAGGGAGAGGGAGGAAACAAGGAG
GCGGTGAAAGGGGATCGACAGGGTATTTAAAGCCACTCATGGAGTCGTATTCCTAGCATG
ATTAGATTACCGGAGTTTGAAGAGGATCTGCAATAGAAGAGGAGACAACACAAAGAA
CTGTTAATTGAAGAGAAGATGAAGCAATTCAAGTTGGTTAATGCGGTTTCCGCATCAT
TTGTGCTTATTGGCTTAGTGTGGCCAATTCAGATTCAAGTGTTCGACAAGTGGACGCGAG
AAGACCTGGCCGATTTATTACGTGATAATAAGAAGAGCTTGGAAAAGTACGCTACAGACT
CCATTGAGGACTTGAAAACGGAGGCATCGCAGGTATGGGACAAACACGCGCAGCCCCAAC
CATGGTGGCAGGTGTGGTCTAGTGACAGCAGTAGCGTGAGCAACAGTAACCCCGGATGGT
TTGGTTATATCTGGTCTTCCGATCACCCAGTTTCTGACTGGCTCTTTGACACCTGGTCCA
CAGACAGTCTACGTAACCTTCTTGAAGAAAAACGGCGTGGATGTTGACGACGCTAAGGCTT
CCAAGGACTCGCTGGTGAAGACTGCTAAGGAGAACTTCAACAAGATTTCCAAATCTTTGA
AGTCGTCGGGATACATCTCTTAGCTCTTACTTTGATAGCTGGTCAACCAAAGATTTGC
AAAACCTGGTTGAATGACAATGGTATCGACTACGACAAGGCAGTTCAAAGCAAGGACGAGC
TAGTTTCAGAAAAGTCAAGGAAAACATCTACCGAACTTCAGAAAAGGCAGAACAGCAGCGTC
TGGGTTTGCTAGAAAAGCTTGGATTGGCTCACCAACAAATATTAGACACATCGGGACAAA
TAAAGACACTGTATTTGACAAGTGGTCTAGTGATCAGTTAACCAATTGGTTGGAGAGCC
ACAAGGTCAATATTGACAAGAACATGGCCAAGAAACACGACTATTTGGTTAGAATGGCCA
AAGAAAATTCGCCAATTTGAAAGATGATATCTACTGGTACCTGGACTATATGAAAAGAG
AGTCTTCTCCATTTTGGACCAAGACCCCAAGAAACGTTGGTTCCGTTTGGGACTCTTCTA
AAAATTTCTCACAAATTTGTACTCCAAGTTCAAGGTAAGACTGACAATGTGATCAATG
ATACTTTTTTGGTTGGCTAGACTCTTGGCCAAAGGACAAATGAAAATGTTTTTAGATG
CTCGTGGTATTAAGTACTCAATGCTGTCTACTGAACATCAATTGAGAGAATTAGTCAAAA
AATCCAGAAACGAAAAACTCAAGATCCTGCCAAAAGACTACCAAAAATACTTTGACAACA
GTAACCTGGTCTTTGGATGACATAAAGGGTGGTTTGGCTGACAAAAGGACGACTTCCAAG
ATTCTCAGACTTACTCCACAATTATGCAGGATTTTGACAAGGTTTCCAAAACACAAATG
ATGCTAAGGACCAAAATCGCTAAGACCTGGTCAAATACCTTTCAAGAGCTGGTCTCAAGAAG
ACCTATTGCAGTACCTAAAATCATTCCGGTGTTCGGTTAAACAGACTTCTACGAAGGACG
ACTTAATCAACTTGGCCAAGCAGAATACGCAATGGTTGTTCCGGCACTGTTAAGGAGCCTG
CTTACAAGAGGTACCTACATAACGTTAAAAACTGGTCAAAAAGCATATTAGGGTTCAACT
AA

YML128C, 513 aa (SEQ ID NO 212)

MKQFKLVNAVSAFVLIGLVLANSDSVFDKWTQEDLADYLRDNKKSLEKYATDSIEDLKT
EASQVWDKHAQPKFWQVWSSDSSSVNSNPGWFGYTGSSDHPVSDWLFDTWSTDLSLRF

LKKNQVDDAKASKDSLVTAKENFNKISKSLKSSGYYPSSSYFDSWSTKDLQNLNDN
GIDYDKAVQSKDELQVQVKENIYRTSEKAEQORLGLLESLLDLAHQQILDTSQGIKDTVFD
KWSSDQLTNWLESHKVNIDKNMAKKHDYLVMAKENSANLKDDIYWYLDYMKRESSPFLT
KTPEYVGSVWDSSKNFLTNLYSKFRGKTNDVINDTFLVGLDSWPKDKLKMFLDARGIKYS
MLSTEHQLRELVKSRNEKLKILPKDYQKYFDNSNWSLDDIKGWFADKKDDFQDSQTYST
IMQDFDKVSKNTNDAKQIAKTWSNTFQSWSQEDLLQYLSFGVPVKQTSTKDDLINLAK
QNTQWLFQVKEPAYKRYLHNVKNWSKSIILGFN

YML130C, 2192 bp, CDS: 501-2192 (SEQ ID NO 213)

ACGAGATCATTTTCTATCTATCTATTTGAGTAATGCTTACTTTTCATATTTTCAATGAAC
AATAGGATATGTAGGAGAATTGATATATTTCACTGCGTATCAGAGAAAAGGTCTACTGACA
TTTTATGGCAAAATGTATTCTACACAAATCGAGAATACCACAGACAATGGTACAAGACATA
CACAAAGAGAAGACTGTTCTAATTAACAAATAATATTGAGCTACCTGCTAAGTATGTCC
TTTTCCCTTTGTCTTTGGTTTCTTATAGAAGACCCTGGAAATTTTTTCGCAATTTTCC
GGCTTTGGCGCTTAGTAAGAACAAGAAAGAGAACAAGAAAGAAACGATACGGGA
GTACGTGTCATAAAAACTTGTTCATCATCCTTGAAGCTAAGTATAAAGAGCTTGAAGAG
GTTTACCCTTAACTGGTTATCTATTTCAAGAGTGTAACATTTTATTGCATATACCA
CAGTAACGTGCAGGTAAAACATGAGATTAAAGAACCGCCATTGCCACACTGTGCCTCACGG
CTTTTACATCTGCAACTTCAACAATAGCTACATCGCCACCGACCAACACAAAATGCCT
TTAATGACACTCACTTTGTAGGTTCGACAGGAATGATCAGTTAGTCCAGTTGTAACG
TAACATTCAATGAATTAATGCCATAAATGAAAACATTAGAGATGATCTTTTCGGCGTTAT
TAAATCTGATTTCTTCAAATACTTTTCGGCTGGATTTATACAAGCAATGTTTCAATTTGGG
ACGCCAACGATGGTCTGTGCTTAAACCGCGCTTGCTCTGTTGATGTCGTAGAGGACTGGG
ATACACTGCCTGAGTACTGGCAGCCTGAGATCTTGGGTAGTTTCAATAATGATACAATGA
AGGAAGCGGATGATAGCGATGACGAATGTAAGTTCTTAGATCAACTATGTCAAACAGTA
AAAAACCTGTAGATATCGAAGACACCATCAACTACTGTGATGTAATGACTTTAACGGTA
AAAACGCCGTTCTGATTGATTTAACAGCAAATCCGGAACGATTTACAGGTTATGGTGGTA
AGCAAGCTGGTCAAATTTGGTCTACTATCTACCAAGACAACCTGTTTTACAATTGGCGAAA
CTGGTGAATCATTTGGCCAAAGATGCATTTTATAGACTTGTATCCGGTTTCCATGCCTCTA
TCGGTACTCACTTATCAAAGGAATATTTGAACACGAAAACCTGGTAAATGGGAGCCCAATC
TGGATTTGTTTATGGCAAGAATCGGGAACCTTCTGATAGAGTGACAAACATGTTTCA
ATTATGCTGTTGTAGCTAAGGCTCTCTGGAATAATCAACCATATTTACCAGAATTTTCAT
TCTGTGATCTAGTCAATAAAGAAATCAAAAACAAATGGATAACGTTATTTCCCAGCTGG
ACACAAAATTTTAAACGAAGACTTAGTTTGTGCAACGACCTAAGTTTGACTTTGAAGG
ACGAATTCAGATCTCGCTTCAAGAATGTCACGAAGATTATGGATTGTGTGCAATGTGATA
GATGTAGATTGTGGGGCAAAATTCAAACTACCGGTTACGCAACTGCCCTTGAATAATTTGT
TTGAAATCAACGACGCTGATGAATTCACCAAAACATATTTGTTGGTAAGTTAACCAAT
ATGAGTTGATTGCACTATTACAGACTTTTCGGTAGATTATCTGAATCTATTGAATCTGTTA
ACATGTTTCAAAAAATGTACGGGAAAAGGTTAAACGGTTCTGAAAACAGGTTAAGCTCAT
TCTTCCAAAATAACTTCTTCAACATTTTGAAGGAGGCAGGCAATCGATTTCGTTACACCA
TAGAGAATCAATTCCTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG
TATTTGATGATTTAAAAATGCCCAAGCAGAAATAGTTTCAAGGCCCTCTAACGGTACAG
TAAATAAATGGAAGAAAGCTTGAATACTGAAGTTAACAACGTTTGAAGCATTACAGAT
TTATTTATAGAAGCTATTGGATTACCCAGGAACATCTGGGAATTATCTTTGATGAAGG
TATACAAATTTTGAATAAATTCATCGGTGTTGCTGATTACGTTAGTGAGGAGACACGAG
AGCCTATTTCTTATAAGCTAGATATACAATAA

YML130C, 563 aa (SEQ ID NO 214)

MRLRTAIATLCLTAFTSATSNNSYIATDQTQNAFNDTHFCKVDRNDHVSPPSCNVTFNELN
AINENIRDDL SALLKSDFFKYFRLLDYKQCSFWDANDGLCLNRACSVDDVEDWDTLPEYW
QPEILGSFNNDTMEADDSDECKFLDQLCQTSKKPVDIEDTINYCDVNDNFNGKNAVLID
LTANPERFTGYGGKQAGQIWSTIYQDNCFTIGETGESLAKDAFYRLVSGFHASIGTHLSK
EYLNVTGKWEPNLDLFMARIGNFPDRVTNMYFNAYAVAKALWKI QPYLPEFSGDLVNK
EIKNKMNDNISQLDTKIFNEDLVFANDLSLTLKDEFRRSRFKNVTKIMDCVQCDCRRLWGK
IQTTGYATALKILFEINDADEFTKQHVIGKLTKEYELIALLOTFGRLSESIESVNMFEKMY
GKRLNGSENRLSSFFQNNFFNILKEAGKSIRYTIENINSTKEGKKKTNNSSQSHVFDLKM
PKAEIVPRPSNGTVNKKWKAWNTEVNNVLEAFRFIYRSYLDLPRNIWELSLMKVYKFWNK
FIGVADYVSEETREPISYKLDIQ

YMR022W, 998 bp, CDS: 501-998 (SEQ ID NO 215)

AACAGTATTGGCTGTTGATTTCATTGCGCTGCAGCAGTCACCTTCAATTTGTGCACCATT
TCGTATTCTGTACTTTGCGATGTAGAGTCTACTAAAAAGCGTCTCTGATAGCCATGGGT
GAAGGTCTTCTCTAGTTCTCACCTTAATTAGCATTTCGGTGAGAATGCCTGCATGTTGAA
GAGCGATGCCCTCTGATGCACGATGCACACGCATATTTGTTCCCATTAATATTATCATC
TCTGATAGAGCTTGAAGAACTTACCAGACTGTTTCAAGTTTAAAAACAAGGCGCCTCATCG
CATCTACCTCACGAAGATGCAGCAGCTTATTGTCTCGAGATCCTTCTTATAACTCCTTTT
CGCCATTACCCGAAAAACGAGATTACAGCCTCTAAACCAAGAGCTCGAAAAGCGCCAAAGT
AAACTCTGGCGTTTAGCGTACGAAGGAGATTATCCTAAAAGGAACTTCCCTAGTAATAGT
GTAATTTGGAAGGGCATAGCATGTGCGAAAACCGCTCAGAAACGTCTCCTCAAGGAGCTTC
AACAGTTAATTAAAGATTCTCCACCTGGTATAGTGGCTGGTCCCAAATCGGAGAATAACA
TATTCAATTTGGGACTGCCTAATTCAAGGGCCTCCAGATACGCCATACGCTGATGGTGT
TTAATGCTAAGCTAGAGTTTCTTAAAGACTATCCGTTATCTCCACCTAAACTTACTTTCA
CAGCCAGCATACTACATCCAAATATTTATCCAAATGGGGAAGTGTGCATATCCATTCTAC
ACTCCCTTGGTGATGATCCTAACATGTACGAATTAGCGGAAGAAAGATGGTCGCCAGTGC
AAAGGTAGAAAAAATCTATTAAGTGTATGAGCATGTTGAGTGAGCCCAATATCGAAA
GTGGTGCCAAACATTGATGCTTGCATCTTGTGGAGAGATAATAGACCTGAATTTGAGAGAC
AGGTAAAGTTATCCATTTTGAAATCATTAGGATTCTGA

YMR022W, 165 aa (SEQ ID NO 216)
MSKTAQKRLKELQQLIKDSPGIVAGPKSENNIFIWDCLIQGPDPYADGVFNKLEF
PKDYPLSPKLTFTPSILHPNIYPNGEVCISILHSPGDDPNMYELAEERWSPVQSVEKIL
LSVMSMLSEPNIESGANIDACILWRDNRPEFERQVKLSILKSLGF

YMR118C, 1091 bp, CDS: 501-1091 (SEQ ID NO 217)
GTCCTTCCGCTTTATATGTTTCGTTATCCTATCACATTATCAAATGACTTTGTGCCACTG
TGTTTGTGACAAAAATTACTGTAATATAATCAATAGTATTTACATGTTTGTACCAGAAGTAC
TTGCATCGCATCCAGTTCTCATGCAATATAGTTGTATACCATGTCGTTGAAAGGAACCAG
AGTAAACACTTCTACCAGTATTTCTTTACGGTTTCGGATCAAACCATCACTCATTTCGGTC
ATTCTTACCGTACGATAAAACCAAAATACAAGGAAAAGTATCCCTAATTAGAGATCACTGC
ATCCGTAATAGTTTTTTTTCTATTTTGGACTTTTGTAAAAAAGGGATTAGGGATACGTTG
CTCATAAAAAAATTGACGAAGATTTTAGATAAATGGCAAATAAAAAATGAAATAGTATCAAT
ATACCGAAAAATTAATCACACTCAATGCGACTGTGATAGCTGATAAGTGGAGCTCAGAAA
TATTCAGAAGCGTAAGAATAATGAAAGCAACCATTCAAAGAGTAACATCTGTATTTGGAG
TTCCCCGAGCATCTGTATTCGTGCCAAGAATCAGCACACCATTTATTTTGCATAATTATA
TCTCTAATGGCAGAATGGACCTTTTTTCAAAGAATTCCACAATGGCCCGGTATCCAAAT
CTGATCTTTGGTCAAGCAACAAGGAAGGAGCTCTTAGTATCTCAAAGGAAAAAAGAC
CGATCTCTCCTCATTTAACTGTTTACGAACCTGAAATGAGCTGGTATCTTTCCCTCTTTAC
ATCGTATATCTGGCGTTTACTGGCTCTTGGATTCTATGCTTTTACAATTACTTTGGGTG
TGACGACAATAATGGGAATGGATACGACTTTTCAGGATCTAAACAAGTGGTATCACGAAA
AGATGCCCTAAGTGGTCCCAATGGGTGGCCAAAGGCTCTGCAGCATATCTGTTTGCATTCC
ATTTTGGTAACGGTATAAGGCATCTCATCTGGGATATGGGCTACGAATTGACCAACCGTG
GGGTATAAAAAACCGGATCAATCGTTTAGCCGGCACACTCGTCTTAGGAACGTATTTAC
TGGCTCAGTAA

YMR118C, 196 aa (SEQ ID NO 218)
MKATIQRVTSVFGVPRASVFPRISTPFILHNYISNGRMDLFSKEFHNGRVSKSDLWSSN
KEEELLVSQRKKRPISPHLTVYEPMSWYLLSLHRISGVLLALGFYAFTITLGVTTIMGM
DTTFQDLNKWYHEKMPKWSQWVAKGSAAYLFAFHFGNGIRHLIWDMGYELTNRGVIKTGS
IVLAGTLVLGTYLLAQ

YMR143W, 1121 bp, exon1: 501-524, intron1: 525-713, exon2:
714-1121 (SEQ ID NO 219)
CCGCTTAGCGCAAACTATCGTGAACCTCGCTGCAACAACCTGAGAGGGCAAGGATATACATA
AAAAAGCCTACAAATCTGAACTCTGTAAAGGAAGCCTCATAAATAAAGGTAGATAGTA
AAGTATACAAGAGAAGAATCCCAAGATGTCAGCTGTCCCAAGTGTTCAGTATGTTTCA
GTTCTGCAGAATGATGTTTGATAGTATCGATAATGGAGTGAGATCAAGAGAAAAAATG
AATATGTCAGCCAACCAAGTTCTGAGTAGGCAGTAAATGAGTACGCATAGTGTATTTATC
CAAAGGAAAGAAATGTTATTTTACAAGCCGAATTGAGATCCAATTAGGCAATGTTTGG
GGAGAGTATTTTGCACAAGATTGGTTAAACTACTACGGTCAGTTCCGTAACCAGTACGATT
GTACACATAAGGAAACAACCTGTAAAGATAAACAATAAGGGCTTCCAATGCCATTGTAAGA

TATCATATTTCCTAAACAAAAATGTACAGCGAATATAAAGCCAGCGTCAGTGTCTTCCTGG
AAGGTTGCGCAACTAAAGAAGTTGAAATTAAAAATGCGAAGCGCTACATTTTTCATCCATTT
TCACTCATCAGATGTCCAAGATTTTCGAAAAATAAATATTCTCATTTTCTCTCAATGAA
ATAATTGTTACTAACATTGAATTTCTCGTAACATAATTGCATTACTTCTTTAGACTTTTG
GTAAGAAGAAATCAGCTACTGCTGTTGCCCATGTCAAGGCCGTAAGGGTTTGATCAAGG
TTAATGGTTCTCCAATCACTTTGGTTGAACCAGAAATCTTAAGATTCAAGGTTTACGAAC
CATTATTGTTAGTTGGTTTGGACAAATCTCCAACATCGATATTAGAGTTAGAGTTACTG
GTGGTGGTCATGTTTCCCAAGTTTACGCCATCAGACAAGCTATTGCTAAAGGTTTAGTTG
CTTACCATCAAAAAATATGTCGATGAACAATCCAAGAACGAATTGAAGAAGGCTTTCACCTT
CTTACGACAGAACCTTGTGATTGCTGATTCTAGAAGACCAGAACCAGAAATTCGGTG
GTAAGGTCGTCGTTCCAGATTCCAAAAATCTTACCGTTAA

YMR143W, 143 aa (SEQ ID NO 220)

MYSEYKASTFGKKKSATAVAHVKAGKGLIKVNGSPITLVEPEILRFKVYEPLLLVGLDKF
SNIDIRVRVTGGGHVSQVYAIRQAIKGLVAYHQKYVDEQSKNELKKAFTSYDRLLLIAD
SRRPEPKKFGKGARSRFQKSYR

YMR174C, 707 bp, CDS: 501-707 (SEQ ID NO 221)

GTCCCATCATTTCTTTACACCTCGTACTGTATTTCATGATCATCTATCCATTTTACATACCG
CTCCCTTTAAGATACGTTTATTTCGTAACCTCCATTTACCAATCACTATGAGCCGTCCACG
TTTCCAAAAAACCTAAACATATGATGCAAACCTCCAATGAGACTCAACGTAACATGCAA
GTAAATACAGAAGGTTAAGAGATAGTTGTCTTAAAGGGGTACCGAAAGCATTTAGGGGAG
GCTTAAGGGGAGGGTGGCGATCCTATGAAGTATTAATACGTAATGCCAAAAGGAATTGTTG
AACATCTGAAGTGGATAGATTAATCGTACAGTAATCGTACAGTACTATGTCCTTACTGATG
TCGGGAATCTCAGGGGCGACCGCCCCGGCTAGAATTATCTATATAACGGTAAAAAGAAAT
AAAATCTATTCTAGTTCTCGCCATTTACCTTGACTTTAATGAACCAATAAAAGAAATTT
CTACAACCAAGACATCCAGAATGAATACAGACCAACAAAAGTGAGCGAAATATTTTCAGA
GCTCAAAGGAAAAATTCAGGGCGATGCAAAGGTAGTGAGTGACGCTTTTAAAGAAATGG
CTAGTCAAGACAAGGACGGCAAGACTACCGATGCTGATGAAAGTGAAAAACACAACCTATC
AAGAGCAATACAACAAGCTCAAAGGGGCGGGGCATAAGAAGGAGTAG

YMR174C, 68 aa (SEQ ID NO 222)

MNTDQQKVSEIFQSSKEKLQGDQVVSDAFKKMASQDKDGKTTDADESEKHNYQEYQYNKL
KGAGHKKE

YMR191W, 1877 bp, CDS: 501-1877 (SEQ ID NO 223)

GGTTCGATACAACACTTGTGCTGGCTGGTATATCAACCATGGGTACGTCAGCATATTGAT
TCGATGTGGCAGTGACGAGAGCCATTCTGTATCGTTGACAAAGTTTGCATGACTTCAT
GTGTGTTTCGTAGCAGTATTTCGTTGGTCCAGATGCAGGAATGCTGGTTATAAAGTTTGTG
TTCTTGGTCCACATTCATCTTTGGATGGCGTTGTTGGTGGCGAATTTGTCTTAGGCCPTT
TGTTCCGATGTGCTTTTGGATAGCCTGGAATACGAAATCTTTGTCTTCCTGTAAAGTCG
CCGTTTCTTTAACCATTGTGCTCCCTTCTTAAGTTATGTGACGGCTTCGTCACCATTA
CCGCTTGTGTGTACGTGTATGATTTTTTAAATATATACAACAATAATCTGTATTTTTTC
CTTTCTCTAGCCAATGACTCCAAGCTGGCTGATAAAAAACAACTAAACGGTAAAGCCAC
AAATCCGAAATGTATACCAATGATCACCCAGCCTGCTAAGTGCCCTCTATTGATCCGTA
TATCAGCTTTTAGATCAGGCTCGAGTTTCTTGTATATGTGCATTGCAAAAGCATAAACA
AATCCTGGCAGCCGAAGCCGGGCAATCCACTTCGAAACGCACGGCTGAACATATATAAATA
TAAAGGACATGTGGAGAGAAGCTTCTCTTCTTCCATTTCGATTTTCATGATCTAAAGT
GGTTCTTTTACAATAGAAGAGCACCAACACGAAATATGGCTGTGGTGGTAATAACTGGA
GCATGTGGCTGCGAATGTACGGGTCCACCTCAGGCAGATCACGAAGTCTCTGGACCGAA
CGCTGATCAGTTTGAGCCATGGGAATTTTCCACCAATATAATCGCAATATTTTGTCA
CTTGGTGGGAAGCCTATTTGAGGCTTCTACAGCTTTTAGGAGGGCAAGTGGTTTAAACGG
TATCTCTCTCACGAGGAGAGGAATCGCAAGGTTTGACCATTTCAGACCTGTTCCTCAATG
TCAGTAAATTTGCTTCTTTTCCAGAGTGCCCAAAGGAGCCCCAAGGGGCTTTTACCA
ACTGGAATATGACTACATCAAGAGATTATTAGGGCAGAGAGCTTATTCGACTTCCAGTA
TCAAATTTACCAAGAAGCCGTGAATAACATGACTATATCTTTGAGGTGTTTTTCAACT
CACTAGGCGGATTAATCAGTGCTCCCACTCTAATTCCTGCAAAGCTTATCAGAATGCGT
CTAATGTTACCTCTAAACAGGATCACGTCCAACCAAGTTGCCCTTAAAGAAGTTATCTCAAA
AGGATATCAATTTCAATTCGTAATTTAGAATTTTAAAGATAATGAAGACCCAGAATGAAG
TCGTTGATGAAACAAGCGCATATTACATGGAACCAACAGGTTCTCTATATTGAATTTACCA

TTTCAGAAATTTAACGTTAATGGGACATTCTCCGCACCTTTGTCAATTTTTAGATCCTTCTT
TGTTAGCGGATTTGGATGAAATGATTAGAAATTACAAATACGAATTAATCAATATACA
GTAGTGTGACATGATCTTGACAGAATTATGGATCATTGCCGATAACTTTTCATCGAAATA
AGATTCGAATACATTTTCCAACTCAACTGTGGTGGAACAGAAAACTAATTGCAGGTC
TGAATATTGCTACGGGTGTTATTTACGCAGATACGTCTCCCGATATCAGTCTAGAAGGTA
CAAAATTTGAATGCTCTGGTTAATGTTGACAATTCAGGAAGCGTATGGTCTTTTGTAAAGG
AGCCCTCGTTTCCCTCTAGGAGCGCTTTTTCACCTATTTTATCAGATGCATCCTATGATA
CTTATGAATTGGTCTAG

YMR191W, 458 aa (SEQ ID NO 224)
MITQPAKCPLLIRISAFRSGSSFLLYVHCKSINKSWQPKPGNPLRNARLNYINIKDMWRE
ASLPSHFADFHLKWFHNRAPTRNMAVGGNNWSMWLRMSRVHLRQITKSLDRTLISLSH
GNFESHQYNRNIFVTWWSLFEASTAFRRASGLTVSPLTRRGRIARFDHFRPVPNVSKFASF
PRVPKGAPRGLFTNWNMTTSKRLLGQRAYSTSSIKFTQEAVNNMTISLRCFFNSLGGLNQ
CSHSNSCKAYQNASNVTSKQDHVQPVALKKLSQKDINFIRNLELFKIMKTQNEVVDETSA
YYMEKPGSYIEFTISEFNVNGTFSAPLSFLDPSLLADLDEMIRNYKYLKSIYSSVDMIL
QNYGSLPITFHRNKIRIHFPNSTVVETEKLIAGLNIATGVIYADTSPDISLEGTNLNALV
NVDNSGVSWSFVKEPSFSPRSASFSPILSDASYDTYELV

YMR230W, 1228 bp, exon1: 501-552, intron1: 553-962, exon2:
963-1228 (SEQ ID NO 225)
ATCAAAATATTGATCGAGTTCATATAAAGCTAAAGAGTAGGAAATATACCATCAATGGTGA
GCACTTATTTTTTTTGGATTTAGATGTGAGACATACTAAAAAAGTTGCTATCAAGCC
TATAATTTGGCTACGTTGTCTTCCGGTGTTTTCAATTGATTTAAGTTACAACACTCAAA
TCTGGGTAATTTGATCTTTTTTAATAATTATTTTAGTGACATATAGTTCTTAGAGTTTCGC
AGATTTATTTTGTCAATTTTTTGGATCGGCGTCTTATAAAATCAAGACATAATACATCCGC
ACATCGCGCATGTGTGGGTGTATATGCCCTTTTACGATTTTTTAAGTTGCGTCTCAAAAT
AGTTTCCGAGTTGGAAGCCTGAGTTTTTCAAAACAATATAGGAATTAAGGTATACGTCT
TTGGATACATGTTATTTGAAATGGGGTAGAACTAGCACAACTGAAACCAAGAAAACACAG
ATCATAACTAACCGTTCAAGATGTTGATGCCAAAGCAAGAAAGAAACAAAATTCACCAAT
ACTTGTTTCAAGGTATGTTTGCATTTTTTAGGTGAAATATGCAGTGATATGCTCCGAAAT
GGATAGCAAAGATGATAAATGAAAATACAATTAAATTGAACCTGAATATCATTTAAAGTG
GTAGAAAACCGATGTTTCAAAAAGATCTTTGTGGACAAGTACGGCAGTGATGAATCCG
AAAGAAAAGTGCAACCTAAGCAGAATTCCATTATTTACGCGTCCATTTTTATAATGTTT
GAACTTTTGAGTCCTTATAGAAATGCTAATATTATGATCAAAGCGATTATATCATTACT
TTACAGTTTTCCGAGTTTCCGTATTATTGCAAAAGGACCACAAACAATTGAAATCATGAT
ATCGTAAGAAATATTATTACTAACAAGGAAGATCATTGAATTACGATCGCATATCGAAAT
AGAAGGTGTTGTCTCGCTAAGAAGGATTTCAACCAAGCTAAGCACGAAGAAATTGATAC
CAAGAACTTGATGTTATCAAGGCTTTGCAATCCTTGACTTCTAAGGGTTACGTTAAGAC
TCAATTCTCATGGCAATACTACTATTACACTTTGACTGAAGAAGGTGTTGAATACTTGAG
AGAATACTTGAACCTTGCCTGAACACATTGTGCCAGGTACCTACATTCAAGAAAGAAACCC
ATCCCAAAGACCTCAAAGAAGATACTAA

YMR230W, 105 aa (SEQ ID NO 226)
MLMPKQERNKIHQYLFQEGVVVAKKDFNQAKHEEIDTKNLYVIKALQSLTSKGYVKTQFS
WQYYYYTLTEEGVEYLREYLNLPFHIVPGTYIQERNPSQRPQRRY

YNL054W, 3998 bp, CDS: 501-3998 (SEQ ID NO 227)
CCCTTCGCTAAATCATTAAGAGGTCATTCATGAAGTTAATTCAGCACCAAAGTTGGACTG
TTAGACACGAGATACACATTGCAGTCCAAATGTGCAGATTTTTTCAGATAATTGTCGTCGC
ACAAGACTGCCCTCCCGTCCTCAGACAGACACAAAATTAGATTTTACGTTTACATAAAG
ATGTACATAACTTGAAAAACGTTAATCCCTCTTAAATTTAGACCTTGTAAGTCTTCTCG
GCCACTCTTTGTGATATATTGTAGTGCAATATATTGATTTCGTTCTTCTTATTTCTTTGTT
CTTAGGCATTTCCGCTTTAGAAAATTCGTTGGGTGGTTTCTGCGACGGGTATCCCTTCG
ATTTTGCAATAATGATCTTCAATTCTACAATAAAATCAAGTAGATACAGGAAAATATTCC
ATAAATTATAGTGTAATCGCCCTGTATACACCTTATCGTTTTCATCTCAGGCAAGTTAAA
GCATTTGGGAAACGTGCTAGATGACAGAAGAAGATAGAAAGCTCACTGTAGAGACAGAAA
CAGTTGAGGCACCCGTGGCAAATAATCTTTATTGTGCGAATAACAGTAATGTAGTAGCAC
CTAATCCTTCTATTCCCTCTGCCTCCACATCTACCTCTCCGCTACACAGGGAAATAGTTG
ATGATTCTGTCTGCTACTGCTAACACCACCAGCAACGTTGTACAGCATAATTTGCCACCA

TAGATAACAATTTAATGGATTCCGATGCCACGTCACATAATCAAGATCATTGGCATTACG
ACATAAACAGGGCAGGAACATCAATGTCAACGAGTGATATCCCAACAGATTTACATTTAG
AACATATCGGCTCTGTTTCATCAACTAATAATAGTAACAATGCCCTAATCAACCACA
ACCTCTGTCTATCTCATCTTTCCAATCCGTCATCTTCATTACGAAACAAGAAGAGCTCTT
TGTTGGTAGCTTCTAACCTGCGTTTGCTTCAGATGTTGAACCTCGAAGAAGAAACCTG
CCGTCATCTCCAATAATATGCCTACAAGTAACATTGCCCTTTATCAAACAGCGAGATCGG
CGAATATTCATGGTCCATCATCAACTTCCGTCATCTAAAGCGTTTCAGAAAGGCTTCGGCT
TCTCCAATAACACGGCAGCCAGCACTAGTAATAACATCGGCTCGAATACACCTCCAGCTC
CTCTTTTACCTCTACCTTCACTATCACAACAAAATAAGCCAAAATAATAGAGAGGCCCA
CAATGCACGTCATAATTCAAGAGAAATACTTTTAGGTGAAAACCTGTTAGATGATACAA
AGGCGAAGAATGCTCCCGCAATTCAACCACACAGATAATGGTCCAGTAGCAAAATGATG
GGCTGCGTATACCGAATCACTCGAACGCAGATGATAATGAAAATAACAACAAAATGAAGA
AGAATAAAAACATTAATAGTGGGAAAAATGAACGTAATGATGACACCAGCAAAATATGCA
CTACATCTACTAAAACAGCGCTTCAACCGCACCTTTGGGCAGTACAGACAATATCTCAGG
CTCTCACTGCTAGTGTCTCCAGCAGTAATGCTGACAATCACAATAATAACAAGAAGAAAA
CCAGCAGCAACAACAACGGCAATAACAGTAATAGTGCATCCAATAAAACCAATGCCGATA
TCAAGAATTCTAACGCCGACTTGAGCGCTTCTACCTCTAACAATAATGCAATAAATGACG
ACTCACATGAGAGTAATTCAGAAAAACCAACAAAGGCGGATTTTTTCGCTGCAAGGCTGG
CTACAGCTGTAGGTGAAAATGAAATTAGTGAATTCAGGAAACATTTGTTTATGAAATCGG
CAGCTAATTCGACTAAAAACCTAATATTTCTGACTCTCCAGCCAGCAGCAGCAGCAGC
AACAGCAACCTCCAAAACAACAGCAACAGCAACAAAATCATGGAATAACCTCAAAGATAA
GCGCCCCATTGTCTAAACAATAACAAAAAATTATTAAGCCGACTGAAAAATTCAAGACATA
TTAGCACTGGTGCCATATTGAATAACACAATCGCGACTATAAGCACAAATCCGAACCTTGA
ATTTAATGTGATGCAGAACAATAACAATCTGATGTCGGGACACAATCACCTGGACGAGT
TGAGCAGTATAAAACAGGAGCCACCGCATCAATTGCAGCAGCAGCAACCACCAATGGATG
TACAATCGGTAGATTTCGTATACCTCTGACAACCCAGACAGCAATGTTATTGCCAAGTCGC
CTGATAAGAGGTCAAGCTTAGTATCCCTATCTAAAGTTTCTCCACATTTACTTTTCATCCA
CATCAAGCAACGGTAACACAATATCGTGTCCCAATGTTGCCACAAATTCGCAGGAATTGG
AACCAACAATGATATTTCAACGAAGAAATCTCTTTCCAATTTACTTTGAGACATTCCT
CTGCTAATAGAAATTTCTAATTATGGTGACAACAAAAGGCTCTTTAGAACAACAGTGTCAA
AGATATTTGATTCAAACCTAATGGAGCTCCTTTACGGAGATACTCTGGGGTACCGGATC
ACGTTAATCTAGAAGATTACATCGAACAGCCGCATAATTATCCAACAATGCAAAATAGTG
TGAAAAAGGATGAATTTTATAACAGCAGGAACAATAAGTTTCCCCATGGTTTAACTTTT
ATGGTGATAACAATGTTATTGAAGAGGAAAAATAATGGTGACTCGTCTAATGTAATCGAC
CGCAACACACTAACCTTCAGCATGAGTTTATTCCAGAAGATAACGAAAGTGATGAAAACG
ATATTTCACTCCATGTTTATTATAATCATAAGAACGATTTAGAAACAAAACCGCTAATAT
CCGATTATGGTGAAGATGAAGACGTAGATGATTATGATCGCCCAATGCTACTTTCAACA
GTTACTATGGCTCAGCATCCAACACGCACGAACTTCATTACATGGAAGGATGCCTTCAA
GATCAAATAATGATTACTACGATTTTATGGTTGGCAACAATACTGGCAATAACAACCAAT
TGAATGAATATACCCCTTAAGAATGAAACGTGGTCAAAGACACCTATCAAGAACAACA
ATAGCATATGAATGGTAGCATCCATGAATGGTAACGATGACGTTACCCATTCCAATA
TCAATAATAACGATATTGTTGGTTACTCACCGCACAACTTTTACTCAAGGAAGTCCCCAT
TTGTGAAAGTAAAGAATTTTCTTTATCTTGCATTTGTTATATCATCACTATTGATGACAG
GATTCATTCTGGGATTTTATTGGCCACTAATAAAGAACTACAAGATGTAGACGTGGTAG
TGATGGATAATGTGATTTCAAGTTCGGACGAGTTGATCTTCGACATCACAGTAAGTGCTT
TTAATCCAGGATTTCTCAGTATAAGCGTTTCCCAAGTCGATTTGGACATTTTTCGAAAAA
GTTCTTACCTGAAGTGCGATTCTAATGGTGACTGTACAGTAATGGAACAGGAACGGAAAA
TTTTACAAATAACGACAAATCTTTTCGTTAGTTGAAGAGAGTGCTAATAATGATATTAGTG
GTGGGAACATAGAGACGGTATTACTAGGAACCGCTAAAAAATAGAGACACCATTAAGT
TCCAGGGCGGCGCATTTAATAGGAACACGATGTGTCAGTCTCGAGTGTCAAGCTTTTAA
GTCTTGGGTCTCGTGAAGCCAAGCACGAAAACGACGATGATGACGATGATGATGGCGACG
ATGGTGACGATGAAAAACAATACTAATGAAAGACAATACAAAAGCAAACCAATGCTAGAG
ATGACAAAGAAGATGATACTAAAAAATGGAAGCTACTAATCAAGCATGATTACGAATTGA
TAGTCCGTGGAAGCATGAAGTATGAGGTGCCCTTTTTCAATACGCAAAAATCTACGGCTA
TTCAAAAGGATTCCATGGTCCATCCTGGTAAGAAGTGA

YNL054W, 1165 aa (SEQ ID NO 228)

MTEEDRKLTVETETVEAPVANNLLSNNSNVVAPNPSIPSASTSTSPHLHREIVDDSVATA
NTTSNVVQHNLPIDNNLMSDATSHNQDHWHSIDINRAGTSMSTSDIPTDLHLEHIGSVS
STNNNSNNALINHNPLSSHLSNPSSSLRNKSSLLVASNPAFASDVELSKKKPAVISNNM

PTSNIALYQTARSANIHGPPSSTSASKAFRKASAFSNNTPSTSNNGSNTPPAPLLPLPS
LSQQNKPKIIERPTMHVTNSREILLGENLLDDTKAKNAPANSTTHDNGPVANDGLRIPNH
SNADDNENNNKMKKNKNINSKGNERNDTSTKICTTSTKTAPSTAPLGSTDNTQALTASVS
SSNADNHNNKKTSSNNNGNNSNSASNKTNADIKNSNADLSASTSNNNAINDDSHESNS
EKPTKADFFAARLATAVGENEISDSEETFVYESAANSTKNLIFPDSSSQQQQQQQPPKQ
QQQQQNHGITSKISAPLLNNNKKLLSRLKNSRHISTGAILNNTIATISTNPNLNSNVMQN
NNNLMSGHNHLDLSSIKQEPHQLQQQQPPMDVQSVDSYTSNDPDSNVIKSPDKRSSL
VSLSKVSPHLLSSTSSNGNTISCPNVATNSQLEPNNDISTKKSLNSTLRHSSANRNSN
YGDNRPLRRTTVSKI FDSNPNGAPLRRYSGVPDHVNLEDYIEQPHNYPTMQNSVKKDEFY
NSRNNKFPHGLNFYGDNNVIEEENNGDSSNVNRPQHTNLQHEFI PEDNESDENDIHSMFY
YNHKNLDLETKPLISDYGEDEDVDDYDRPNATFNSYYGSAANTHELPLHGRMPSPRSNNNDY
DFMVGNNNTGNNNQLNEYTPLRMKRGQRHLSRTNNSIMNGSIHMNGNDDVTHSNINNNNDIV
GYSPHNFYSRKSPFVKVKNFLYLAFVISSLLMTGFILGFLLATNKELODQDVVVMDNVIS
SSDELIFDITVSAFNPFFSISVSQVLDLIDIFAKSSYLKCDSDNGDCTVMEQERKILQITTN
LSLVEESANNDISGGNIETVLLGTAKKLETPKLFQGGAFNRNYDVSVSVKLLSPGSREA
KHENDDDDDDDGDDGDDENNTNERQYKSKPNARDDKEDDTKKWKLLIKHDYELIVRGSMSK
YEVPPFNTQKSTAIQKDSMVHPGKK

YNL067W, 1076 bp, CDS: 501-1076 (SEQ ID NO 229)

GACGACTATTGATGCCAGGCAAATTTTGGAATTTACTGCTCCTCTTTTAAGAAGACAAGTG
TGTGATATCGTAGCGGTAGGAACCAATTTTGCAATCGATTTACTTACAGCCAAGAAAATC
TATTTTCATGTTTAGCATTGCCATTTCTTCTGTGTACACGTTGTGCTTGCCAGGAACATA
TAGGAGAGACGTATACAAGCATCAATGTTACGAATGTACGATCCCGTTTGCATCTGATGT
GTAAACTCATGTGGTGCCTGTTGTTTCCAAGACTGCCTATTAACCTGGGAATTTT
TTTTTCTTCTAGTGAATTTTTTTTAAAGCGACGCACAGGAAAAGTGAAAATTTATTTAA
ACGGACGGCAAACATGAAAAAAATTAACCAACCATATTTCTATTTCTTTCCCTTTTAC
CTATTTCTTTTGAAGTAGTTTCTTCTCTCTGAAACGACAATAAACCAAACTCTA
GCCTCCAATAGTCACTAAAGATGAAGTACATTCAAACCGAACAACAAATGAAATCCCAG
AAGGTGTTACTGTCAGCATTAAGTCCAGAATCGTCAAGGTTGTCGGTCCAAGAGGTACTT
TGACCAAGAACTTGAAGCATATGATGTTACCTTCAACCAAGGTCAACAACCAATGATCA
AGGTTGCTGTTTACAACGGGTGACAGAAAGCAGTTGCCGCTTTGAGAACCGTTAAATCTT
TGGTTGACAACATGATCACTGTTGTCACCAAGGTTTACAAGTACAAGATGAGATACGCTCT
ACGCGCATTTCCCAATCAACGTCAACATGTTTGAAGGATGGTGCTAAATTCATTGAAG
TCAGAACTTTTGGGTGACAAGAAGATCAGAAACGTCCCAGTTAGAGATGGTGTTACTA
TCGAATTTCTTACTAAGTAAAGGACGAAATCGTCTTATCTGGTAACCTGTTGAAGACG
TTTCCCAAAATGCCGCTGACTTGCAACAAATCTGTCGTGTTAGAAACAAGGATATCCGTA
AGTTTTTGATGGTATCTACGTTTCCACAAGGGTTTCATTGTGCAAGACATGTAA

YNL067W, 191 aa (SEQ ID NO 230)

MKYIQTEQQIEIPEGVTVSIKSRIVKVVGPRGTLTKNLKHIDVFTKVNQLIKVAVHNG
DRKHVAALRTVKSLVDNMITGVTKGYKYMRYVYAHFPINVINIVEKDGAKEIEVRNFLGD
KKIRNVPVRDGVITIEFSTNVKDEIVLSGNSVEDVSQNAADLQQICRVNRKDIRKFLDGIY
VSHKGFIVEDM

YNL075W, 1373 bp, CDS: 501-1373 (SEQ ID NO 231)

TCGATGGATATCCCATCCAAGAACAGGAATACTGGGTTTTTGAAGACCAGAATGGAGATC
TCTGAGGAAGAAAAGATGGTACGTACAATATCACGGCTTGACAATACGAGTATTGCAAAAC
AGTAATGGAAATGGTAATGATGACACCTCTAATCAGAGAACGGAAGCACTGGGGCGTAAG
ACGAGTAATGGAGGGCGAATATGATTACTAAGTTAAATAAATCAGATACAGTATTTAAAG
TTCTTTCAAAAAAGATAATGTCTATATTTTACTATCTACGCAGTGAAAGAGTTCCCTTC
TAATGACACACTATTCATCTCGGGTAACGGATATTGTGTACTGAAAAATATAAAAAATTT
TATCCCGGAAATGCGATGAGATGAAAAATGCATGAAGTAGCGTATATATTGATTGATGAG
GTTGGACTTGAAAGGGCATATATACTCGGTTTTATCATTGATTCAAGTGTTCACATAAAT
AATAAAACAGTTAAATCGAAATGCTAAGAAGACAAGCCCGTGAAAGGAGAGAATATCTAT
ACAGAAAAGCGCAAGAATTACAAGATTCTCAACTGCAACAAAAACGTCAAATAATTAAC
AAGCGCTAGCTCAGGGGAAGCCATTGCCAAAGGAAC TAGCAGAAGATGAGAGTTTACAAA
AGGATTTTCAGATATGACCAAGTTTAAAGGAGAGCGAAGAAGCAGATGATCTACAGGTTG
ATGATGAATATGCTGCCACAAGTGGTATAATGGATCCAAGAATCATCGTCACAACATCTC
GTGACCAAGCACTCGTCTCTCGCAATTTGCCAAAGAAATTAACCTGCTATTTCCAAATG
CTGTCAGGCTGAACAGAGGTAATTATGTGATGCCAAATCTAGTGGATGCTTGTAAAAAT

CCGGTACTACAGATTTGGTGGTATTACATGAACATAGAGGTGTTCCAACCTCTTTGACCA
TATCACATTTTCCACATGGACCCACTGCACAGTTTAGTTTACACAATGTTGTTATGAGAC
ATGATATTATAAATGCTGGTAACCAAAGCGAAGTGAATCCACATCTAATATTTGATAACT
TTACTACCGCTTTAGGGAAAAGAGTAGTCTGTATTTTAAAGCACTTGTTCAATGCGGGGC
CCAAAAAAGATTCCGAAAAGAGTAATCACTTTTGCGAATAGGGGTGATTTTCATTAGCGTTA
GACAGCATGTATATGTGAGAACAAGAGAGGGAGTAGAGATTGCCGAAGTTGGTCCTAGAT
TTGAGATGAGGTTGTTTGAAGTGGGAACTTTAGAAAATAAGGACGCTGATGTTG
AGTGGCAGTTGAGAAGATTCATAAGGACTGCCAATAAAAAAGACTATTTGTGA

YNL075W, 290 aa (SEQ ID NO 232)

MLRRQARERREYLYRKAQELQDSQLQKQRIKQALAQGKPLPKELAEDSLQKDFRYDQ
SLKESEEADDLQVDDEYAATSGIMDPRIIVTTSRDPSTRLSQFAKEIKLLFPNAVRLNRG
NYVMPNLVDACKKSGTTDLVVLHEHRGVPTSLTISHFPHGPTAQFSLHNVVMRHDIIINAG
NQSEVNPHLIFDNFTTALGKRVCILKHLFNAGPKKDSERVITFANRGDFISVRQHVYVR
TREGVEIAEVGPRFEMRLFELRLGTLENKDADVEWQLRRFIRTANKKDYL

YNL096C, 1418 bp, exon1: 501-644, intron1: 645-989, exon2:
990-1418 (SEQ ID NO 233)

AAACACCTACTTATAGACACGACCAAACTTTCCACAACCTTTTCATCAGAGAGAAATGTTG
ATCAAGTTGAATGCGTGAAAGTAGCAATTCGAAACAACAACCTACCTGTCATTCTGCATAG
TAGTAGTTACGAAAGGCACAGAAAATAACAAAAAAGTCAATTTTCTACGGT
CTCCATCCGTACCTCTTTAAATCCGTACATTATTGTTTTGCTTAATTTCAATATTTTCGGA
AAAAGCGAGCGCCCTGGTAAATGTGGTTCAAGCCTGCGAGCCTTTGCTTGGTAACTCAC
CAAATGCAATTCAGTCACGTTCCACACAGTTTGGGTTTCCAGCCTGGCTTTAGGGAAGAA
TGGGCTCCTAGGCGTTTATAATACGCGGAGGGGAAATACCAAATGCTATTGATTATGG
TTAAAATATGTGTTATTTGACTTTGTATATACAAACAGAGAAGAAACCAACACACTAAAG
ACTAGACACATAACTGACCAATGTCTCTGTCCAATCCAAGATCTTATCCCAAGCTCCAA
GTGAGTTGGAATTACAAGTCGCAAGACCTTCATCGATCTAGAAAGCTCCTCTCCAGAAC
TAAAGGCTGACTTGAGACCATTCGAAATCAAATCTATCAGAGAAGTATGTTAAAAGTTAT
ATAATTTGGAAGCAGCAACATTTGTGATTTCTTCTAAAGGGGTTCTTTGCAGTAATTTTTT
CAAAAAGAGTGATTTTGAGCAGTATCTGTATGAAATTTTCATGTGTTTCGAGAAAAATAG
TAATTCGAGAGCTGTCAATACCATGAACGTTGCGATGAGCCTTTGAACTATAAAGGCCT
CCTTGGTCAGTACCAATATCGATGAATAAAATAGAAGCACGCGAAAAAGACCTTACCCCA
AGGAGAAGAAATCACAAACCTTTTGTGTTATGAATGAACCAATTCAGTTACTAATTTTAT
TTCAACGCTGCTTGATTCTTATTGTTTAGATTGATGTCACCGGTGGTAAGAAAGCACTAG
TCCTTTTGTGCCAGTTCCAGCTTTGTCTGCATACCATAAGGTCCAAACCAAAATGACCC
GTGAATTTGGAAGAAATTCCTGACCGTCATGTTATTTCTTGGCTGAAAGAAGAAATCT
TGCCAAAACCATCTAGAACATCTAGACAAGTCCAAAAGAGACCAAGATCCAGAACTTTGA
CTGCTGTTTACGACAAGGTTTGGAAAGACATGGTTTTCCCAACTGAAATTGTCGGTAAAA
GAGTTAGATATTTGGTTGGTGGTAAACAAGATCCAAAAGGTTTGTAGACTCCAAGGATG
TTCAACAAATCGACTACAAGTTGGAATCTTTCCAAGCTGTCTACAACAAGTTGACTGGCA
AACAAATTGTTTTTGAAATTCGAAGCCAGACCAACTAA

YNL096C, 190 aa (SEQ ID NO 234)

MSSVQSKILSQAPSELELQVAKTFIDLESSSPELKADLRPLQIKSIREIDVTGGKKALVL
FVPVPALSAYHKVQTKLTRELEKKFPDRHVIFLAERRILPKPSRTSRQVQKRPRSRTLTA
VHDKVLEDMVFPTEIVGKRVRVYLVGGNKIQKVLDDSKDVQQIDYKLESFQAVYNKLTGKQ
IVFEIPSQTN

YNL162W, 1333 bp, exon1: 501-504, intron1: 505-986, exon2:
987-1333 (SEQ ID NO 235)

TTCATACCAATATAGACTAATGCGTTTTTGAACGCCAAACCGCAGTGACAAATAGCAAA
TATGTAGCTGTCTATATCGGCATATAATAACAGTTTTCTACCAAATGCTGTCTACATTCA
GAGATCTTACATCCTTACATCTAAAGTAAAACCTAGACATTTACTTCGAGTTATAC'TTTT
TTTTTATTTATCTATTTTTTCTCTTGCAGACATTTAACACCTGAATTCGCCTAACGCCA
GGACTGATCTGCCAGGGAAGGGAGCTTTGTCTAGTGCCAATAGGCCGAGCAGTAGGAA
GGTTACAGCAGCTGGCCCCGAGAGTGATTGGGTACAGGAAATAGCGCAACCTTCTCTTT
TGCCCGGGAAGGCGGTTCAATCTACCTTCGAAGGGCTAGTACATGAGCGGAAGGAGGC
AGATAATAGCACCATTAAAGTGGTCCAAATGCATCTTGAAATCTAATCCTTAATAGAGGAA
ACAACAATTATCAGTAAAAATGGGTATGTTATAACCATAATTCCTAATGGTGAATAAAA

TCAGGACCAATAAAGAAAAGCTAATTTGATTTTTATTGTCAATGAAATTTTCATAATCGTC
ATGAATGCATAAAACAGACACACCTAGCAACTGTATAATCTGCGCCTAAAAAGGGCGTATA
CACAAAACATAACGATGCGCAATAAAAGTTTCAGCAGTCAGCAATGAAACCGAGATATGCA
GCAACAGAGTATCATATGCATGGAGGATCCTTTCTGTTTTTCTGATAATATGCTCTGAAA
AAGCTCCAAAACAGCACAGTAGCCTATTTGTGAAGCTCAAAAAAGGCTTCTATTTCCCTCG
CTATCTTCAGATTGTGCAGTGATATTCTTTGAGGAAGGAAACGTAGAGGGGATAAGTTGG
ATAACTGTATTATTCTTTCAATATGCTAGATTTTGCTTACCACCTTACTGATTTTTTCTTA
ATAATAAACTTTTTTACTAATAGTAGATGTCTCATCTATTTCTTCTATTTAGTTAA
CGTTCCAAAGACCAGAAAGACCTACTGTAAGGGTAAGACCTGTCGTAAGCACACTCAACA
CAAGGTTACTCAATACAAAGCTGGTAAGGCTTCTTGTGTTGCCCCAAGGTAAGAGACGTTA
TGACCGTAAACAATCTGGTTTCGGTGGTCAAACCAAGCCTGTTTTCCACAAGAAAGCTAA
GACTACCAAGAAGGTTGTTTTGAGATTGGAATGTGTCAAATGTAAGACCAGAGCCCAATT
GACCTTGAAGAGATGCAAGCACTTCGAATTGGGTGGTGAAGAAGCAAAAGGGTCAAGC
TTTGCAATTCTGA

YNL162W, 116 aa (SEQ ID NO 236)

MVRCLYFFYLNVNPKTRKTYCKGKTCRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGF
GGQTKPVFHKAKTTKKVVLRLCEVKCKTRAQLTLKRCKHFELGGEKKQKGQALQF

YNL178W, 1223 bp, CDS: 501-1223 (SEQ ID NO 237)

GGTCCACGTCAAGTTCCACACAATAACATTTACGTAGTGTTACGCGAAGCAGTTACATCT
CAACTAACATAATTGCTGGTGAGCCTACAACACTGCATGCGTAAACGTCAACGGGATTAC
GTTAGTATTTTTGGCCGCCGTAATTTCTCTGTTTTTTTTTCTTGATTTCACTTCTTTT
CATGTTCTTTTGAATAATCTAATTCCTCATGATTAAATGAGACTGTTTTTTGTTTTCCGT
AACATCCATACCTTTTCTGTATAATATTCTTGCTGTAAAGTTTGTTTTTTTTATGAAAA
AACATTTTCTTTCTTGAGATGAGGCGCCGAGCCTTTCTCCCATGGGCAGTGGTAAAT
TTTCCAAATCAATGCAGCTCTTTGAAATACAACAGCATTTTTTCATACATTTTAAGCAATT
TCTAGTTTGTAGATATTGTTAGATTAGTTTTTGAACATTGTTTTGATAACTGAAAATAAA
ACAGCAAACAACACTACAAAAATGGTTCGCTTTAATCTCTAAGAAAAGAAAGCTAGTCGCTG
ACGGTGCTCTTCTACGCTGAATTGAACGAATTCTTCACCAGAGAATTAGCTGAAGAAGGTT
ACTCCGGTGTTGAAGTCCGTGTCACTCCAACCAAGACCGAAGTTATCATCAGAGCTACCA
GAAGTTCAAGATGTTTTGGGTGAAAAACGGTAGAAGAATCAACGAATTAACTTTGTGGTTC
AAAAGAGATTCAAGTACGCTCCAGGTACTATTGTCTTATATGCTGAAAGAGTTCAAGACC
GTGGTTTGTCCGCTGTGCTCAAGCTGAATCTATGAAATTCAAATTGTTGAACGGTTTGG
CTATCAGAAGAGCTGCTTACGGTGTCGTAGATACGTTATGGAATCTGGTGCTAAGGGTT
GTGAAGTTGTTGTTTCCGGTAAACTAAGAGCTGCCAGAGCTAAGGCTATGAAATTTGCTG
ACGGTTTCTTGATTCACTCTGGTCAACCAAGTCAACGACTTCATTGACACTGCTACTAGAC
ACGCTCTTGATGAGACAAGGTGTTTTGGGTATCAAGGTTAAGATTATGAGAGACCCAGCTA
AGAGCAGAACTGGTCCAAAGGCTTTGCCAGATGCTGTCAACCATCATTGAACCAAAAGAAG
AAGAACCATTCTTGTCTCCATCTGTCAAGGACTACAGACCAGCTGAAGAACTGAAGCTC
AAGCTGAACCAGTTGAAGCTTAG

YNL178W, 240 aa (SEQ ID NO 238)

MVALISKRRKLVDGVFYAELNEFFTRELAEEGYSGVEVRVTPTKTEVIIRATRTQDVLG
ENGRRLINELTLVQKRFKYAPGTIVLYAERVQDRGLSAVAQAESMKFKLLNGLAIRRAAY
GVVRYVMESGAKGCEVVVSGKLRAARAKAMKFADGFLIHSGQPVNDFIDTATRHVLMRQG
VLGIKVKIMRDPKASRTGPKALPDAVTIIEPKKEEPI LAPSVKDYRPAEETEAQAEPEVA

YNL182C, 2168 bp, CDS: 501-2168 (SEQ ID NO 239)

CTTTGATAAAATTAATACGTAAGATACCGTGTAAGTATTATAATAACTGCCACGCTTAT
AGCATGTACGCTATACATTTACGTGCTGAGCTCCTAGGAAAGCTCATGAGCAGCCACTGT
ATCGTGGAGCATAACTACAACAAAGAATACACAGCGTCACATAGAGGGTTTTTGAGAGGA
GAAGTTGAAATAGGACTTGATCTTGGGGGAGAGGGGATTGAAAGCACCCATTACAGGAGT
ATGTGTCTGTAATTGAAGTGTTAGCGCGGATTACCTGTAATAAGAGTGATGATTTGAT
AGCGCCATTCTACATCATATGGCAATGTTGAAAACTGTACGCGCGAAGTAAAATTTTT
TTTTACATCCCCTAAATGAAAATTTTAAATCGATGCCATTCCAAATATGCTTATTTCGA
AGGACGGCTCTGACAAGGGCATATGCGTTAAGATTGATTGTTCAATATTCATAAAACAGG
ATCTTTCAAGGGACGATAAAATGGATGAGCAAGTTATTTTTACAACAAATACCTCAGGAA
CAATAGCTTCTGTACACTCATTTGAACAGATAAAATTTGAGGCAATGCTCCACTCAATCAA
GAAATAGCTGTGTTCAAGTAGGAAATAAATACCTTTTTATTGCTCAAGCACAAAAAGCAT

TAATCAATGTCTACAATCTGTCAGGTTCTTTCAAAAAGAGAATCTGTTGAACAGCGCTTAC
CATTACCTGAAATCCTAAAATGTCTGGAAGTAGTTGAAAATGATGGTGTGCAGTATGATA
GAATTCAGGTGTCAATCATAATTTACCAGACTTCAATCTTCCGTACCTTTTACTTGGCT
CCACCGAATCGGGTAAATTTGTACATATGGGAGTTAAATTCAGGGATTTTATTGAACGTGA
AGCCTATGGCTCATTACCAAAGTATACCAAGATTAAGTCCATTTTAAACGGCAAGTATA
TTATTACTTCTGGTAACGATTCGAGAGTTATTATATGGCAAACCTGTTGACTTGGTATCAG
CGTCCAATGATGATCCTAAGCCTTTATGTATCCTTCACGATCATACTCTACCCGTGACAG
ATTTCCAAGTTTCTTCTAGTCAAGGAAAATTTTATCATGTACTGATACGAAACTCTTCA
CAGTATCTCAAGATGCTACCATTAGATGCTATGATTTGAGTTTAATAGGCAGCAAAAAGA
AGCAGAAGGCAACGAAAATGACGTTAGTATTGGTAAGACCCAGTATTGCTTGCACAT
TTACAACCTCCTTATCTATCAAATCCATTGTACTGGATCCTGCTGACAGAGCATGCTATA
TTGGTACTGCGGAAGGTGTGTTTTCATTGAATTTATTTTATAAACTAAAGGGTAATGCTA
TCGTTAATCTGCTACAGTCCGCCGGAGTAAACACAGTTCAAAAAGGTAGGGTTTTTTCCC
TAGTGCAACGTTAACTCACTAAGTGGCGGCAAAAATGAAGATTGGATGCACATATATGCAA
TGGGCCAAGTTGCTGTGAGAAATGCTTAAATTCAAATGTGTCATGCCTAGAAATATCAA
TGGATGGTACATTATTATTGATCGGTGATACGGAGGGGAAAGTTTCTATTGCGGAAATTT
ACTCAAAACAAATCATTAGAATATCCAAACTTTAACTACATCACAGGATTCAAGTTGGAG
AAGTGACCAATCTCTTAACCAACCCCTTACAGACTCGAACGTGGAATTTACTTTTTGAAG
GAGAATCCAAAGGCAACAACCTAGTAATAATAATGGTCACAATTTTATGAAGATACCAA
ACTTACAAAGAGTTATCTTTGATGGTAAAAACAAAGGCCATTTACACGATATTTGGTATC
AGATAGGAGAACCAGAAGCAGAGACAGATCCTAACCTCGCATTACCACTTAACGACTTTA
ATGCCTATTTGGAGCAGGTCAAACGCAAGAATCGATATTTTACATATCGGTAAGGTGT
CAAGCAATGTAAAAGTGATTGACAATAAAATCGACGCCACTTCATCTTTAGACAGCAATG
CCGCTAAAGATGAGGAAATTACAGAACTTAAGACCAACATAGAAGCATTAACTCATGCCT
ACAAGGAGTTACGTGACATGCACGAAAAGCTGTACGAGGAACACCAACAGATGCTTGACA
AGCAATAA

YNL182C, 555 aa (SEQ ID NO 240)

MDEQVIFTTNTSGTIAVSFSEQINLRQCSTQSRNSCVQVGNKYLFIQAQKALINVYNL
SGSFKRESVEQRLPLPEILKCLEVVENDGVQYDRIQGVNHNLPDFNLPYLLLGSTESGKL
YIWELNSGILLNVKPMHYQSITKIKSILNGKYIITSGNDSRVIIWQTVDLVSASNDPK
PLCILHDHTLPVTDQVSSSQGKFLSCTDKLFTVSQDATIRCYDLSLIGSKKKQKANEN
DVSIGKTPVLLATFTTPYSIKSIVLDPADRACYIGTAEGCFSLNLFYKLGKNAIVNLLQS
AGVNTVQKGRVFSLVQRNSLTGGENEDLDALYAMQVLVCENVLNSNVSCLEISMDGTL
IGDTEGKVSIAEIIYSKQIIRTIQTLLTSQDSVGEVTNLLTNPYRLERGNLLFEGESKQ
PSNNGHNFMKIPNLQRVIFDGNKNGHLHDIWYQIGEPEAETDPNLALPLNDFNAYLEQV
KTQESIFSHIGKVSSNVKVIDNKIDATSSLDNSNAKDDEITELKTNIEALTHAYKELRDM
HEKLYEEHQMLDKQ

YNL190W, 1115 bp, CDS: 501-1115 (SEQ ID NO 241)

AATGCGCTCCCGTACGTCAGTGGCTGTGCTGAAACGAGACAATTTCTCAATTCGTTTGT
TTGTGTACTGTATTTGTTATCTTTACTATATATATGTTGTTAAGTTTCTTTTACCAATTA
GTGCTCACTTCTCTCGTCTTTTATTAGGTGTGTGTGTGTGCGTAATTTTCGTTTCGCTG
ATTACTTTTATATAGTGTAGTTTGTCTTGAATGTAATAAAGACTTCTGTTTTATTTTGT
TTGTTATTTAGAAAAGTCTATCTGGTTAACTTAAACGAGTGAGCTTAAGATAATCTGA
CTACAAGAAAACCAAGCTTCTATTACTTTGTTTCTTTCTCTTTTTTCTTTTTTGAATAAA
GAATTTTCTTTAAGGAGTAACTTAAGCATTTAGCTGCACATTAACACTTTTTTTTTTTA
CTTCTAACTCACACTTTTGAAGAACATTTATTTTTTTCGACCTTCTTTCCCAATACC
CAGCGCTTTATAATGAAATATGAAGTTCTCTTCTGTTACTGCTATTACTCTAGCCACCG
TTGCCACCGTTGCCACTGCTAAGAAGGGTGAACATGATTTCACTACCACTTTAACTTTGT
CATCGGACGGTAGTTTAACTACTACCACTCTACTCATACCACTCACAAGTATGGTAAGT
TCAACAAGACTTCCAAGTCCAAGACCCCAACCACTGGTACTCACAAGTACGGTAAGT
TCAACAAGACCTCCAAGTCTAAGACCCCAACCACTACCGGTACTCACAAGTATGGTAAGT
TCAACAAGACTTCCAAGTCCAAGACTCCAACCACTACCGGTACTCACAAGTACGGTAAGT
TCAACAAGACCTCCAAGTCTAAGACCCCAACCACTACCGGTACTCACAAGTATGGTAAGT
TCAACAAGACCTCCAAGTCTAAGACCCCAACCACTACCGGTACTCACAAGTATGGTAAGT
ATGCCGCCCTTGGTCCATCTAATTTCAACTCCATAAAATGTTTGGTGTACCCTGGTA
GTGCTGCCGTAGCCGGTGCTTATTACTATTATAA

YNL190W, 204 aa (SEQ ID NO 242)

MKFSSVTAITLATVATVATAKKGEHDFTTTLTLSSDGLSTTTTSTHTTHKYGKFNKTSKS
KTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTSKS
KTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTKHDTTTYGPGEKARKNNAAPGPS
NFNSIKLFGVTAGSAAVAGALLL

YNL208W, 1115 bp, CDS: 501-1115 (SEQ ID NO 243)

GGTTATACACATATATATATATTTTCATTTTTAATGTCTTAGCTTTTGTATCTTAGATGAA
GTTTTAGTTCTGTATATCACGATCAAGATATCATAAATCATAAATTCAATTATCTTCT
GTTTCCCTCTTTGAGGCATCAAACGAGTGTGTTGACTGATACACACCAACATACATAAGGCA
ACTTTTCTGGCTGCCCAAAGCTGTGGCAGTATGAACTGCTTTTCCGGCTGCATAAAACA
ACCATGTGGAGTTTTACTGTATTTCGCATTTCCGCCCCGCTAGCATTCTTCGTTTCATGCTA
AAAAAGAGCGTGGGCTAATATTCAGTATTAATAATTCCGGCACCCGCACAGCCCATACC
GGAAAAGGGGCTGGCTGTGTTGGGCTTGGCAAAAACTCAATCTGAGCAGTCATTTATAAAG
AAAGACTTTAATTTGTCTTGTCTTAAACACTTGTAAAGCCTTCCAAATATAGATCACTTAAGA
CAATCTAAAGTGTCCAAATGTCTGCAACGAATTCTACTCAAGTGGCCAACAAGGTC
AATATAACCAGCAAAACAACCAAGAAAGAACTGGTGCTCCAAACAACGGTCAATATGGTG
CCGACAAATGGTAACCCCAACGGTGAACGTGGTTTATTTTCCACTATTGTAGGTGGCAGTG
CCGGTGCGTACGCTGGATCTAAGGTGTGCAACAACCATTTCTAAGTTGAGTGGTGTGCTGG
GCGCCATAGGTGGTGCATTCCTTGCCAACAAGATATCTGATGAGCGTAAAGAGCATAAGC
AACAAAGACAATACGGCAACTCAAACCTTCGGAGGTGCTCCTCAAGGTGGACACAACAACC
ATCACCGTCAGACAATAACAACAATAACGGTGGATTTGGCGGTCCAGGCGGCCCTGGCGG
TCAAGGTTTCGGAAGACAAGGCCACAAGGATTTGGAGGTCTGGTCCACAAGAGTTTGG
TGGTCCAGGTGGCCAAGGATTCGGTGGTCCAAATCCTCAAGAATTCGGCGGCCAGGTGGC
CAAGGATTCGGTGGTCCAAACCCCTCAGGAATTCGGGGGCCAAGGTTCGTCAAGGATTCAT
GGCGTTACGTTGGTGAATGGCTCAACAGAGTGA

YNL208W, 204 aa (SEQ ID NO 244)

MSANEFYSSGOQGOYNQNNQERTGAPNNGOYGADNGNPNGERGLFSTIVGGSAGAYAGS
KVSNNHSLKSGVLGAIGGAFLANKISDERKEHKQOEQYGNNSNFGGAPQGGHNNHRTIT
TITVDLAVQAALAVKVSIEDKAHKDLEVLVHKSLLVVQVAKDSVVQILKNSAARWPRIRWSK
PSGIRGPRSSRIQWRFITLVNGSTE

YNL210W, 1313 bp, CDS: 501-1313 (SEQ ID NO 245)

TCATAACGGGTTCTTTTCAAAAAACCGTAAAAATTTGAGGTACACCAACTAAATACAAA
TTGTTTCATCACGGTGACTATATCAAGAACTTCGTAAGGAAACATTTAGAAAACCTCAATA
TAGTAAAGTTTTCATCAGCAATCTTATCTGAGTAATATTATCTACGATCTAAATATAGGAT
GATCTGCCGATTTAGGAATCGTACTGTAGATTGCTCTTGGCGACAGATATAGTGAAATAC
CTTTTACAAAGTGGATACAGGTTGCCTATCACTACCGCCATTTCACTAGCAAGTAGAGTA
TTGAGAAAACGGTAAACTTTTGAAAGTTGCAGATGCAGAATATATATCTGGTTTTGTAGTT
CTATCCGCTAAACGGGACGATCGCATTTTAGCCGCCGACAGTGTTAATATAAGTAATGAA
CTTGGGTTAATTTGATTACGCGTCACAGCTACTAATAAAATAAGACCGAGAGTTTTAATC
AGCTAGTGCATACCAAAACAATGAGTAACCAACACAGCCCTCAGCCATTTTGTGTTGGACA
CCAAATTTGGTGAAGCTATTAGAAGAGCTCCAGGAGGGAAAGCAATTCACAATAAAAACA
TATTCCTCCGAAAAAGCATTATATTTGAAGCTCGCTCTTGATTATTCTTTCTTCAGAAAGA
ATTTACTAGAGTTTTGCGTCCACCTTGACAAGATAAAAGGAGTCATTAGACCAAACTATG
ACACTATATATATTTTGTGCCTGTTGGAGGTGGATCTCTCAATCTGGTATTTACCGACA
ATATATTTGGAAATATGTTTGGCCAGGTTTGTGTTTCAAGGGAGGACTTGAGGGTTTTTAATA
ATACTTTTTACACATATCACGATAACCGCTACGTATTCTCCAAGAAGACTTTTCTCAAT
TGTTCAAAAAAATCAAACTAAGGCTTCTGTACTATGTTTTACAGTTGAGGAAATTTTTC
TGACAAACCAAGAAATTTTACCTCAAAACTCAACAGTGGCAGAACTGCAAAAGAGCACTA
ATAAAGTACAGACAAAATGGGCCGCAACGGCAGGATTTTCATAGTCACTCTAGAAATAAAC
TGAACAAAACACAAAATCACCTTTCCTCATTGGAGCTAAAGGAACGAGAATTGAAAGCTTGA
GGGAAAAATCAGGCGCCAGCATAAAAATAATACCTATTAGTGATAAAATGACTGCACATG
AAAGGAACCAACCTGAATCTGTTCAACAAACAATACTAATTTCCGGTGACTTATACTCAA
TTGCATTAGCCGTCACAGTATAGAGTCTGCATTAATTACTTTGGATTTATAG

YNL210W, 270 aa (SEQ ID NO 246)

MSNQHSPPQFCLDTKLVLKLEELQEGKQFNKNIFPEKALYKLALDYSFFRKNLLEFCV
HLDKIKGVIRPNYDTIYILCLLEVDLLNLVFTDNILEICLPRFVSREDLRVFNNTFYTYH

DNRLRILQEDFSQLFKIKTKASVLCFTVEEIFLTNQEILPQNSTVAELQKSTNKVQTNQ
PQRHDFIVTLEIKLNKTQITFLIGAKGTRESLREKSGASIKIIPISDKMTAHERNHPS
VQQTILISGDLYSIALAVTSIESALITLDL

YOL031C, 1766 bp, CDS: 501-1766 (SEQ ID NO 247)

AGTTTTTTTTCTCGAGAAATTGTGAACAAAAGAAAGACACAGAAGATGATAAGAG
AGAGAAACAACGAAGAAAGAACAAATGTGGGGTTACCCGAGAGATATTGACATACT
GACCTTAGAAAAGGCATTACTGAGGCTACTGACTAAAGCGGTTACATAAATGCATAGTA
TATTTCTTGTGTATACGCAGCGGCCAACTAGTGGCAGCAAGAATGTAATGAACGATTCA
TCTGCAGGTTTGGAGGCCGCAACTAGATCAAAACGTAAATAGCGGGTGAAGTGTCTGGA
CGTTAGAAGTAACGTCCGCAGATCGAAGCTAAACACGAGATTAGATTTCTGGGTAACGGAA
TTGTGATAATTAAAGAAAGACCAGACTATGTGAAAAGGCCACGTAAATGATAGAGCACACA
TTAGCAACTATAATAGACTAGTTTTTCGCATCGCTGGAAGTTCTCGATATTGAATATCACT
TCCAAGAAGCAAACTTAGAATGGTCCGGATTCTTCCCATAATTTTGAGCGCCCTATCTT
CGAAATTAGTGGCGAGTACAATATTGCATTCATCCATACACTCAGTGCCATCTGGAGGCG
AAATCATATCTGCAGAAGATCTTAAAGAACTTGAAATTTTCAGGGAATTCGATCTGCGTTG
ATAATCGTTGCTATCCTAAGATATTTGAACCAAGACACGATTGGCAGCCCATACTGCCAG
GTCAAGAACTCCCCGGTGGTTTGGACATTAGAATAAACATGGACACAGGTTTAAAGAGG
CAAACTAAATGATGAGAAGAATGTCGGTGATAATGGTAGCCATGAGTTAATTGTATCTT
CAGAAGACATGAAAGCATCGCCTGGTGACTATGAATTTTCCAGTGATTTCAAAGCAATGA
GAAACATCATAGATTCTAACCCGACTTTATCTTTCACAGGACATTGCCAGATTGGAGGATA
GTTTTGATAGAATAATGGAATTTGCGCATGATTACAAGCACGGCTACAAAATTATTACCC
ATGAATTCGCCCCTCTTGGCCAACCTTAGTCTCAATGAAAATTTGCCGTTAACATTGAGAG
AGCTCAGTACTAGAGTCATTACCAGCTGCTTGAGAAAACATCCTCCTGTAGTCGAGTTCA
TTAATGAAAGTTTCCAAATTTTAAAGCAAAATCATGGCCGCTCTGTCAAATTTGAATG
ATTCTAACCCAGATCCTCTAATATCCTAATAAAAAAGATACTTGTCCATTTTAAACGAAT
TACCTGTACATCCGAAGATCTTCCTATATACTCTACGGTTGTTTTACAAAATGTATATG
AAAGAAACAACAAGGACAAACAGTTACAAATAAAAGTCCTGGAGTTGATCAGCAAAATTT
TGAAGGCCGACATGTACGAAAATGACGATACAAATCTAATTTTGTTCAAAAGAAATGCTG
AGAATTGGTTCGTCAAATCTGCAAGAGTGGGCAACAGAGTTCCAAGAGATGGTCCAGAACA
AAAGTATAGATTGAACATACATACAAGAACCTTTTGTGACACCCTTACAACTTGAAGAAAA
TTTTTCAAAGTGACATCACGATCAACAAAGGGTTTTTGAATTGGTTAGCGCAACAATGTA
AAGCCAGGCAATCTAATTTGGACAATGGGCTCCAAGAGAGAGATACTGAACAAGACTCAT
TTGATAAGAACTTATCGACAGCAGACACTTGATCTTTGGCAACCCCATGGCTCATAGAA
TAAAAAATTTTCAGAGATGAACTCTGA

YOL031C, 421 aa (SEQ ID NO 248)

MVRILPIILSALSSKLVASTILHSSIHSVPSGGEIISAEDLKELEISGNSICVDNRCYPK
IFEPRHWDQPIILPGQELPGGLDIRINMDTGLKEAKLNDEKNVGDNGSHELIVSSEDMKAS
PGDYEFSSDFKEMRNIIDSNP TLSSQDIARLEDSFDRIMEFAHDYKHGYKIIITHEFALLA
NLSLNENLPLTLRELSTRVITSCLRNPVVEFINESFPNFKSKIMAALSNLNSNHRSS
NILIKRYSILNELPVTSEDLPIYSTVVLQNVYERNNKDKQLQIKVLELISKILKADMYE
NDDTNLILFKRNAENWSSNLQEWANEFOEMVQNKSIDELHTRTFDFDTLYNLKKIFKSDIT
INKGFLNWLAAQQCKARQSNLDNGLQERDTEQDSFDKKLIDSRHLIFGNPMAHRIKNFRDE
L

YOL048C, 821 bp, CDS: 501-821 (SEQ ID NO 249)

TAAGTACATGATTTTTGTGTTGCATTGATATGACTTGTTTTATGACTAACATATTTAATTT
TTATTTGTAAACCGTAGGGGTTTTATGAAGTGCTGACGAATCCTGTTTATTGGAAGCATA
TTTTACTGTTTGGCGTTTGCTATGCCCTGATTTTTGTCACTATTGCTGGTCTCTTTTATG
TCACACTTGTACCGCTTTTAGTGACATGGGCCATACTGTTATTAGGGCCTCTTGGTGTGA
TACTGGTTCAATTTCAATGGATTTTACAAACGAATGTCTTGACTGCCTTTGTTTGTAGAA
CACTGGTCCCTGACCCATATTACGAATCAGATATTTGATATATCTTTGGTGTGTGAAGACC
AAGATGAATTTCTAAACGAGGTGAAGGTATTGCCTAAACCACAAAAGCCACATAGAAAAA
TCGATGAACCTGATGCGGTGAGAAATTTCAACACAATAAAGGGAAGTCGGATTTTTAAGA
TTCCCAGATTACTATTTCAGAAATGTTTTTAAAGTCTCCAATTTTACTTCACTAACATTAC
TGTCGCTAATTCCTATTGTAGGACCAATCTTGGCAAATCACTAATGGCCCCAAAAAGAA
CCTTTACCTATTTGCAGAGGTACTTTTTACTAAAGGGATTGAGTAAGAAACAGGCCAAAG
ATTTTCAGTACGAGCATTACGCAAGTTTCATATGTTTCCGGTATGTCTGCCGGTCTACTAG
AGTTAATACCTTCTTCACAATAGTCACCATATCTAGCAACACTGTTGGTGCAGCTAAAT

GGTGTACTTCGCTACTAAAGGGTGAAAGAAAGAAGGAATGA

YOL048C, 106 aa (SEQ ID NO 250)

MFFKVSNFTSLTLLSLIPVGPILANQLMAPKRTFTYLQRYFLLKGFSKKQAKDFQYEHY
ASFICFGMSAGLLELIPFFTIVTISNTVGAANKWCTSLKGERKKE

YOR010C, 1256 bp, CDS: 501-1256 (SEQ ID NO 251)

ACATTTCCCAAAAAAGACATTTCTGTCCAAAAAGTAGAAGGCAAGAAAAACCCTGGAGGAAT
CATAGGCAAAGAAAGAAAGAAAGAGTTTCATCTTTAACTACCTTTCAAGCCTTTATTC
GTTCCTCGTAAAGGACACACGAAAAAATAACAGTACCTTGCAGAAGGAGTGCAGAGTT
AGGTCGCAGGGAATCCCTTGAAAGCCAAGAGTTTTTTTCCGTAATGATCTCCCAAAGCAA
CCATCAACATTGTGGTGCAAGTTTAGTGTAAGATGTTCTACTGAACTATCTTAATAGCT
GAGCATCATGTGAGTAAACGAGTAAGCAAGAAAAACAACAAAGTAATGTTCAACTTTCGTA
ACTACGGAATAATATATAAGTAGTTAACGAAATTCGAACAATGAGAGCTCTCACATAT
CATCTTCTTTTCCAGTTTAGCCATTATCAGCACAATAATACAAAACACACTCGTACACTC
GCTTCAACTATAACAAAAAATGGCTTACATCAAGATCGCTTTATTAGCTGCTATCGCTG
CTTTGGCTTCGCCCCAACTCAGGAAGAAATGACGAATTGAACGTTATTTTGAATGACG
TTAAGTCCAACCTTGCAAGAATATATTAGTTTGGCTGAAGATTCTTCATCTGGATTTCCT
TAAGCAGTCTGCCATCTGGTGTTTTAGACATCGGTTTAGCTTTGGCTTCGCCCACTGATG
ACTCCTACACTACTTTGTACTCTGAGGTTGACTTTGCTGCTGTTAGCAAGATGTTGACCA
TGGTTCCATGGTATTCCTTCCAGGCTTCTACCAGAATTGGAATCCTTGTTAGGAACCTCTA
CCACCGCTGCCCTCTTCTACTGAAGCTTCTTCTGCTGCTACTTCTCCGCTGTTGCTTCCT
CCAGTGAACACTACTTCTTCTGCCGTCGCTTCTCCAGTGAAGCTACTTCTTCTGCCGTCG
CTTCTTCCAGTGAAGCTTCTTCTTCTGCTGCTACTTCTTCTGCTGCTGCTTCTTCCAGTG
AGGCTACCTCTTCCACCGTCGCTTCTCTACCAAGGCTGCCTCTTCCACTAAGGCTTCTT
CCTCTGCTGTTTCTTCTCAGCTGTTGCTTCTTCCACCAAGCCTCCGCCATTTCTCAAATCA
GTGATGGTCAAGTTCAAGCCACTAGCACTGTTTCCGAACAAACTGAAAACGGTGCTGCCA
AGGCTGTCTATCGGTATGGGTGCTGGTGTCATGGCCGCTGCCGCCATGTTATTATAA

YOR010C, 251 aa (SEQ ID NO 252)

MAYIKIALLAIAALASAQTEIDELNVILNDVKSNLQEYISLAEDSSSGFSLSSLP
VLDIGLALASATDDSYTTLVSEVDFAAVSKMLTMVPWYSSRLLPELESLLGTSTTAASST
EASSAATSSAVASSSETTSSAVASSSEATSSAVASSSEASSAATSSAVASSSEATSSSTV
ASSTKAASSTKASSAVSSAVASSTKASAIQISDGQVQATSTVSEQTENGAAKAVIGMG
AGVMAAAAML

YOR019W, 2693 bp, CDS: 501-2693 (SEQ ID NO 253)

CATTGATCTCGAGCACAGCTGCTCTTTTCTCTCAATGAATTACGTTATATGTTAATCACA
CAAGCATCAGTTTTTCATCGCAAAAGAAATATTTAGAGTTCTTGCAATTCAGATGTACC
TCAATTAATAACTCAATCACCTCTATGTTCTTGCTGGTAGTACTGCTTTTGTCTTAAT
ACTGCTGAATCAGCCTTCTAGAAGACCGTTCTGTTTTCAGCCGCTCGCCCCCTTTTCAAAGC
TTGCGCGGCTGAGTTTTATGAGGGGCGGCTTTTTTGTGAATGGCAATCTACCATTATTAG
TAGCAATATGATTTGCAGATAGATACATATATATCCTTCTGGGTTTCATGTCTCGTTACCA
TCCACACTAATGCATAGGACCAGAAAGAAAGGACATCGAATCCAACACGTATTAAATAA
GGACTCCTCATTAATAAGGCTTTTAATATTCAACTTGCTATAGATCACGCACCCTTTTGG
CAAGTCAACCTTAAATTATATGATTTCTGTTTGCCCCACAAATGACTTGCAAAATGCT
ACAGAAGCCTCACATTGATGTTCCAGGACAACAATTGGAAGAGAGAAATGAACAAAACC
TTAAAAAACGGGCCAAAAAGAAAGGAGTTTCCAACCATCTGTTGCCTTTGACACAGTGC
CTTCCACCGCTGGTTATTCTTCTATAGACGACAGCAGGGAAGGATTCAAAGGTGTACCTG
TTCCCAACTATTACACGATGGAAGAGTGCTATGACGATGAAACAGACTCTTTTTCGCCAA
ATTTGCAATATTTATTTGAGAGATACATTCCAATCATCACCTTTTCTGAATACTAGAAAAG
AGAACAATCTGAATCCAGTAGTTTTCATGAGATCCTCAAAGTTGTTGAAAAGAATT
CTGACATCAAAAAATATTTCTTGGTATCCAAGAATGGAAAAATAGTGAGGAGAGACTATC
CAAGCACGCCAGTAATTTGCAACGAAACGTTGATGATAAACAGGTTTGAAAAGAAGTGA
TAAAGTTATGGCGCCAAAGAAAACTACAAATAAATGAAAGGCTGAATGACAAAAAAAT
GGTTTACTTACCAGAACTTATCTTCTGAAGAGCGTATTAAACGTTATATAGAGGAG
ATGATAGTGACCATGTACAAAAAGAACAAAAAGAAAGCATAAAATACTTCAACAAAAGG
TCGGATATCCCAATAACCCTAAGACAATAGTTTGTACATTAAACGGAAAAAACATACGT
GGGTTGCCCTAGACTGGACAGTCTACAAGTTTGCACGAAATCTTGATCACATTGTTGTCA
TAACTACACTGCCAAAAATGATTTCTAACAGGAAAAAACTGCAAAAGATGATACAGAAT

GGGCACCGGGATATCAAAAAGAAGTAATAGATCAAAAATTAAACGACATTTTTGATTATA
TTTTACAGCTAGTAAAAGTGGTCAAAATATCCGTCAAAATTACTTTAGAAATAATTGTAG
GCAAAATTAAAAAAGTCTGGTAGATGTCATTAATGTCCATACTCCAGATTTCTTAGTTC
TTGCTACTTTTAAAGCACGAGCGAAATGAGAATCTTATTACATATAAATCCAAAAAGCTGA
CAGATGTCCTTCCCTGTTAGTTATCCGATTCCCACATTTGTTGTTCCCTCGAAACGAATGT
ATTCGTTTCGAACGAATCTACAAAGAGAAGTAAATGAACATTATGTCTCAAAAAATCATA
TGAAGCACGAACACACTGACGTTGAGAGCATGAGCAGTTCAATGTTCAAAAAAATACAA
TATCAGATATTTCTTCACATATTTCCGTAGATTTCGTACGCCGAAGATTTCAAAAGGCAAG
GCTACATCAAAAAGCAGTTCAACACCTCTAATGATTCCATTCCAAGAAAATTGACCCGGTC
TCGCCCAGCATTTCAAGAAGGAAGATCACGGGTGATATAGAAAAATTACAAGACGATGAGA
AAGATAGAGAATGTACTAAGGAAAAAATTTTGTGTAAGAAAATTGATATCATAATTAGAG
AGTCATTGAAGTCTTCTTTAGCGATAGAGACGTTGCCTGGTAAAAATGTATCGCAGTCCA
GTCACGGTGACCAAAATTTCCAGCTTTAAGAATGCTTTGATAGGCAATGGGTGCAAAAACA
CAAAGTTTAGAAAACTCTTAATACCATATTTCTCCTCAGAGGAACAAAATACCACAACAA
CTATTAACTCAGTAGCTCGCTACGTCCCAAATCAAGTTTGCAACCTCTGTAAACACA
AAGATGGAAGACGCCGCCCTTGCGAAAGCCAGAAATCTGCCTGATATAAGGCACAGTATTT
CCTTCGACAAAGAAAATTCCTTTGATCCATCTGATAAAAGCAGTAGTGTGATAATAGCA
TTCTTTGAGGAAAGTTAAAGTGCCGGTGCCTTAAGAAAAGTCAAACTAATGACTCCT
CAAGTAGTGCAGGGTCAAAGAAAAGCTCGTCTAGTTTGTAGTACTGTGAACACCTTCACTG
GGGTGAGAGTTGGGATTTTAAAGGTGTTTAAAGTGGAAGTTCCTCTGGAAATAAATCAT
CCAGTAGAAGGAATAGTAGCAGTGGCGATGTTTGTGAAAGTGATGATCGTAACGACAAGA
AAAAGAAGAAGAAAAAAGAAGAAATCATTTGTTCTTATTTCGGCAAAATATGA

YOR019W, 730 aa (SEQ ID NO 254)

MISVCPQNDLQKCYRSLTFDVPQQFEERNEQNLKKRAKKGSFQPSVAFDTPVSTAGYS
SIDDSREGFKGVVPVNYTMEECYDDETDSPNLYYLRTDFQSSPFLNTRKENKSESS
SFMRRSSKLEKNSDIKKYFLVSKNGKIVRRDYPSTPVIIVNETLMINRFKKNWIKLWRQR
KLQINERLNDKKKWFTYPELIFSEERIKPLYRGDDAPCTKEQKRKHKILQQKVGYPNNP
KTIVCHINGKHTWVALDWTVYKFARNLDHIVVITTLPKMISNRKKTAKDDTEWAPGYQK
EVIDQKLNDFDYILQLVKVVKISVKITLEIIVGKIKKSLVDVINVHTPDFLVLATLKHE
RNEENLITYKSKLTDVFPVSYPIPTFVVPVPSKRMYSFELNLOREVNEHYVSKNHMKHEHTD
VESMSSSMFKKNTISDISSHISVDSYAEDEFKRGYIKKQFNTSNDIIPRKLGTGAQHSRR
KITGDIEKLQDDEKRECTKEKLLKKIDIIRESLKSSLAIETLPGKNVSQSSHGQDIS
SFKNALIGNSGKNTKFRKSLIPYSSSEEQNTTTTIKLSSSPTSQIKFATSVKHKDGRAAL
GKARNLPDIRHSISFDKENSFPDSDKSSSVDNSIPLRKVSAGALRKVKINDSSSSAGSK
KSSSSFSTVNTFTGGGVGIFKVFKSGSSSGNKSSSRNSSSGDVFESEDRNDKKKKKKKK
KKSFLFLFGKI

YOR027W, 2270 bp, CDS: 501-2270 (SEQ ID NO 255)

AAATTTTCCCCCGTCATAAGTTCTATACACGGCTGGCTCTGATGGCATAATTTTCATGCT
GGAACCTACAAACCCGCAAGAAAAATAAAAAATTTGCGCAAATTTAACGAAGACAGCGTGG
TTAAAAATTGCTTGTTCGGACAATATCTATGTCTGGCAACTTCTGATGATACTTTCAAGA
CAAACGCCGCAATTGACCAAACTATTGAACTAAACGCAAGTTCAATATACATAAATTTTG
ACTATGAGAACTGATATCTTCGTGAAGATTTCGTGTAGTATGATAGAACATTCCAGAAAAA
AAATTCAGATTCATCGCTCTCTCTTCGCTTCTCCTCCTTTAAGGAATAAAGAAAAAATCA
CATACATAGATTAAAGTAAATAGGATCTGCTAGAAAAATTATATATAGATCAATCATCTTA
TTAAGGTATCTTGTTTAAGCCCAAAAGTCTGCTCCCAAATTCCTCACTGTAGCTACTAAA
ACAACCTATACGCAAGAAAGATGTCAATTGACAGCCGATGAATACAAACAACAAGGTAACG
CTGCATTTACCGCTAAGGATTACGATAAAGCGATAGAGCTCTTCACTAAAGCTATTGAAG
TTTCTGAAACTCCAAACCATGTTTATATTCTAACAGGTCCGCTGTTATACTTCTTTAA
AGAAATTTAGTGACGCATTGAATGATGCTAATGAATGTGTCAAAATCAATCCATCTTGGT
CTAAGGGTTATAATAGACTCGGTGCCGCCCACTTAGGTCTTGGCGATCTCGACGAAGCTG
AAAGCAACTACAAAAAGCCTTGGAGTTGGATGCCAGTAACAAGGCCGCAAGAAGGAT
TGGATCAGGTTTCATCGTACCCAACAGGCAAGACAGGCACAGCCTGATTTAGGGTTGACAC
AGTTGTTTGTCTGACCCAAATTTAATTGAAAATTTAAAGAAGAACCAAAAACTAGCGAAA
TGATGAAGGACCTCAATTAGTGGCTAAACTGATTGGGTACAAACAAAATCCGCAAGCTA
TTGGCCAAGATCTGTTTACTGATCCAAGATTAATGACCATCATGGCTACATTGATGGGGG
TTGATTTAAACATGGATGATATAAACCAATCAAACTCCATGCCAAAGGAACCGGAACCA
GTAAAAGCACTGAACAAAAGAAAGATGCTGAACCACAAAGCGATTCCACTACGACGAAGG
AAAATTCCTCTAAAGCACACAGAAAGAAGAAAGTAAGGAATCCGAGCCAATGGAAGTTG

ATGAAGATGACTCTAAAAATTGAGGCCGACAAGGAAAAGGCCGAAGGTAACAAGTTTACAA
AGGCACGTCAATTTCGATGAAGCTATAGAGCACTACAACAAGGCGTGGAACATGCATAAAG
ATATTACCTATTTAAACAACCGTGCTGCTGCTGAATACGAAAAAGGCGAATACGAGACAG
CTATTTCTACCTTGAATGATGCTGTTGAGCAAGGTAGAGAAATGAGAGCGGATTACAAGG
TCATTTCCAAATCATTTGCGCGTATTGGTAATGCCTATCACAATTTGGGTGACTTGAAGA
AAACTATAGAATACTACCAAAAATCATTGACCGAACATCGTACTGCTGACATTTTGACCA
AGTTAAGGAATGCTGAAAAAGAATTGAAGAAAGCTGAGGCGGAGGCGTATGTTAACCCTG
AAAAGGCGGAGGAAGCCCGTCTTGAAGGTAAGGAATATTTTACCAAGAGTGATTGGCCGA
ATGCTGTTAAGGCTTACACTGAAATGATCAAAAGGCGACCTGAAGATGCTAGAGGATATT
CTAATAGAGCTGCTGCACTAGCGAAGTTAATGTCTTTCCCTGAAGCTATCGCAGATTGTA
ACAAAGCCATTGAAAAAGATCCAAATTTTCGTGAGAGCTTATATCAGAAAGGCCACCGCAC
AAATTGCTGTTAAAGAATATGCTTCCGCTTTTGGAAACACTAGATGCGGCCAGAACCAAAG
ATGCTGAAGTGAATAATGGTTCTAGTGCAAGGGAAATTGATCAACTGTACTACAAGGCAA
GCCAACAAAGATTCCAACCTGGTACCAGTAACGAAACCCAGAAAGAACCTATCAAAGGG
CCATGAAAGATCCTGAAGTGGCTGCGATCATGCAAGATCCTGTTATGCAAAAGTATTTTGC
AGCAGGCCCAACAGAATCCCGCTGCTTTACAAGAACACATGAAAAATCCAGAAGTATTCA
AAAAGATTGAGACGTTGATCGCTGCTGGTATCATCCGACTGGCCGCTAA

YOR027W, 589 aa (SEQ ID NO 256)

MSLTAD EYKQQGNAAFTAKDYDKAIELFTKAIEVSETPNHVLYSNRSACYTSLKKFSDAL
NDANECVKINPWSKGYNRLGAAHLGLGDLDEAESNYKKALELDASNKAAKEGLDQVHRT
QQARQAQPDGLTLQFADPNLIENLKNPKTSEMMKDPQLVAKLIGYKQNPQAIGQDLFT
DPRMTIMATLMGVDLNMDDINQSN SMPKEPETSKSTEQKKDAEPQSDSTTSKENS SKAP
QKEESKESEPMVEDEDDSKI EADKEKAEGNKFYKARQFDEAIEHYNKAWELHKDITYLNN
RAAAEY EKGEYETAISTLNDAVEQGREMRADYKVISKSFARIGNAYHKLGLDKKTI EYYQ
KSLTEHRTADILTKLRNAEKELKKAEEAYVNP EKAEEARLEGKEYFTKSDWPNAV KAYT
EMIKRAPEDARGYSNRAAALAKLSFPEAIADCNKAIEKDPNFVRAYIRKATAQIAVKEY
ASALETLD AARTKDAEVNNGSSAREIDQLYYKASQORFQPGTSNETPEETYQ RAMKDPEV
AAIMQDPVMQSI LQQAQQNPAALQE HMKNP EVFKKIQT LIAAGIIRTGR

YOR031W, 710 bp, CDS: 501-710 (SEQ ID NO 257)

CTGCAGAAGTACAGCTGCCTTTATTTCTTGTGGTCATTTATTGCTTTTATTTTCAAGTCA
GATATACAAGAAAATCAAATCCCATCGTCAACGTCACGTATAAACGATTAATTTACAGTA
ATACCATACTCTACCAACATTATTTTAGTCCGACGTTACGTCTGTAGGTGTTCCAAATC
CTTCTGGCATTGACTTCTGTGCAGAAACCCCTTCAAATGAGTTCCACTTTACGTCAGATC
GCATAACAACCGGTCATATATTTTCTTTTGTCTAAACCCCTTACTGCAAGCACTTTTA
AGAAAAAGAAACAATAAATGCGTCTTTATTGCTGTGTGGAAGTGATTTTTGTCTTTCCGGAC
AAAAAAAGGATAGGGATGCGAGAGGGCTGTGAAGTAGTGATCAAGCGGGGCCCTATATAAG
AAGGGCGCACATCGTCCCCCTAAGAATAGCGAAGCGATATTACACTGAACACTACAATG
TCAAATAGTACTCAATAAATATGACTGTAAAAATATGTGACTGTGAAGGCGAATGTTGTA
AGGACTCTTGTCAATTGTGGGAGCACCTGCCTTCCAAGCTGTTCTGGCGGTGAAAAGTGCA
AATGTGATCACAGCACCGGAAGCCCTCAATGTAAAGAGTTGTGGTGAAAAATGCAATGCG
AAACCACGTGCACTTGTGAAAAGAGTAAATGCAATTGTGAAAATGTTAG

YOR031W, 69 aa (SEQ ID NO 258)

MTVKICDCEGECKDSCHCGSTCLPSCSGGEKCKCDHSTGSPQCKSCGEKCKCETTCTCE
KSKCNCEK

YOR096W, 1474 bp, exon1: 501-644, intron1: 645-1045, exon2:
1046-1474 (SEQ ID NO 259)

AAACCCATACACAATGAACCTTATCACACCCAAACATATGATATGGTATTAAAAAATGAA
AAAAATTCATTATTTCTTTAGCGTAATTATTGAAGAAAAACAGTGC GCGCGGTAATTTTT
TGTCACTCAGTAAGTACTAGAGAGAAGCCGAATGTACTCCCCCGGCTAGCTGGAGACCATGGC
TCTGCCTAGGATTTCTCTTATGCTTTCTTTTACCAATCACTTTGTTCCGGCGAGGCCCG
CGAAGCTCGCTTTCTTTCAGCCTAGCAATCATGTTCTTGCCAGCGTCGTAGACTACTGTA
TGGCAGTTGCTGCACTTGCCATGAATATCCTAGTGAAGCCTCTATGCAATAATCCAGTTA
CTGCGTTAGAATCCTGGTAAATGTCTAATCTTATTACATTACAGCAACGTATTAGATTT
TGATTGAAAAATTAGTCTTGCAGCTTGGTATATATCTTATTTTAAAGAAAGCTGAAAGGAA
GAAAGATCATCAGGAACAACATGTCTGTCTCCACAAGCCAAGATTTTGTCTCAAGCTCCAA
CTGAATTGGAATTACAAGTTGCTCAAGCTTTCTGTTGAATTGGAAAATTTCTTCTCCAGAAT

TGAAAGCTGAGTTGAGACCTTTTGCAATTCAAGTCCATCAGAGAAGTATGTTATTAATTTG
AATCTAAACTTAAGAATAATGGAGAGTAACAAAGGAAAAAAGTGTGAACGGGACGATACC
AGAATGTTTCAATCTAGAAAAGTATAAAAGATAAGGACTAGGACTCAAATGTATTTGGCT
GACTATCGCCTGAACCTTGATGCTAAGCAAATACCATATCTTCAAGAAAAAGCCTACTCC
AGTGTTTAAGAAGAAGGGAACGATTTACTAGATCATGCTATACGCAGTAAGGTTCTGATA
GTTAATTACAATCGGTCCAAGTTC TAAGCGGTGTCGTCCATGCATATATCATTTACAAGT
TACTGGCGTCAACTCTTCAAATATTCAAAATATCACCTAATCAAACCTACTAACATTTTC
CTTTTTTGTTCCTTCTTTTATAGATCGACGTTGCTGGTGGTAAGAAGGCTTTGGCCAT
TTTTGTTCCAGTCCCATCTTTGGCTGGTTTCCACAAGGTTCAAACCTAAGTTGACCCGTGA
ATTGGAAGAAGAAATTCGAAGACCGTCATGTCATCTTCTTGGCTGAAAGAAGAATCTTGCC
AAAGCCATCTAGAACATCTAGACAAGTCCAAAAGAGACCAAGATCCAGAACCTTGACTGC
TGTTTCATGACAAGATCTTGGAAGACTTAGTCTTCCCAACTGAAATCGTTGGTAAGAGAGT
TAGATATTTGGTTGGTGGTAACAAGATCCAAAAGGTTTTGTTAGACTCAAAGGATGTCCA
ACAAATCGACTACAAAATTGGAATCTTTCCAAGCTGTTTACAACAAATTGACTGGTAAGCA
AATTGTTTTCGAAATTCGAAGTGAACTCATTAG

YOR096W, 190 aa (SEQ ID NO 260)

MSAPQAKILSQAPTELELQVAQAFVELENSPELKAELRPLQFKSIREIDVAGGKKALAI
FVPVPSLAGFHKVQTKLTRELEKKFQDRHVIPLAERRILPKPSRTSRQVQKRPRSRTLTA
VHDKILEDLVFPTEIVGKRVRYLVGGNKIQKVLDDSKDVQQIDYKLESFQAVYNKLTGKQ
IVFEIPSETH

YOR248W, 803 bp, CDS: 501-803 (SEQ ID NO 261)

ACCCATTTTACAAATTTTTTTTGTATTTGAGCCATAGTACCCATTAATAGGTCTCGTCC
ATTCCTTTGTTTTTTTTTTTATTGTTTCAATTACACTACATAATTAAAAATCAGATCACTT
TCACTCTCACCTTAGTCGTTCTTTATCAACCAAAAAATAAAAAATGCTTCAATCCGTTGT
CTTTTTTCGCTCTTTTAACTTCGCAAGTCTGTGTGTCAGCGATTTATTCAAACAATACTGT
TTCTACAACCTACCCTTTAGCGCCCGAGTACTCCTTGGTGCCCCAAGAGACTACCATATC
GTACGCCGACGACACCCTACCTTTTTTGTCACTCAACGGTCTACTCCACGAGCTGGTT
CACCTCAACTTCAGCCACCATTACCAATGCGGCCCTCCTCCTTGTCCACCTCTTCGGC
CTCTGGATCTGTAACCCAGAAATCCACCCATGAAATTACCTCCACCTCGACTATCACGTC
CACTTTGCTGCTAACCCTTCATGACTCCACTACTTTGTCTCCATCATCTACTGCAGCAAG
TGTCAGTGACGAAGATTCAAACAACAAGATGCAAAGGTCAAGTCCTTTGAACAGGCTTC
AACTTCCAATGGTTGCGTCCCAATCACAAAGTTTGTCACTGTCAACCAATGAGCCCGTTAC
CCAGTACGTTACAGTCACCCCAAATACGACTACACAATACGTTACTGTCAACGGTGCACC
TTCTGTTACCCTACCTCTCCAGGTAACGTACAATGGTACAACACCACTTCGATTACTAA
TTCGACCAGTTGGTGAATTATGA

YOR248W, 100 aa (SEQ ID NO 262)

MTPLLCLHLLQQVSVTKIQTTKMQRSSPLNRLQLPMVASQSLSLSPMSPLPSTLQSP
QIRLHNTLLSPVHLLPLPLQVTYNGTTPRLRLIRPVGEL

YOR293W, 1255 bp, exon1: 501-552, intron1: 553-989, exon2:
990-1255 (SEQ ID NO 263)

AACTTTTCGAAATATATACTCTGAGTTCTTGCTCCCCGTTTTGTACGATGTTCTTAATGCA
AACACACGTCCCTTTAAAGATCCCCTGATAGGTTTCATTAAAGGCAACTTCCATACAGTT
GAAGTGCCAATTTTTTCCCTACATCCAAGCATCTGGGTTTGTATGGGTGTTACACCGGT
TTTTCTTTTTTATTTCCAGAGAAGTACAATTTTAGGCGGGTTCAAATTTCCCCTGTGTG
CGAGAAACGCTCCGCTACGCTAGGCTCACTCCGGTCTTCTCCCATTCTATCAGCGC
GATAGGCATACTGTGGGAGAGCGGCACTAGGGAGACCGGTGGGAAGCACCGTATCTAGTA
ACGCACGCTCTTTTGCAAAAATATCCATTAATTCATGTAAGTAACTAGATTAACTAGGTT
TAAGATTTTCGCAATTTTGGGCTGGATTATTAAGGTGAGTAGCAAAGTTTAGCAAGAACA
GTACGAACCTAAGTAGCCAAGATGTTGATGCCAAAGGAAGACAGAAACAAGATCCACCAAT
ACTTATTCCAAGGTATGTTTTAGAATAACTTTAGAAAGCATGAAGATACACGGAAAGTC
AAGCGAGGGAAGTTATGCGTATACACAGTAGCGGTAGTGTGATTACATACACGATGTT
TCAAACACACAGATGGATACCATGCATATGAGGTTAAAGGATTTCTTATGAATATATTAG
TGGATTACATAGAAGAAATTACAAGGAACCGTGTGACGACATTTTCGAAAGGACAGCACA
AGGCCATCGACCCCTGGAGACGTATGAAATATGGTATACGTCCTATATTTGGGCAAGAAAA

CGGTAAACTGTTTTACGCGGAGATCCAACTTTTGATCCTTACCGAGTACCACGAATCAT
CTATATGATCTTTTTACTAATCTATCTTCAATTTCAACGGAGAGATGTAAACATCATTCT
CTCCTATGATAATTTCTTTTTTATACAGAAGGTGTTGTTGTCGCCAAGAAGGATTTCAA
CCAAGCCAAGCACGAAGAAATTGACACCAAGAAGCTTGTATGTCATTAAGGCTTTACAATC
CTTGACTTCTAAGGGTTACGTCAAGACTCAATTCTCATGGCAATACTACTACTACACCTT
GACTGAAGAAGGTGTTGAATACTTGAGAGAATACTTGAAGTTGCCAGAACACATTGTTCC
AGGTACCTACATTCAAGAAAGAAACCAACTCAAAGACCACAAAGAAGATATTAA

YOR293W, 105 aa (SEQ ID NO 264)

MLMPKEDRNKIHQYLFQEGVVVAKKDFNQAKHEEIDTKNLYVIKALQSLTSKGYVKTQFS
WQYYYYTLTEEGVEYLREYLNLEPHIVPGTYIQERNPTQRPQRRY

YOR312C, 1432 bp, exon1: 501-507, intron1: 508-914, exon2:
915-1432 (SEQ ID NO 265)

TATTTACAAGCTAGATAAAAAAAAAAATCAAATAGCAAGCTATTCTGTTCATATCTTAAAGGT
GCTGATTGTTGTAGGCACGAAGTAAACAAGCTCTTCCCCAAAACAATAAATACGGTTTTT
CGGGACTGTTACCCGTACATTTTACGTTTCCGACGGCGCGATGCTATCTTTGAATTTTT
ATCTCTTTACAGTAACCCCATGACCAGTAGGGCGGCTTACTACCGAAGAGAAAAATGTCC
GCGGCTTAGACAGTTACTTCCCAGGCCAGGGCCAGGCCACACGGACAGAGGCAGATTCCA
AGTTGTTCCGCATAGTCTGTCTAGCTCTTTCTCAATTTTCCGCCAGATTCTGTCTAAATTT
CTTTCCGCTCGAGTTGGCAACAGTACGAAGAAGTAACTCTAATAGATAGATATAACCGTT
TTTGAGGGCATTATTTTTGCAGAAGATAATAGAAGAGAACCGTAACAAAGGAATCAAGCA
AAGAAAAAGTATGTAATAGAATGTATTGTATGCTTGTGGAATGAATGTCAATGTAGCTAT
TTTATATGGTGAGCTCAAATGGAATGAACATATCGTGGAAATTTAAATACTGAAGAATA
CCCAATAAGTCAATGCAACCTGTGAATGTTTTCTCTGAAATACGCCGAATACTGAATACG
ATTATTACCATAAATTGCTTCTAGAAGGAAGGCGGTGTACCATTTAATACTGATGATAG
GTTAATATCATTTGAGAACTCTTCACATGAGGACTATAGAATACTACCATCCAGGAATTATA
GAGGAAATTAAGTGAATCAGAGATCTATTTTGAAACATTCAATTTACATGTAATTTGCTGTC
AATAAAGCAATATTTTTGAAATATGCAAGTTTACTAACAAGAATAAATTTCTTTTTTGATT
TTTATCTTTAACAGTGGCTCATTTTCAAAGAATACCAAGTCATTGGTCTGCTGTTTACCAAC
TGAATCCGTTCCAGAACCAAAGTTGTTTCAAGATGAGAATTTTGTCTTCAAATGAAGTCAT
CGCCAAGTCTCGTTACTGCTATTTCTTGCAAAAATTGCACAAGGTTAAGAAGGCTTCTGG
TGAAATTTGTTCCATCAACCAAATCAACGAAGCTCACCCAACCAAGGTCAAGAACCTCCG
TGTTTGGGTTAGATACGATTCCAGATCTGGTACTCACAACATGTACAAGGAAATCAGAGA
CGTATCCAGAGTTGCTGCCGTCGAAACCTTATACCAAGACATGGCTGCTAGACACAGAGC
TAGATTTAGATCTATTACATCTTGAAGGTTGCTGAAATTGAAAAGACTGCTGATGTCAA
GAGACAATACGTCAAGCAATTTCTTGACCAAGGATTAAATTTCCCATTTACCTCACAGAGT
CCAAAAATCTACCAAGACTTTCTCTTACAAGAGACCATCAACCTTCTACTAA

YOR312C, 174 aa (SEQ ID NO 266)

MYLAHFKEYQVIGRRLPTESVPEPKLFRMRIFASNEVIKASRYWYFLQKLHKVKKASGEI
VSINQINEAHP TKVKNFGVWVRYDSRSGTHNMYKEIRDVSRVAAVETLYQDMAARHRARF
RSIHILKVAEIEKTADVQRQYVKQFLTKDLKFLPHRVQKSTKTF SYKRPSTFY

YOR369C, 932 bp, CDS: 501-932 (SEQ ID NO 267)

CTTCTTACAAGTTAATGAATAGTATATATATGTAAAAAAAATTTCTGCTTCATGTATATA
CGCACCTCGTTATTGAGGTATTGCGAATGTAGCAGTTGAATAAGCAAAGACGAGGTTTGT
ACATCTTGGCATATTAAATGGTTATTTCCGGGTTTTGTTTCCGGCTCAACGGTGATATAAAA
AGAAATCCAGTACTGTTTACCATTGTGCATCCGTACATTTGATTTGTTTACAACATCTTC
ACATTTCCATTGTGGAATCATTTTATTTTTTTTTCAGAATACCTTACCCGCAAGCAAACCTT
CAAGCAAACCTTACAATTTGCAAAATTTTCATCGAATTTCTCCGCAGGACATATTATAAAAGT
TATGTCATCTCTTATCACAACAGGTCTATAAGTGTTCCTTGTTCATTTGTTTTTCCCAAT
TCAAAACCTTTACCGGAGCAGTTTAATTTACTTCTGTCGAAGAAGTCAAAAACCTAGACT
ATATATTATTGAGAAGAAAAATGTCTGACGTTGAAGAAGTCGTTGAAGTTCAAGAAGAAA
CTGTTGTTGAACAACTGCCGAAGTTACTATCGAAGATGCTTTGAAGGTTGTTTTGAGAA
CCGCTTTGGTTACCGATGGTCTAGCTAGAGGTTTGAGAGAATCTACCAAGGCTTTAACCA
GAGGTGAAGCTTTATTGGTTGTTTTGGTCAGCTCTGTTACTGAAGCTAACATTATCAAGT
TGGTTGAAGGTTTGGCTAACGACCCAGAAAAACAAGGTTCCATTGATCAAGGTTGCTGATG
CTAAGCAATTAGGTGAATGGGCTGGTTTGGGTAAGATCGACCGTGAAGGTAACGCCAGAA
AGGTTGTCGGTGCCCTCCGTTGTTGTTGTCAAGAAGTGGGGTGCTGAAACTGATGAATTTGT

CCATGATCATGGAACACTTCTCCCAACAATAA

YOR369C, 143 aa (SEQ ID NO 268)

MSDVEEVVEVQEETVVEQTAEVTTIEDALKVVLRTALVHDGLARGLRESTKALTRGEALLV
VLVSSVTEANIIKLVEGLANDPENKVPLIKVADAKQLGEWAGLGKIDREGNARKVVGASV
VVVKNWGAETDELSMIMEHFSQQ

YPL047W, 800 bp, CDS: 501-800 (SEQ ID NO 269)

GGTTAGGGGCCAAGATTACGTTCCAGCTTTCGATGTCGCACCAGATTGGGAATCTTACGA
CTATGCAAAGTTGGATCCAACCTAACGACGACGACAAAGAATTCATCAATAACATGTGGGC
CTGGGATAAGCCAGTTTCCGTCAATGGCGAACCAAGGAAATTGTTGACGGTAAGGTCTT
AAAATAATCTCTTCGTACTATCCTTCATGTCGCCTTTTATTATAAAGTATGCTAGGTAGT
TTTATCTATATCTTATTTATGACGCAATATAGGGTAACAGAGTTTTCTGCTCTGAAACT
TCCGCAGAAAAAATCAAGTTTTCTTTCGTATCTTGGATTATTGTTATATAATAGAT
GCATGTATTATATGTATAGCAGTGATTGCTTATTTCTTGATTCTGAGGAATCGAAGAA
GTAACCTAGCGTTTCTTCCGTTGAGCAGAGCAGTATAATAATCCTTCAAATTCCTTAGGT
TACGGGGTTTTCTGTGCGATGACCGAAGAACTATTACTATAGATTCTATTTCAAATG
GGATACTGAATAACCTGTTAACCACATTGATCCAGGACATTGTAGCTCGGGAAACCACTC
AACAACAATTGCTGAAGACAAGATATCCGGATCTTCGCAGTTATTATTTGACCCGAACG
GATCTCTCGATATTAATGGACTACAGAAGCAACAAGAGTCTCTCAGTATATTCACTGTG
AGAATTGTGGCAGGGATGTGTCCGCAACAGACTAGCAGCTCATTTACAGAGATGTTTGA
GTAGGGGTGCTAGACGTTGA

YPL047W, 99 aa (SEQ ID NO 270)

MTEETITIDSISNGILNNLLTTLIQDIVARETTQQQLLKTRYPDLSYYFDPNGSLDING
LQKQQESSQYIHCENCGRDVSANRLAAHLQRCLSRGARR

YPL090C, 1605 bp, exon1: 501-506, intron1: 507-900, exon2:
901-1605 (SEQ ID NO 271)

GTAAGCAGAAGCCGGAAGAAGACAGAGTTTCATTTCAGAGAAAACATCCGTACATTCGAG
TTCTCATTTGAACCCATACATTTCAACTATTTTTACATAGTTTCGTTTTTCATGTGTAAT
TGTCATCGACGCGCCGAGCATCGGAAAGTTGGAACGTGCGCGATTGCACCAATCCCACT
GGGGCCGTGCATTCTGTAGGCAGGAAGCCACTGGACACTCTGCCCGTTCCCACTTGGAAG
ATTGGCGTAATTCACGCTCCTCTATCGATTCTAGCGGGAAAGTTATCTCTCTGGTAAG
CGTTGGAGGAATGCCGCTACCTAGGTAAGTCTACTGGGTGGGAATTCAGTACCGACGTC
TAGGAACATCATGATGCTGCGAGTTCTTTGAAATTTTCATATACAGTGTTACCAAGGATAA
AGTGGTTAATGCTTATTCGTCATTGAATTTTTATATTTGCTTAAGAGAAGTGACAAAAGA
GTGAAGACAGACTATACATCATGAAGGTATGATTTATGATACTATTATTGAGGGGCAACA
GAGAACTTTATATGTGGAAAAATGCGATGAAAGTTTGAAAGTGAGAAAGAACTAAACAGA
ACCAGACGTCGTAAAGATTTTAGAAATTTTTATGGAAAGAAGCAGGAAGACTACCATAT
ACTAATTGATGCGTTTGTGGCGTTATTTTAAACAAACAGAGCGGGTTTACATATCTGT
TACTACAAACCGTGAAATTTGAAGCAGTTTCATATACTTGGAGTATAGTCAATAAAAGACAA
GCTTTTTTCATCTTCCACTTAATAATTTCTCTAGAGTAATAAACTTCACCCTATTCAAACA
TTAATTTTGCAATAGTATACATAACAAATTTCTTAATAACCTGTTGAAATTTTAAATAG
TTGAACATTTCTTACCCAGTTAACGGGTCTCAAAGACCTTCGAAATTGATGATGAACAC
CGTATTTCGTGTTTTCTTCGACAAGAGAATCGGTCAAGAAGTCGATGGTGAAGCCGTTGGT
GACGAATTCAAGGGTTACGTCTTCAAGATCTCTGGTGGTAACGACAAACAAGGTTTCCCA
ATGAAGCAAGGTGTTTTGTTGCCAACTAGAATCAAGTTGTTGTTGACCAAGAAGCTTTCT
TGTTACAGACCAAGACGTGATGGTGAAAGAAAGAGAAAGTCCGTGAGAGGTGCCATTGTT
GGTCCAGATTTGGCTGTCTTGGCTTTGGTCATTGTCAAGAAGGGTGAGCAAGAATTGGAA
GGTCTAACTGACACTACTGTTCCAAAGAGATTGGGTCCAAAGAGAGCTAACAACATCAGA
AAGTTCTTCGGTTTGTCCAAGGAAGATGACGTTTCGTGATTTTCGTCATCAGAAGAGAAGTC
ACCAAGGGTGAAAAGACTTACACCAAGGCTCCAAAGATCCAAAGATTGGTTACTCTCAA
AGATTGCAAAGAAAGAGACACCAAGAGCTTTGAAGGTGAGAAACGCTCAAGCTCAAAGA
GAAGCTGCTGCCGAATACGCTCAATTGTTGGCTAAGAGATTGTCTGAAAGAAAGGCTGAG
AAGGCTGAAATCAGAAAGAGAAGAGCTTCTTCTTTGAAGGCTTAA

YPL090C, 236 aa (SEQ ID NO 272)

MKLNISYPVNGSQKTFEIDDEHRIRVFFDKRIGQEVGDGEAVGDEFKGYVFKISGGNDKQG
FPMKQGVLLPTRIKLLLTKNVSCYRPRRDGERKRKSVRGAIVGPD LAVLALVIVKKGEQE

LEGLTDTTVPKRLGPKRANNIRKFFGLSKEDDVRDFVIRREVTKGEKTYTKAPKIQRLVT
PQRLQKRHRQALKVRNAQAQREAAAEYAQLLAKRLSERKAEKAEIRKRRASSLKA

YPL137C, 4331 bp, CDS: 501-4331 (SEQ ID NO 273)

GTCTCAGTGATGCAATCATCATGGCACGGGCATTAATTAAGGTTAAGGAACCACTTCTCT
ACGCCATACTCCAAACAATAACAATATTAGACCTAGCCAATTGATACCCATGAGCGTGCA
GTCATTGCCATGGATTATTCATCTCTTTTCGCTGTTCTCTTTCTTTTCAAGTTTGTCTATC
ATCATGCGCTTCACTTTTGCCTTTCCATCTTTCTTTTGTCTGCAAAATAAAGGGAAGAGGG
GTAAAAACGCAAGGAAGAACAAGAAGAAGAGGGTAGTGCAAGAAAAAGAAAAGAAGAAAA
AAAAAAGTAATCTTGATACCGTGAGCAAAATAAGCTAACGGAAAGCGTAAGAAAGAA
GAGCGTGTTTTGGGAAATAACACCACAGCATAAAGCTAAAATTTCAGTTTATATAATCTAT
AGTAGTCCATAGAAATTGCGAATAACGGAAACAATAGTCCACCAAGCAAGCATAGGGA
GTGGAGATAGCATCTAGGTTATGATAACTAACACCGAGTTCGATGTGCCCGTAGATTGGT
TGTATAAAGGTAAGAGTAGACGGAAGACAAATACGAAGCCATCGAGGCCTTCTACGTCCG
CAGCCTCCCTCTTCATCTACGTCCCTTTCGAAAAACGGAGACAATAGCACGAGTGGTAACA
GGTCTAGCAATGATAAGCCTCGTGCGAGGTCGTCTATCTGTATCCAATGCAGCACTTTGTA
ATACTGAGAAACCAGATTGAAGAGGAACGATGGTAATACCTCTGCATCAGACACTGATA
ACATACCGCTACTTACTCCTATTAATAGCGGTAACCGGAGCGATTCCGCTGACATTGATA
ATCCGGCTACCGTAGACGCCATAGACCTTATAGATAATGATGACAACGGCTCAAGTACTC
AATTTGTAAGGAAAAACGTTCCACTTCTATATCCAATGCTGTGGTCTCGTCCAAACCAA
GACTGGCCAGTTCTGCCATAAAGCCACCGCATCTTCTTCTGTTGGCAAGGGAAGCAACC
CGCCAATTTCTTACCATCTAATGCTACTCTCAAGAGAAGCAACTCGACTAGTGGAGAAA
AGACTAAAAGGTGCGATTTTTGGATCTTTGTTTAGCAAACGGTCTACCTCTTCTTCAGCTT
CCACTGCCAAGAAACCATTACCTGTTGTTAATACTAGCACGACTGAGAATGAGTCTGGTG
GCATTAAAGCAGTTGCGACTCCTGATCCACGGGTGAAGGAGATATCATCACCATGAGAG
GAGTGGCCACCAACAGCTAGCAAGCCACAGACACCTATACTCCCTCCCTGCACTTGCAG
TAAAAGACCTATCTACAGTTTCATTGAAAAGGGTCTCGTTTGGCGTCGATAAATTGCAAT
CCGATCCTCCCAACAACCTTCTTCAAGAACCCCAAAAAAGGGAAACATCCTTATCCCTG
ATGACATGATAAGCGAGGTTCCTTCTATTTCCGTGGGTATTTCCAGTAGCAACCAATCGG
CCAAGTCAACCAATTCCAACATTAAGGGACCGTTGTACACTAAGAAGTCTAAAGAATATA
TACTCGCCCTGGAAAAATCAAAAGTTGGCTTTAAGGGAGGCTGCTAAGCATCAGCAAGAAG
CTCATTTTGTCTGCTAATAGAATAGCCTTTTGAAGTAGCCAATTTTAAGACTGCTTCGGATG
CAGGCGGTAAAGCTTACTGAAAAGTCATCAGAAGGCACCATTACGAAGCAAAGAGAAGAGG
TGTCACCTCCAAATGTTGAAGCTGATCGGGAGCTTGAGAATAATAAACTTGCAGAAAACC
TCTCAAAGCCGGCATTGATAAGCCCATTTCATATGCATGAGCACTATTTCAAGGAACCTG
ATCAAGATAAGTACCAAGACGGTCATTCTATTGAAAAATAACGAAGTTACGCTGGATGTTA
TTTACACAAGATGCTGCCATTTAAGGGAAATTTTACCATTCCGCTTACCCTAAGCAAG
TAAAGGACAAGACAGCTCCCTTGCAAATATTGAAGTTTTTGAACCCTAAGCCTACCTTGA
TCGATATTCTTTTCTTTTGTGATTTCATCACCATTGCTCCATTACACGATTGTTTTCTG
ACAATGTAGCTTTAAACCAGGATATGTTTCAAGAATAATTATTTCTGCTTTGGTAAACTCCA
CAGTTTTTGGACAAATTGAGTTTAAGAAATGTACGAATCGACCAAGATGGATGGAAATTAC
TATGTAAGTTCCCTTTTGTCTAAACAAATCACTGAACAAGCTCGACATTTCCCAACGAAAA
TCAAATCTGACCTTGCTGAATCACTATATCGCCATAACATGGATTGGAACCTTGTCTACTG
ACGCTTTGTCTCAGAGATCTCACAACCTATAGAAGAATTGTTATTCAATGGTATTCAAT
TTAGCAAAATTCCTTACTCATGCTTTGCACGTTTACTGACATCCTTTGCTACCCAAAAAA
ACTTTCCAGAATCGGGCATCAGGCTTGGTTTAGCAGGTGCCACTACTTCCAATATCTCTC
AGGATTGTCTGAAATTTATCTTCAATTGGATGCTCAATATAACGTCCAGGGTGTGGATC
TAGCGTTTAAATGATCTGTCCACTATGATTAAAGCCAATGGTTGGTAAACTATCTGCTCTAT
CATATGATAACTTAAGATATTTCAATTTGAACAGCACTAATATTTTCGACTTCTTATGATT
TAGCTTTGTCTTTGAAATATCTTTCTAAGTTGCCTAACTTGATTTTTTTTGGATTTGAGTA
ATTTGTGCGCAATGCTTTTCCGTGACATTTTACCCTACATGTACAAGTATTTACCAAGATTTT
CGAACCTGAAGAGGATACATTTGGATAGCAATAATTGACATTAAAGGAACCTAGCTGTCTG
TTTGTAAATTTTGTATTAAGTGCAAAATCGCTCTCGCATGTGTCAATGACTAATCAAAACG
TTGAAAACCTCTATCTAATGAACGGCACAGATTCTCCCGTTCAACAAACTAACACAGACG
GCGACTTGGATAGTTTCGAGCACATTGGACGTTAAGGGCCAATTTGCTAAAAATAGTTTTT
CATCCACACTTTTACGCATTTGCTAGAGACTCTCCAACTTGATTGGTTTTAGATTTTGA
ATGATTTGATATCAGAAGAGATTCAATCAAGAATAGCACTGTGCTTGTATGAGAAATATGA
AACGGACCATGGATTGCACTTTCCAGTTAGATGAATTGGATTGCAAGATGATTTGCTAT
TCGATGGCTCTTTAGTAACATATGACCGCTGAAAGTGTTTTAGAAAAACTGAACCTGTTAA
GCGATAAGAGTACAAAGGTCAAAAAAGACACCACGAAGAGATATTTGCTGAAAAATATA

TTGAAAAGTTCCATATCTTGCACCATAATGTTTCAGCATACAATAGATACTATGTTTCGAAA
AAAGGAAATCAGGTGAATTGCCATTGCAAGAAAAAGAAAACCTTGTAAGATTACTCCTTT
TGGAACAAAACCTTATGCAATATACTAGAAATGTTTTTCGCATAATCCGAATCTGAATGATG
TCCTTGGATCCAGCAGGGATGATTCTGAAGGAAAGTGTGACTCCAGCGAAGATTCAAAAT
TACCAGCATTGAAGCACGTTGAATCCGGATACCATGTTCCCGAAGAAAAAATACAACCTG
AGAATGATGTAATTACAGCAAGACCACATTTAATGGCCACCGATTCTGGTAAAACTATTG
ACGTTTTTCACAGGCAAACCATTTGGTGTTCAGCATACATCATCTAGTACTTCTGTAGGTT
GTAAAAAGCAGGAAGAAGAAGGTTGAATACATAAATGGGGTTTCTTCGTTTCAGCAGC
AGAGGTCTTTTATACCCTGAAAATGAATCAACAAGGCAGACACCTTTTGCATCAGGTGATA
CGCCTATCAACACAGAAACAGCTGGTAAGTCAACTTCATCTCCTTCAGTTTCAACTTCTA
ACAATGAAACTGCTACCACCTAGTTTATTTAGCCAGCTAATCCTAAGATTTTACCAAAAA
TTCCATCCGGTGTCTGCTTAAGATCGGCAATCATGAAGGCTAAAGGTATTGATTCTATCG
ATGATTGATTGAGAACGTTAACTCCAACAACATAGAATTGGAGAACATTTATGGTGAAT
CCATTGAGAAATAGCGCTTCGACATTTACACCAGCGTGGATTCTGATGTATCTGCGCCCA
ATACCAGATAAAGGATCCGTAGAAACATTGCCTGCAGTCTCAACTGACGACCCAAATTTGTG
AAGTCAAAGTCACTGCTACCTATGACAACTATTAAATAATTTGTGATGGAGAGGTCAA
TCAGACTTTGA

YPL137C, 1276 aa (SEQ ID NO 274)

MITNTEFDVPVDWLYKGKSRRTNTKPSRPSTSPASSSSSTSSSKNGDNSTSGNRSSNDKP
RARSSSVSNAALCNTTEKPD LKRNDGNTSASD TDNIPLLTPI NSGNRSDSADIDNPATVDA
IDLIDNDNGSSSTQFVRKKRSTSI SNAVSSKPR LASSAINATASSSVGKGKHPPISSPS
NATLKRSNSTSGEKT KRSIFGSLF SKRSTSSSASTAKKPLPVVNTSTTENESGGIKAVAT
PDP RVKEISSPMRGVAPTASKPQTPI LPSALAVKDLSTVSLKRV SFAVDKFESDPPQQL
PSRTPKKGNILIPDDMISEVPSISVGISSNQSAKSTNSNIKGPLYTKKSKEYILALENQ
KLALREA AKHQEAHFAANRIAFEVANFKTASDAGGKLTEKSSEGTITKQREEVSPNVE
ADRELENNKLAENLSKAGIDKPIHMEHYFKEPDQDKYQDGH SIENNEVTLDVIYTRCCH
LREILPI PSTLRQVKDKTAPLQILKFLNPKPTLIDILSFCDFITIAPIHTIVFDNVALNQ
DMFRIIISALVNSTVLDKLSLRNVRIDQDGWKL LCKFLLNLSLNLKLDISQTKIKSDLAE
SLYRHNMDWNLF TDVLSQRSHKPIEELLFNGIQFSKIPYSCFARLLTSFATQKNFPESGI
RLGLAGATTSNISQDCLKFIFNWMSQYINVQGVDLAFNDLSTMIKPMVGKLSALSYDNLRY
FILNSTNISTSYDLALLKYL SKLPNLIFLDLSNLSQCFPDILPYMYKYLPRFPNLKRIH
LDSNNLT LKELAVVCNLIKCKSLSHVSMNTQNVENFYLMNGTDSVPVQQTNTDGDLDSSS
TLDVKGQFAKNSFSSTLYAFARDSPNLIGLDFDYDLISEEIQSRIALCLMRNMKRTMDST
FQLDELDSQDDLLFDGSLVTMTAESVLEKLNLLSDKSTKVKKD TTKRYLLKKYIEKFHIL
HNVQHTIDITMFEKRKSGELPLQEKENLVRL LLLLEQNLCNILELFSHNPNLNDVLGSSRD
DSKESVDSSSEDSKLPALKHVESGYHVPEEKIQPENDVITARPHLMATDSGKTIDVFTGKP
LVFKHTSSSTSVGCKKQEEEEGELHKWGFVQQQ RSLYPENESTRQT PPFASGDT PINTET
AGKSTSSPSVSTSNNETATTS LFS PANPKILPKIPSGAVLRSAIMKAKGIDSIDDLIQNV
NSNNIELENIYGESIQNSASTFTPGVSDSV SAPNTDKGSVETLP AVSTDDPNCEVKVTAT
YDKLLNNLSMERSIRL

YPL159C, 1262 bp, CDS: 501-1262 (SEQ ID NO 275)

AAACAAAGCGATTTGAGTATTACGTTAAGATCTCCATTTGCTATGCTAAATCCTGCCTAC
TCAAACAGCATTTATATCGCTACCAACAGGTGTGGTCAAGAGGTCAATTGACTCTTCTCTGTC
GGTATGAAAATTTAAAAATATATAAATAACATAAGTTTGCATTCAATTAATATAATAAAA
TCAACGTATCAACCATAAGAACCATAATCATAATAATTGTTTACCTTAATGGCGATATCG
CCTTTTATCACCATCGACGATAACAAACGCCTATTCTGTCTACCGTTTCTTTTTTTCGCT
CGCAATATCAGAATCGTTTATCCCAAAGGGTAGTTATAGCAACTATTTAAATAACTTAGA
TGTTTCTTTAACTTATTCGGTCATACGTACACAAACACCCGCTAGATATAGCACTCCTTG
CTGTCGAACATTATAAAGGTGCTTTTAAAACTACTAATCGTATATTTCAGCAGGTCAAGAC
GCAAAGTCGGACGATAAACTATGTTGAAGCTAGCTCGTCCATTATTCCGCCTTTATCAA
GGAACAATGCCATTTCTTCAGGAATAGTTCTCACTTCTAGAAGATTTTCAGTCTTCTTTTA
CGTTCTTAAGTAACCACTCTTTACTATCTAAAAATCAAATGAAATCCAAAAGAAAAAAGG
GCAGTAAAAAGGCAGCGTACCATCGTCAACCCCGGAACACGAACATACTGCACCACTTA
TAAAGCAAAACAAGACAATCACAAAGAAAGACATAGCGATGTGAGAGGTTCTCATTTAA
AAAAGAAAAAGAAGCGATTTTTCTGTTGGCTACCAAGAGTACCATCCACCTCACATTTAAAGC
AGAGTGACATGACCACAAATGTACTCTATTCTGGATATAGACCCTTATTCATCAATCCCA
ATGACCCGAAGCTAAAGGAAGACACCGGAAGTACGTTATACGAATTTGCGATGAAGCTTG
AAGATTTAAATGAACCTCTATCACCATGGATTTCCTCTGCCACTGGACTTGAATTTCTTTT

CAGAGTGGGAGAATATACCTAGTGAAGTACTGAAAAATTTGAAGCCTTTTCATCCACCTA
AGGAAAAATCAATGAACACAAATGAGCTTATTCATGTAAGTGCTAAGAGAAATACATTAG
TTGACAATAAAACAAGTGAGACGCTTCAGCGGAAAATGGATGAATTTTCAAAGAGAAGAG
GAAAGGGGAGAAAAAAGTCAGTAGTGACGTTGCTCCAAATGAAGAAAAAAGTTGAGGGAT
GA

YPL159C, 253 aa (SEQ ID NO 276)
MLKLARPFIPPLSRNNAISSGIVLTSRRFQSSFTFLSNQSLLSKNQMKSKRKKGSKKAAY
HRQPPEHEHTAPLIKQNKITITKKEHSDVRGSHLKKRSDFSWLPRVPSTSHLKQSDMTTN
VLYSGYRPLFINPNDPKLKEDTGSTLYEFAMKLEDLNEPLSPWISSATGLEFFSEWENIP
SELLKNLKPFPPEKESMNTNELIHVSAKRNTLVDNKTSETLQRKMDEFKRRRGKGRKKS
VVTLLQMKKKLEG

YPL175W, 1940 bp, exon1: 501-514, intron1: 515-568, exon2:
569-1940 (SEQ ID NO 277)

ACGTTATTTTCAAAACACATACGAAATCGCTGGACTTTCTCACTAAAGGCTTCCGGAGCC
TGCGGTTCTTCCATCCCCATCTCTTCCACATATACCGGGGGTTCTGATGGCAITTCCTATA
GCTTGCTCAAAGTCTGCGAGTTTAGCTCATCTTGTGAGTTATTTGCTGGTCTTCAACA
TTCGGAAGAGTAGTGTAGCCCCTAGTATTACCATATCCTTTGTATACTCATATGCGAAC
TTGTCTAATAACAATGTATACCAAAAATAACAGCTTGAAAAAATCTCAGGGTCTTTTCAT
TGAATAATCTCATTTCTGCTATTTTAAGTTTTTCGTTTGCAACCCGAGACTGTCGAGCTAG
AAAAATTCATTGATACGATTTAAAAATAATCGATGCCAGTAATAGCCTCAAAAACTTAT
GCAAAAATACGAGATACTATAAACTACAGCTTAGCTAACTCTAACATTATTATATAAAAC
AATGGGCTTCAATATAGCGTATGTCTAGCTCACAGCATGTGTTCCAAATACATTAAAGAA
GATCTCTTTTGTGTGTTGATACTAACAGTAAAGTTGAGAGTTATAACAATGAAAAATAGGA
TGCTGTGCGACTTTTTTTATCCACAGTTAGGTGGAGTGAATTCATATATATCATTTAT
CGCAGAAACTAATCGATTTGGGCCATTCTGTCTGCTATTATAACTCACGCTTACAAAGATC
GAGTCGGCGTACGACATCTTACCAACGGTCTAAAGGTCTATCACGTACCATTTTTTGTGA
TTTTACAGAGAAACCACTTTCCCACTGTTTTTTTCAACATTTCCAATAATAAGGAATATTC
TTCTCAGAGAGCAGATCCAAATGTTCATTCTCATGGTAGCGCTTCCACGTTCCGCTCACG
AGGGAATTCCTTCATGCTAATACTATGGGATTGAGAACTGTGTTACGGACCATTCACCTCT
ACGGTTTTAATAACTTAACGTCGATTTGGGTGAATAAGTTGCTAACATTTACCTTGACAA
ACATAGATCGGGTTATATGTGTTTTCTAATACATGCAAGAAAAATATGATTGTTAGAACAG
AATTAAGTCTTGATATAATCTCAGTAATTCCTAACGTCAGTGGTGAGCGAAGATTTCAAA
CAAGGGATCCTACTGGTGGCACCAAGAGAAAAACAAAGTAGGGATAAGATAGTGATCGTGG
TCATCGGAAGGCTCTTTCCAAACAAAGGGTCCGATTTACTTACTCGCATAATTTCCGAAAG
TTTGTTCCTCACATGAAGATGTGCAATTTATAGTAGCGGGCGATGGTCCAAAGTTCATAG
ATTTTCAACAAATGATTGAAAGTCATAGACTACAAAACGTTGTGCAACTCTTAGGCTCTG
TTCCACATGAGAAAGTCAGGGATGTATTATGTCAAGGTGACATATATTTACACGCTAGTT
TAACAGAAGCATTTGGTACAATTCTAGTTGAGGCCGCATCTTGTAATTTGCTAATTGTAA
CGACACAAGTCGGAGGAATTTCCGAAGTGTTACCAAAATGAGATGACTGTTTTATGCAGAAC
AGACATCCGTTTCTGACCTTGTTCAAGCAACAAATAAAGCTATCAATATCATAAGAAAGTA
AAGCTTTGGACACTTCCTCTTTTCATGATAGCGTGTCTAAAATGTACGACTGGATGGACG
TAGCCAAAAGGACAGTAGAGATATATACTAATATATCTTCTACTTCTTCCGCTGATGATA
AAGATTTGGATGAAAATGGTAGCAAATCTTTACAAAAGAGATGGAATCTGGGCTAAACATC
TTTATCTGTTATGTGGAATTGTAGAGTACATGCTTTTTTTTCTCTTAGAGTGGCTATACC
CCAGGGATGAAATCGATCTAGCTCCAAAATGGCCCAAGAAAACAGTGTCTAACGAGACGA
AGGAAGCAAGAGAACTTAA

YPL175W, 461 aa (SEQ ID NO 278)
MSSSHKVESYNNENRMLCDDFFYPQLGGVEFHIYHLSQKLIDLGHSVVIITHAYKDRVGV
HLTNGLKVYHVPFFVIFRETTFTPTVFSTFPIIRNILLREQIQIVHSHGSASTFAHEGILH
ANTMGLRVTFTDHSLYGFNNLTSIWVNKLLTFTLTNIDRVICVSNTCKENMIVRTELSPD
IISVIPNAVVSDFKPRDPTGGTKRKQSRDKIVIVVIGRLFNPNGSDLLTRIIPKVCSSH
EDVEFIVAGDGPKEIDFQQMIESHRLQKRVLQSGVSPHEKVRDVLCOGDIYHLASLFEAF
GTILVEAASCNLLIVTTQVGGIPEVLNEMTVYAEQTSVSDLVQATNKAINIIRSKALDT
SSFHDSVSKMYDWMDDVAKRTVEIYTNISSTSSADDKDWKMKVANLYKRDGIWAKHLYLLC
GIVEYMLFFLLEWLYPRDEIDLAPKWPKKTVSNETKEARET

YPL180W, 2900 bp, CDS: 501-2900 (SEQ ID NO 279)

CTCAATGGGAATTGAGTGAAGATCAGTCTGATCGAGAGGAATTTGTACGATTCGTGGAAA
ACCAGCATTTTCGTAGAAAAAGTTGATACGATTTACAACGGTTATAATGAAAGTCTATCAA
TGATGGACGACCTGACTAGAGAGTTACTACTATGGGAGAAAAAATATTCAAATAACACTA
ATGCCATTCAATAAACGCAAAACACTGCAATATTATTCTCAACCAAAGTATAACTGTAAT
GAGGCGAACAAACACATCTATACATATATATACATCTATATGGATATAAAAAAGACTAAT
TCAACGTTGTTTTTATCAACCGAGCTTACTCTGTACGGGTAACCGCAAGGATAGCTAGT
TGCGGATGGTATAGCGATTTGGCTGGCAGCATGATTAAGGAATCCAAACATCTAATGGAC
TAGCACATTTCTATCGATTTACGGGTCAAGGTAAACATAGATATTGGGATATATCATATATC
CTTACTGAGTAACTATAATTATGGTTCATCGAGGAAGGACTTTGAAGTCAGACACTGATG
TAACATCTCTTAATGCGTCAACAGTATCACACCAGTCAAAGCCATTTAGACAGTTTTTCGA
CTAGGTCGAGAGCAAAGAGTAACGCAAGCTTCAAAGGTTTGCCTAGAGTTTTTAACACATG
ATGGCACCCCTGGATAATGATTATTTTAATAAGCACAAACGTTTCTCAGAAATGCAAGAGTT
CTGATGCCATTTTTAGAAAGCGAACGATTAGTGGGTTGAATATGACAGCTTTAACAAGAG
TAAAGTCCAACTCAAGGAAAAAGATCAGCATCCTTTTCATAGTCCGGTGCATAAATACGCTGC
TCAGTCCAAAGAACAGCAGTCAATCTAATACTGGAAGTCTGGTTTTCGGCCTGAAACCAC
GAAGAGTAAAAGTACCAATCTGTTCTGAGTCTTCGAGATGCGCAAGAATCTAAAAAGA
GTGAATCTACTACTGACGAGGAGGTGGAATGTTTTTCGGAAGACAACATTGAAGATGGAA
AGGTGAATAATGATAAAGTAATAGCCGAGCATGTTATGCCTGAAGAAAAAAGAATGTGC
AGCAATTAAGTACGAATGAATTACAATCCCCGATTCAATAGATGAACAAGAAGAAGATA
AATCAGGTACTGATGGAAAGGAAAAATCATAGAGCTGTATCCTTACCATTACCTCATTTAT
CTTCCAATAACTATTTTCGGAGAATCAAGCCATTCTATAGAACATCAGAAAGATGGAGAAA
CATCTCCAAGCTCAATTGAAACAAAACCTGAATGCAACAAGTGTAATCAATGAAGAGGGGC
AATCAAAGGTGACGAAGGAAGCTGATATTGATGACTTGTCCAGCCATTCTCAAAATTTGA
GGCCTCATTTGGTTAAAGCGGGCGATAATATATCAGAAGCACCATATGATAAAGAAAAA
AAATTTCTTGATGTTGGTAATACCTTAGCTGCACATAAAAGTAATCAAAAACCAAGTCATT
CAGATGAACAGTTTGATCAGGAAGATCACATTGATGCCCCTAGGAGTAATTCATCAAGAA
AAAGCGACTCGAGCTTTATGCTCTTAGGAGACAAAGTTCTAAACAACACAAATTTATTAA
ACGAAGAAGAAGATCTAATCAAGCCTGATGATATTTCTTCCGCTGGTACCAAGGATATTG
AAGGGCATAGCTTACTGGAAAATTATGCGCCTAATATGATTCTCTCCAGTCGACTGGAG
TTGAACGTAGATTTGAAAATTCATCATCCATCCAAAATTCGCTTGGGAATGAAATTCATG
ACTCGGGTGAGCATATGGCTTCAGGTGATACTTTTAATGAACTGGATGATGGCAAATTCG
GCAAGAGCAAGAAAAATGGTGAAGATCTCAACTTGGCCAAAATATACCGAAGTCTCAGT
CTACTTTCCCCACCATTGCTAATCATCGGTAGTAAAGATAATAATGTACCACAGCACAACT
TTTCGACCTCCATATCGAGTTTAACCAATAATTTGAGGAGAGCTGCTCCTGAAAGCTTCC
ATGGTTCAAGAAATGAATAATATTTTTCACAAGAAAGGTAATCAGAATCTACTTCTGAGT
CCAACGATCTCAACAAAAATTCGAGCCCCGGCCTCTCCATTGTCCAACGAACATATTA
CATCTAGTACGAACTCCGGTAGCGATGCAAACAGACAATCCAAGTCCAGGTGCCAAATTTA
ATAGCTTCGCCCAGTTCCTTAAATCAGATGGGATTGATGCAGAATCAAGAACACAAAGAA
AATTATGGTTGCAGAGGGAGAAATCTATTATGGACTTAAGTTACAAAATGACGGTAGTG
ACTCTATCTTTTATGGCAGGAAACATTGATGCGAAAAGGGAGTTTGAGAGAATATCCCATG
AATACTCTAATGTAAAAAGATTTTACAACCCATTAGATGAAGCATTGTTGAGAGTACAAC
CTATAATAACGGGAAATGCAATAATATCAGGAAAAAAAGCCATAACGATGCTCAGTCAA
TCGCACATTTAGCAGTGATACAGATCATAAGGATGAGGACGATTTGCTCTTTACTAAGT
ATGACAAAAAATTTGATGATCTTTATCCACATCTTGCAAGTGCAAGATTCAGGCAGTGT
TGTCCGGTATATGGAAGCGAAAGTTACTTATTTAACAAGGATGTTAATCCAATCAACA
AGAATAGGACAACGAGTACAAACACAGCGTTGGCCACACTGCTTCACAGAATGCACGTA
ACTTGCTGAGGGGCCGATGGGTTCCAGCACGACTTTGCACCACCAACGCGTCATTAAGT
CTCTGCAGCCGACTACGAGGCAGTGAATCGCAGGATGGAAGATGTGGGCTACATGCATA
CACAGCCACAACAAAGGTGA

YPL180W, 799 aa (SEQ ID NO 280)

MVHRGRTLKSDTDVTSLNASTVSHQSKPFRQFSTRSRAKSNAFSGLRRLVTHDGTLDND
YFNKHNVSQCKSSDALFRKRTISGLNMTALTRVKSNOGKRSASFHSPVHNTLLSPKNSS
HSNTGTAGFGLKPRRSKSTQSVLSLRDAQESKKSESTTDEEVECFSEDNIEDGKVNNDKV
IAEHVMPEEKKNVQQLNQNELQSPDSIDEQEEDKSGTDGKENHRAVSLPLPHLSSNNYFG
ESSHSIEHQDGETSPSSIEKLNATSVINEEQSKVTKEADIDDLSSHSONLRASLVKA
GDNISEAPYDKEKKILDVGNTPLAHKSNOQKPSHSDEQFDQEDHIDAPRSNSSRKSDFSFM
SLRRQSSKQHKLLNEEDLIKPDIDISSAGTKDIEGHSLLNYAPNMILSQSTGVERRFEN
SSSIQNSLGNIEHDSGEHMASGDTFNELDGKLRKSKKNGGRSQLGQNIIPNSQSTFPTIA
NIGSKDNNVPQHNFSTSISSLTMNLRRAAPESFHGSRMNNIFHKGNQNLNLLRSNDLNKN

SAAPASPLSNEHITSSTNSGSDANRQNSNGAKFNSFAQFLKSDGIDAESRTQRLWLQRE
NSIMDLSSQNDGSDSIFMAGNIDAKREFERISHEYSNVKRFYNPLDEALLRVQPIITGNA
NNIRKKSHNDAQSIAHSSSDTDHKDEDDLFTNYDKKFDDLYPHLASAKIQAVLSGIWKS
ESYLFNKDVNPINKNRTTSTNHSVGHTASQNARNLLRGPMGSSTLHHQRVINSLOPTTR
AVNRRMENVGVMHTQPQQR

YPL218W, 1212 bp, exon1: 501-528, intron1: 529-667, exon2:
668-1212 (SEQ ID NO 281)

TGATACAAGACAGGCATTAGGAAACACATGAGTTTTGCATATGTATTATGCAGGTTTCATT
TGTTCCCTCCCTTATTTCTTTTCATAGTATTTATTTTATTTATTTATTTATTTT
GGATTTTATTTTATTTCTTTTAAATGCTAAGAAAGTAAATCCGCATAATTAAACGTGTG
CTGGCCTCGATAGGTACCTATAGTATACAGAAGCTTACGAAAAGCTCCTGCAGGATGGCA
CTTCTAAATTCGCGCTCAACATGGCCGATTGTACATTATATCGTTCTATCATTATATC
GTATACGCCCGCATTACCCGACAACCTCCGTCTGCAACGCGTTGACCAGAAAACCTCGAACA
AGAGATCGCATAAAAAACCAAAAGGAAACGAATTACTTGTCAAATAGTTATTGTAATGGA
TCCTCTAGAAAGGCAACAGTAGATTTATTTCTTCTTTCTAGAAACATCATTATAACT
AACAATATATAATTGGAATAATGGCTGGTTGGGATATTTTGGTTGGTGTATGTTATCAC
CCTGTTACGTTTTTCGGATACTTAGTTTTATTCAATGTGGTAAACATTGAATGTTTTCA
GCTTAAGATCTATTTTTTTTTTCTAGAAGAAATTGCGTCTTTTACTAACTTTTATTTTAC
TGTACAGTCAGAGATGTGTTGGCTTCCCTTGGTCTGTGGAACAAACATGGTAAACTACTT
TTCTTGGGTTTTGGATAATGCCGGTAAGACCACATTGCTACATATGTTAAAGAACGATAGA
TTGGCAACCTTACAACCAACATGGCATCCAACCTCTGAAGAACTGGCTATTGGTAACATT
AAGTTTACAACCTTTCGATTTGGGTGGTCATATTCAAGCTCGTCGTTTATGGAAGGATTAT
TTCCCAGAAGTTAATGGTATCGTCTTTTATGTCGATGCTGCTGACCTGAAAGATTGTAT
GAAGCACGTGTGCAATTAGATGCTTTATTCAACATTGCCGAATTGAAGGACGTTCCCTTTT
GTAATTCTTGGTAACAAGATCGATGCTCCAAACGCCGTTTCTGAAGCGGAGCTACGTTCT
GCTTTAGGATTATTGAATACCACTGGCTCTCAAGAATTGAAGGTCAAAGACCAGTTGAA
GTTTTCATGTGTTCCGTTGTTATGAGAAATGGTTATTTAGAGGCGTTCCAATGGTTATCT
CAATATATTTAA

YPL218W, 190 aa (SEQ ID NO 282)

MAGWDIFGWFRDVLASLGLWNKHGKLLFLGLDNAGKTTLLHMLKNDRLATLQPTWHPTSE
ELAIGNIKFTTFDLGGHIQARRLWKDYFPEVNGIVFLVDAADPERFDEARVELDALFNIA
ELKDVFPFVILGNKIDAPNAVSEAELRSALGLLNTTGSQRIEGRPVEVFMCSSVMRNGYL
EAFQWLSQYI

YPR102C, 1025 bp, CDS: 501-1025 (SEQ ID NO 283)

TTCTTTACAATTCACCTTGCATTATTGAAGGAGTGCTATTCTTCGTTTTGCCACCCTTTT
GCTGTTTTCCCTCATATCACATAATACCCGGAGAGGCTCTTTCCTGCGACAGCGCAACAT
CCAACCATCTAAAGGTATGGGTGTAAGTACGATGCGATTATTTTATTAAAGTTCTGTCTT
TTTTGTATATAAGAAAAAGAACGGTGAAATCCATAGAAATACAGAGAGCGACGCAACA
GCGCGCAGACTCTACGGGTAATAGACTCACATCCACGTGACCAGTTTCCAATCGAACTTT
TTCACCTTTCAGGGAATTATTGTTTCACTAGCAAAGGTAGCCCACTTACCACTCAGCTAT
GCGAAAGTTTCATTGTTTGATACATCTTGATAGTAACCGCAGGCTTCTTTCTTAGTTTAT
ATTTTATTGTATTTCAACTAATATTATTTTTTTTTTTCAGTGAAGGGAAGGTGAACCAAGA
ACATACAAACATAGCCAAAGATGTCTGCCAAAGCTCAAAACCCTATGCGTGATTTGAAGA
TCGAAAAGTTGGTCTTAAACATTTCTGTTGGTGAATCTGGTGACAGATTGACCAGAGCCT
CCAAGGTTTTAGAGCAATTATCTGGTCAAACCTCCAGTTCAATCCAAGGCCAGATACACTG
TCAGAACTTTCCGTATCAGAAGAAACGAAAAAATTGCTGTTACGTTACCGTCAGAGGTC
CAAAGGCTGAAGAAATTTTGAAAGAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACA
GAAACTTCTCTGCTACCGGTAACCTTCGGTTTTCGGTATTGACGAACACATTGACTTGGGTA
TCAAGTATGACCCATCCATCGGTATTTTTCGGTATGGATTTCTATGTCGTCATGAACAGAC
CAGGTGCTAGAGTCACTAGAAGAAAGAGATGTAAGGGTACCGTTGGTAACTCCCAACAAGA
CAACTAAGGAAGACACCGTCTCTTGGTTCAAGCAAAGTACGATGCTGATGTTTTGGACA
AATAA

YPR102C, 174 aa (SEQ ID NO 284)

MSAKAQNPMRDLKIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIR
RNEKIAVHVTVRGPKAEILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSI
GIFGMDFYVVMNRPGARVTRRKCKGTGVSNSHKTTKEDTVSWFKQKYDADVLDK

YBL003C, 899 bp, CDS: 501-899 (SEQ ID NO 457)

TATATGACGGCAAGTGTCTCACTGTTGCATTACGCGATGTTTCTTTTCTTTGTTCTTGTAAAG
CGCGATTTTACCAGAACTAGATGGCGCTCGTGATCCTGAAAACGGGGAGAAATTTTGAGAAC
ACCGCTTTTATTAGGCGAAGCGGTGGGCACAGCTCACGCGTAAGGTGTTCCATTATTTCTCA
AAGTGATGCGAATTTTCAGAGAACACATTAACCTGGGGGCCATAAACGCGACGTGCTACCATT
TTCGTTACGTATACTTAGGCCAGAGATTACAACATGACTACTAATATCAAACATAACTCTAT
ATATAAGGGATGAAGATGTATGCTTTCTTAGAATTTCAAACATGTTCCGTTAAAGTTTTTACT
TTTCGATTTCAATTTGACTGCATGATGCTTTTCTTAGGTAGTTTTTTGTTATTAAATAGTA
TCATAAATTTCTTGTCTTTTACATAAGAATTAGGAAAGTACAGAACAAGAGCAAATTTAATA
TATAATGTCCGGTGGTAAAGGTGGTAAAGCTGGTTTCAGCTGCTAAAGCTTCTCAATCTAGAT
CTGCTAAAGCTGGTTTAAACATTCCCGATTGGTAGAGTGCACAGATTGCTAAGAAGAGGTAAC
TACGCCCAGAGAAATTGGTTCTGGTGCTCCAGTCTATCTAACTGCTGTCTTAGAATATTTGGC
TGCTGAAATTTTAGAATTGGCTGGTAATGCTGCTAGAGATAACAAAAAACAGAATTATTC
CAAGACATTTACAATTGGCCATCAGAAATGATGATGAATTGAACAAGCTATTGGGTAATGTT
ACCATCGCCCAAGGTGGTGTTTTGCCAAACATTCACCAAACTTGTGCCAAAGAAGTCTGC
CAAGACTGCCAAAGCTTCTCAAGAACTGTAA

YBL003C, 132 aa (SEQ ID NO 458)

MSGGKGGKAGSAAKASQSRSAKAGLTFPVGRVHRLRRGNYAQRIGSGAPVYLTAVLEYLAA
EILELAGNAARDNKKTRII PRHLQLAIRNDELNKL LGNVTIAQGGVLPNIHQNL LPKKSAK
TAKASQEL

YDR442W, 893 bp, CDS: 501-893 (SEQ ID NO 459)

TGAACGGGTGCAAAATTTACTTTAACACCCAAAAAGTATATGCGTATATATATATATTTATC
CTTGTTATTTTTGTAAATTGAGCTATGCAACATAAGATTCTCGCATGTAAGAATACTTGC
TAATCAAGAGAACTTCAACAATTTTCCATCGCAGAGACGAAAAAACTGAAAAAAATAAAAA
GAAAAAATTGAAAAAGAAATCGCGACTTCCGATTACATAACCTTATACGGAGTATGATACCAT
TCTTGACATCATCAACACACCATCGCAGACCCACGTGGCCGCTTCGTGTGCCTTGAAAAATAC
AGCCTTAAACGCAATCTCAATTCGCGTTCTGTGGAAATGTCTCGGACTACACGCTGGGCGTG
CATCACAGTGAAAAATGCCGTACCGCCCCGCTTCCGGTTTTGTTTTTATAAATCCGACTGGA
GAAATAGACTTCTGGGTTTACACCCCGGAATAATACTAAAACCAAACTGGTAAATAGGGCT
ACAGATGAGCAGGAAAACGTTGCCGGAAGTTATTTATCCGAGAGAATAATTGATGAAG
AAGTAGCGGTATGCACAGTAGCGGCGGAAGTATTAGCAATTTTACTCTGGTGTGCACAAGA
GTGTTCACTCATTTTTTTCACGGCTAGGATATGCCATGGAATATGGCCATCTTCGCCATCAGA
GAGACCGTACCACACGTTTAGAGCAGCCAGGTTGCGAACTCTTCTAAGATGGTTTTCCAGCA
ATTGTGTACTATCAGAATGTGGACAGTTTAAAAGGTTGACTGCGAATTTGTCCCAAACCGTA
TCACCGTCGCATTTTTTGAATTTGATCAAAGCACCACCTCTAATAGCACAGCGATGCTGTGA
GTGTGCCAGTGGGAACGGGTGCTGA

YDR442W, 130 aa (SEQ ID NO 460)

MSRKTLPKVVYLSERIIDEVAVCTVAAEVLAIFTLVCTR VFIIFFTARICHGIWPSSPSE
PYHTFRAARLRNSSKMVSSNVLSECGQFKRLTANLSQTVSPSHFLNLIAKPLLIAQRCEC
ASNGC

YDR529C, 884 bp, CDS: 501-884 (SEQ ID NO 461)

GAGTCTCCGGAGTTGACCAAGTCATACAATGTGCTACTGACCAAGAAATGGATCTGTGTAGT
TCCAAGATCGCATGCCAAGAGTGGACCGCCATTGATGTTAAACATTAACTCCACGGGGTACT
GTGGTATGATCCTCGTTAAAGACAGAGAAAACTAGAGAACCTCACTGAAGATCCTCATCTT
GTGGACAAGTCGTTACTGCAATGCGGTTTCCCCAACACAGCAGGCCAAAAACCAACAGAGTA
TCACTATTAAGGTCTATTAGCCATATGTACATTGTCTATAGATGTGTAACCTGCGCTGTGATC
TTGTTTTGACCAATCAGGAGCGACGCTTTTTATCGGGTCAACCCGGCGGGGGGCTGACA
ATTTACTTTTCATAGAGCAGTAATAAAAGGGAAGAGATGTAAGCTTGAAAAATAGCAGTA
AAGGTTGTTGTTGGACAAATTTATCAGAATATTAGTAACTGTAATTAAACGTTCCAGAAAGAA
CAAAATGCCACAGTCTTTTACGTCTATTGCGAGAATTGGTGACTATATTTTGAAGTCAACCG
TCCTCTCCAAGTTATGTGTTCCAGTTGCCAATCAGTTCATTAACCTCGCAGGTTACAAGAAG
TTAGGGCTCAAATTTGACGACTTAATTGACAGGAAAAATCCCATCATGCAGACCGCTTTAAG
AAGACTCCCTGAAGATGAATCTTATGCCAGAGCATATAGAATAATCAGGGCTCATCAAACCG
AGTTGACTCATCATTTACTGCCAAGAAACGAATGGATCAAAGCCCAAGAGGATGTTCTTAC

CTGTTGCCATACATATTAGAAGCTGAAGCTGCAGCTAAGGAGAAGGACGAGTTAGACAACAT
AGAGGTCTCCAAATGA

YDR529C, 127 aa (SEQ ID NO 462)

MPQSFTSIARIGDYILKSPVLSKLCVPVANQFINLAGYKKLGLKFDDLIAENPIMQTALRR
LPEDESYARAYRIIRAHQTELTHLLPRNEWIKAQEDVPYLLPYILEAEAAAKEKDELNDNIE
VSK

YGR085C, 1025 bp, CDS: 501-1025 (SEQ ID NO 463)

TCCTTACTTTAGTCTATTATCAATATCTCTTCCCTCCTAAATATGTACTCTTTTATTTTT
TTTAATTGTGAAGGAACAATTCAAGTTAGAACTCTTTTGATAGGAAACATTATTTCTGTGT
AGCCTAATGTTTAAATGCCAATTTTTTTCTAAATGCAGCAACATACATATGTTGAGTCGTA
TAGACATCTATATATAACAAGCACAGAACCGTCTAATTGGTATTTTTTCAGGACATTTTAAAC
ATCCGTACAACGAGAACCACATACATTACTTTTTTAAATATTCTTTTTGTTTTACCAGCCTTC
TTTTTATTTTTATCCGAAGATCTTTTGAACCCGCTCTGCGAATAGCGAAGCTAGGATACCA
AATTGAACTTGGACATAACTCATCTTAAAGAAGTATACTGTTAAGAGAGGCATTCAATTC
GTGTATTATAACGTTTAGCATCAGTTACCCCTTGAAAGCCCCAATATACAAAAATACGCGTC
CAAGATGTCTACTAAAGCCCAAAACCCTATGCGTGATTGAAGATCGAGAAATTGGTCTTGA
ACATCTCCGTTGGTGAATCTGGTGACAGATTAACCAGAGCCTCCAAGGTTTTAGAACAAATTA
TCTGGTCAAACCTCCAGTTCAATCCAAGGCCAGATACACTGTCAGAACTTTCGGTATCAGAAG
AAACGAAAAAATTGCTGTTACGTTACCGTCAGAGGTCCAAGGCTGAAGAAATTTTGGAAA
GAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACAGAACTTCTCTGCTACCGGTAACCTC
GGTTTCGGTATTGACGAACACATTGACTTGGGTATCAAGTATGACCCATCCATCGGTATTTT
CGGTATGGATTTCTATGTCGTCATGAACAGACAGGTGCTAGAGTCACTAGAGAAAGAGAT
GTAAGGGTACTGTTGGTAACCTCCACAAGACAATAAGGAAGACACCGTCTCTTGGTTCAAG
CAAAAGTACGACGCTGATGTGCTCGATAAATAA

YGR085C, 174 aa (SEQ ID NO 464)

MSTKAQNPMRDLKIEKLVLNLSVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIRRN
EKIAVHVTVRGPKAEIILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSIGIFG
MDFYVVMNRPGARVTRRKRCGTGVNSHKTTKEDTVSWFKQKYDADVLDK

YGR106C, 1298 bp, CDS: 501-1298 (SEQ ID NO 465)

GCAACATTACCACTTTGTACGGAGCGTCAGAAAGAACGCACCTCATCTATTATGAGAACA
GTACGATAACTTCTGTCGAGATACGCTTCCTGTTTATAATACAAGTGAAACCGCCACGGAT
AATTAGCAGCAATTGAACACAAGGGATATCATTTGTGTGACCTTTGTTCTCTCATAGTTGC
TGTGAACCTTTTAGTAACATTAATGTTTATTTTCATGAGACTAGTCAAAACATTCAATAACA
GTTTTTCTATATGAGAAAAAAGCAACAGTACGATTATT
ACACTGACTATGCTGCAGTTCCGCAATAGCAAAATGTGTACATTACACGAAAGAAAGAA
AGAACGCTATTTCTTATAAGAGCAAACTGTGTGATAAGTTTATAGCAAGAATAAAAAGGGTAA
AAAGTCATTGATAATAACCACTGCTGTGACTATATATAATAAGAATCGAACTGTAAAGTTAA
AGCAATGGTGTTCGGTCAGCTGTATGCCCTTTTCATCTTCACGTTATCATGTTGTTATTTCCA
AACTGTGCAAGCAGATTTCATCCAAGGAAAGCTCTTCTTTATTTTCGTTTCGACAAAGAGAGT
AACTGGGATACCATCAGCACTATATCTTCAACGGCAGATGTTATATCATCCGTTGACAGTGC
TATCGCTGTTTTTGAATTTGACAAATTTCTCATTTATGGACAACCTTGATGATTGACGAAGAAT
ACCCATTCTTCAATAGATTCTTTGCCAATGATGTCAGTTTAACTGTTTCATGACGATTTCGCCT
TTGAACATCTCTCAATCATTATCTCCCATTTATGGAACAATTTACTGTGGATGAATTACCTGA
AAGTGCCTCTGACTTACTATATGAATACTCCTTAGATGATAAAAGCATCGTTTTGTTCAAGT
TTACCTCGGATGCCTACGATTTGAAAAAATTAGATGAATTTATTGATTCTTGCTTATCGTTT
TTGGAAGATAAATCTGGCGACAATTTGACTGTGGTTATTAACCTCTCTGGTTGGGCTTTTGA
AGATGAAGATGGTGACGATGAATATGCAACAGAGACTTTGAGCCATCATGATAACAACA
AGGGTAAAGAAGGCGACGATGATATTTAAGCTCCATCTGGACTGAAGGACTACTAATGTGT
TTAATAGTTTCTGCGTTGCTATTGTTTCAATTTTGATTGTTGCACTTCTTGGATATCTAATTT
GGATATCACATATGGTGCGTTGGAAAAATCAACAACCCAATAAAAAAACAATTAA

YGR106C, 265 aa (SEQ ID NO 466)

MVFGQLYALFIFTLSCCISKTVQADSSKESSSFISFDKESNWDITISTISSTADVISSVDSAI
AVFEFDNFSLLDNLMIDEEYPPFNRFANDVSLTVHDDSPNLISQSLSPIMEQFTVDELPEP
ASDLLLEYSLDDKSIVLKFKTSDAYDLKKLDEFIDSCLSFLEDKSGDNLTVVINSLGWAFED

EDGDDEYATEETLSHHDNNKGKEGDDDDILSSIWTEGLLMCLIVSALLLFILIVALSWISNLD
ITYGALEKSTNPIKKN

YGR182C, 854 bp, CDS: 501-854 (SEQ ID NO 467)

CCAAGTATCATGGGCTTTGGAAATTAGTTTCCACCGATGAGCGCAACGACTTAGCGAAGCT
TATGAAATTGGTGACAGCAGCTCTATGAATATGTTCCATGCGTTTCCATTACAGGTACTAAC
AATGCATAAAATTATGAGTAGTCTTTTTTCATCACTATATAAAACCTTTTTCAAACGAAACGCT
GTTTTTGTGGTACTATCTTTGCAGGTGCCTTTGTTTTCCAACTGTATTTGATACTGCTAT
TACTTTCATGGTACGAGAATCACAACAAAGGAAAATTATGGAAAGATGTCAAGGCTCGAATAG
CTGCAGGCGATGGAGACGACGATGATGAGTAAACGCTGATTATGTCACACATATACGTGCAA
ACGCTCTCTCTCTCTCAAGCTATATAAGTGGCACTCGTCTTATTTATTATTTTTTTTATTT
TGGCTGGTTGTTTCATGTTCAACCCAACTCATAAAGGCACTCAACTTCATATTTTGACACAA
ATCTATGTCTCGCCAAAGCGCATTCAAATTTTCAAGTGGAAATAGACACGAACGAGCCTGTC
TGTCAGATGTTTCAAAAATCCTTATTATAATTTTATATTCTACTAAAGGAAAAAGAGAATTA
GGAAAAAGAAATAACTCATTTTATGTATATACATATATTTTGTACATATCTATACCAAGCAAG
TATAGTCAATACTGTTCTTCGACGTTATTAACGTAATAGCATTCTTGGTATCCTTTGA
ATCTTATATACAAGTACGAGTACATACTGCGCAGTAAATTGATCCTGATGGTGTGTTTAGAT
TTCGCCAGAAGCGGAGGCGTTCTGGATTCTGGAGATGTAAGCCTTTGA

YGR182C, 117 aa (SEQ ID NO 468)

MSRQSAFKFQGNRHERACLSDVHKILIIILYSTKGKRELGKRITHFMYIHIFCTYLYQASI
VQYCSSTLLNVIAFSWYPLNLIYKEYILRSKLILMVCLDFARSGGVLDSDGVSL

YGR183C, 914 bp, exon1: 501-503, intron1: 504-716, exon2: 717-
914 (SEQ ID NO 469)

AAATACAAATCCAAGAAACCTCGATGAGGATGACTCTGATGATAATGATGACTCTGATGAGC
GAGAGATTTGGTAGATTCAAGCCCTCTACTATGTTTTATAGTTGACATATTTGTATATAAAA
ACTTATACATTATTAAACATTTGCGCGTCGATTGACTTTTTATTATTATTAACAAAGAAGTA
ATACCAACCTAATTACAAATACTTCGAAGTGACTATCATAAGTTTCCTTATCTAGCGAAGGC
AATTTTTGAACCTCCCAAGTTGTTAATATGTATCATTATACACGACCAATCAAACGCGGGGA
AGTCAATGCCGAAAGAAATCTAGGACCTAAAAGCTGCTCAATCCTTGGGCTTTCCCTAATG
ACATCCCCCTCTCAAACCTTAGCTTAGCAGTTGTATTTAATGTCTGTACGGATAGTCAATA
ATCGTTGAAGTTGATTTTCATATCCTTCGCAATTTTCGTAAAGCAACAATAGCAATACGGAC
TAAATGGTATGTTGGTGTGTGTGTGTGCTGCTTCACATTTACAGGCTAAAAATGTTATCCGT
GGAATCTTCCCTAGCCAAGTATCATGGGCTTTGGAAATTAGTTTCCACCGATGAGCGCAAC
GACTTAGCGAAGCTTATGAAATTGGTGACAGCAGCTCTATGAATATGTTCCATGCGTTTCCA
TTCAGGTTACTAACAATGCATAAATTATGAGTAGTCTTTTTTCATCACTATATAAAACCTTTT
TCAAACGAAACGCTGTTTTGTTGGTACTATCTTTCAGGTGCCTTTGTTTTCCAACTGTA
TTTGATACTGCTATTACTTCATGGTACGAGAATCACAACAAAGGAAAATTATGGAAAGATGT
CAAGGCTCGAATAGCTGCAGGCGATGGAGACGACGATGATGAGTAA

YGR183C, 66 aa (SEQ ID NO 470)

MSFSSLYKTFKRNAVFVGTIFAGAFVFQTVFDTAITSWYENHNKGKLWKDVKARIAAGDGD
DDDE

YKR040C, 1004 bp, CDS: 501-1004 (SEQ ID NO 471)

GGGCTTTTCCAGTGCCGCGGCTCGAGATCCAGGCACCAGGAAGTGGCACGCTGTGTATTC
TAACACATTGAAGGGCCTAGGCCCGCTGACGTGGGGTCTAGTTCCACTTTTTTCATTACCTTT
TCTCGGTCTTTCTTGCTCCACAGGCCGTTAATGGCCTGAAACAGTTTTGTGACTTTGGAC
TTATGATAACGATGTTTGCCGGGTGCCACCGGATTCTATCGCGGCGAATCAAGTCTAGTCT
GTTTGCATCCATCAAGGCACTGCTCATTGTGTAAAAATTGTTCTACGCTTTTGTCAATCA
TATCTAAACTCACAGCCGCTAGGGTAGGTGCTGTCAGTGTAAGGTAGCCGGCTCGTCT
TTGGTCATGCGCCAATACTGTGCAACGCGCCGCGTAGCGTTCTTCGGCTTCAACCTTAGA
GCTGATACCTTTTGCTGGTCAAAGGCGAAAACGTCTACCTCGCTTTCACTGCTGCTTTTCGC
TTTCATGACTTCGTTTCAAGCGGTCTCTTTTCGCTCTCGGTTGTAACACACTTGTAGCCTGCT
ATGCTTTACCCGTACTCGAAAAGCGTAGCCTCATGACTAGTTGTACCAACGCCCTTTCTTTT
CTTTTTTTTCTCTTGACACTTCGGCGTATTCATCGCCACTGGTACAAGCCGTATGGTGGCTTT
TTTGCTCATTTTCGTTTTCGCTTTCGATGGTTTCGCGGACCAATCGCATGGGTGGTGGTGG
ATGTTGCTCTTTGCTAGTTGCAACGTAGTCTTCTCTCTCTGCGCTTTCTGACGAAAATTGG
CCTTACGTATCTTTTTTCGGCGTCGTTGTGCTCATCGCTGTTTCATATAATCGTCGCTCACTCA

TATCGGCGCTTTTACTGCGTGTCTTTTGAAGAGAGTTTCATTGAAAAGTAGTGAAGAAA
AAAAAAAAAAAAAAAAAAAAAAAAAGGAAAAAGCTTACATACGGAAGAGAAAAAAAAAA
AAGAAATTTTAA

YKR040C, 167 aa (SEQ ID NO 472)

MTSFQAVSFALGCNTLVACYAFTVLEKRSLMTSCTNALSFLFLLTLRRIHRHWKPYGAFL
LIFVLTLRWFRGPiAWVVVDVVFASCNVVFSPALSDENWPYVVSFFGVVVVIAVHIIIVTHI
GAFTACCLLRVSLKSSEEKKKKKKKKKEKSLHTEREKKKKKF

YOL127W, 1343 bp, exon1: 501-513, intron1: 514-927, exon2:
928-1343 (SEQ ID NO 473)

TCTTATCTTGTATGCCGATATAGCAACCTTGTTGGTACCAATCTAACGGTTTCCGTACTTT
GCAATGAAGAGATGAGGAGGCATGGGTCACTTATTTAATATGTACGGGTGTTTACATGGAGT
TGCTTTCTTTTTTGTCTCAGCAGTCATTGTGCGCCAAAAAAGAGAAAAACCGTGAGCCGAA
GTCCACGCTCTGGAGTTAGGCTCTCCCATACGGAGAGAAGCATTTCTCAGCCTGGGAGCC
CCGTTGGAACAGTCAGGCTAAACTGGGCCTTCTACCCACTGCTTGCTGTTTCTCACTGGAC
GCACAAGGGGATTTTCTTTCTACCTTCGGCTTGCCTCACTGCGTTGGGGCTTCCCAATGCAA
CTTCGTTCTGATGCATACAACTCTTTAGATATTATCTTTTAAATATTATTTTAAACAATTTT
AAATGTATCTCATATGCTTTTCTTCTGCTGTTGAAAAGGCTAAACAAAGAAGATCAATAAGA
TAAAAATGGCTCCATCTGGTATGTGAAGTCAATATTAATAGCACGAGAAAAATTGAGAGGAAG
ATAGATGGGAACTAGTAGAGTTGATATTGATGAGATACGAAAACACACGTAAATAAACTAT
CCGACGACAAGAATAGTGCATTAAAGACTTGATTAAGATATGGTGAGCAACGTAATTATCGG
GCTCAACAGTTTATTAGCAATCGTTTGTATAGAAGCGTTGATGCTGTGGAAGTTGTTCTTTT
TACTACCAACAGCCATTAACAAATCCATTAGAGTGTTTCGTTTCGTTTTTCTGCTCAGATTCAA
GAAAATTATTCCATCCTCATTATACTTTTTTCTTCTATTTTCGTGCTCCACGTCGAGGTATCA
AGGAACATAGTTTACTAACAATTAAACGAATTCATCTCCTATGAATTTACTTTTTGTATAGCTA
AGGCTACTGCCGCTAAGAAAGCTGTCGTTAAGGGTACTAATGGTAAGAAGGCTTTGAAGGTC
AGAACTTCTGCTACCTTCAGACTACCAAAGACCTTGAAGTTGGCTAGAGCTCCAAAATATGC
TTCCAAGGCTGTTCACATTACAACAGATTGGACTCATACAAGGTCATTGAGCAACCAATCA
CTTCTGAAACCGCTATGAAGAAGGTTGAAGATGGTAACATTTTGGTTTTCCAAGTTTCCATG
AAAGCTAACAAATACCAAATCAAGAAGGCCGTCGAAGGAATTATACGAAGTTGACGTATTGAA
GGTTAACACTTTGGTTAGACCAAACGGTACCAAGAAGGCTTACGTTAGATTGACTGCTGACT
ACGATGCTTTGGACATTGCTAACAGAATCGGTTACATTTAA

YOL127W, 142 aa (SEQ ID NO 474)

MAPSAKATAAKKAVVKGTTNGKKALKVRTSATFRLPKTLKLARAPKYASKAVPHYNRLDSYKV
IEQPITSETAMKKVEDGNILVFQVSMKANKYQIKKAVKELYEVDVLKVNTLVRPNGTKKAYV
RLTADYDALDIANRIGYI

FIG. 2:

YBL051C_homolog_1 1229bp PathoSeq: 1..1229; CDS: <1..>1229 (SEQ ID NO 285)

AGAGAACGTATTGAAGAGGAGAAAAAGGGAGAAAAGAGGTCAATTGGAAGAACAACATCGTTCTGCA
TCAAATGCTTCTATGGCTTCTTTATTGTCTAGCTGCTTCAACTACAGCAGCAACTAAAAATTTGAGT
GTGGCTGGCACAAATCCTTCTCATACCACTGAAAGAATGTTTTTAAATTTACCTTTTAAACAATTCC
CTGTTCAATGCCCCACCAGTAGAAATTAATTTTAATGATCTTGAAGTTTTGGAATTGTACACTCAA
TTAGTATTATACCGAGATGATATTACCAAATCTACTTTTGAATTAGCTATATCACCAGCAAATTTG
AATATTTCTCAACGGAAAAATCATATCAATTTTATGTAATTATTTGAATTTATTAGAATTGTTTGAT
AATGGGTTGATAATAATTAGAAGAAAACCAGGATACATTGCTCAGTGTATAACTCAACAATCTATT
ATTCTTAATTCTCAACAGGTGTCTGGGCCAACTCACCCGCAACAACATCAACAGAATCAACTTCAA
CAACAGCAACAGCAACAACATCAACATCAACATCCTTACATTCATCGATGATGAACCTTCAT
CAATTGGGTGGTACATTAGCTGTTCCAGCGCACCTTGAATTATTAAGATCCCAATCGCAATCAGCA
TTACCGTTGCCAAGATTGAGACAGCAAACCTCTACACCAATTCAACAAAATCAACAAGTTCAGCAC
CAAAATCAACCACCACAACAACAGCAACAGCATGTTCAACCACAATATAATTATTACAATCAG
CAATCTATTCAAAGCCAACCACATTCTGCGAGACCTTATTCTCAATCATATAATATTTATCAACAA
CAACAGCAACAGCAGCAACAACAAGCTCAACAACAAGCTCAACAACAACAACAACAACAATTACAA
TATCAACAGGGACACCAGTCACAAGTTTCAACACCTACATTGAATTTCTTAGTGCTGCTGCATTA
CTTAGATCAAGTAGCAGTAGATCATTTGTTGATGTGAGATCCACACCTCCCAAGTAGTTTTGCT
CAACAGCAACAACAACAACAACAACAGCAACAGCCGCCACTAATTTCATCAATCCATGATTCT
CCAACACCACATCATATTTACCCTTCAACAGCAGCCACCACAACCAATCATTACCTATCCAAT
TACCATCAGGGGTTGGATCTCAACCAAAAACCTCCATTGGC

YBL051C_homolog_1 409aa (SEQ ID NO 286)

RERIEEKREKRGQLEEQRHSASNASMASLLSAASTTAATKNLSVAGTNPSHTTERMFLNLPFNNS
SFNAPPVEINFNDLEVLTYQLVLYRDDITKSTFELAI SPANLNISQRKIIISILCNYLNLELFD
NGLIIIRKPGYIAQCITQQSIIPNSQQVSGPHTPQQHQQNQLQQQQQQQHQQHPSHSSSMMNLH
QLGGTLAVPAHPELLRSQSQSALPLRLRQQTSTPIQQNQVOHQNQPPQQQQQQHVQPOYNYNQ
QSIQSQPHSARPYSQSYNIYQQQQQQQQQQQAQQQAQQQQQQQLQYQQGHQSQVSTPTLNSSSAAAL
LRSSSSRSFVDVRSTPPTSSFAQQQQQQQQQQQPPLTSSIHDSPTPHHHLPLQQQPPQPNHYLSN
YHQGVGSQPKTPL

YBL051C_homolog_2 2153bp public: 1..2153; CDS: 501..2150 (SEQ ID NO 287)

ATAAACAAAAAGAAGCACGAACTGTGGGCAACAACAACAACAACAACAACAAAAAATTT
CTGGAAAATCAAAATGAACTCCAACCAGCAGCGCGCGCGACAGAAAAATATATTAACAGAAT
ACTTTTTTGTATTCAACTCTCTAACTCTTCTATTTTTTTTTTTTTCTATATACACTGTTAAATC
AATCAACAATAGCAGGATATCCATTATATACAAATAGATAAACTGTTTAATTAATTAATTAAGT
ATTTGATTTTGGGAAAAAACAATTTTATATTTGGAGAATTGAATTTCAATCATTTTAAACAATTCA
AAGCTTTAATTTCCACCTATCAAATTTTATTATTTTGTTTTTCATTATTTTTTTTTTCCCTTTC
TTTCTTTCTTTCTTTCTTTTGGAAACAAAGTAATAGCCGATAAAATAAATAATTCACATAGCCCA
ATTATATTACATTGACTTTTGGACAGAGGTATATATAATGGATTTTAGAAATTTATCAACTACAC
CGAATCAAATGGGCACTGTAATGCAACGTCGTCCTCTCTATCATCATTTATCGTCAGCCTCGGGCT
ATTCTTCTTCCAATTATGGTGGAAATCCTACACCCAATCCCAACAATCCAATACCAATAACAATA
GTAGTGGCAATAGTAATAACAACACTCATGGCAATAAACAATCCCAATTTATCAACTCAAAGATTGA
CAAATAATAGGAATTTACAATCCTTGTGGATAAACCAACCATCTATTGCTCCTTCTAATGTTGTTT
CTTGGGTGGAACAGCAACAACAACAACCCCTTGATCTGTTGGAAAATAATACTAAAACAGACTCCA
GTAATGATGCTTCTGCTACTAATAATAATGTTAATGTTAATGTTAATGCCAATGCCAATGTTA
ATGCCAATGCCAATATCCATGCCCCAACCCATGTCAACACAAATGTTAATGCAAAACACAACAGCAA
CTAGTATTAAATGCTTCCACGATTTTAAATACTACACCAAGTATTAATGACACTAATGATAATGCCA
AAAAATTAATGTTTCCATGATTAGTAATAACAATAACAATAACAGTAACAATAATAACAACAACA
CTAACAATAGTAGTACAGGAAGTTCTAACATTGCAACATGCTTCCTTCTGTTTCTAATGCAACGA
CAATGAATAACAGTAATAGTATCAATAGCACCACAAACAATACTACAATTAACGAAGCTGATGATG
ACGAGTTAATTCCTACTGCGATTGTGATTAAAAATATTCATTGTCATTAAAAAGGAACAATTGT
TAGATGTGATGACAAAATTAACCTTGCCATTACCATATGCCTTTAATTATCATTTTGATAATGGTG

MDFRNLSTTPNQMGTVMQRRPSLSSLSASGYSSSNYGGNPTPNPNNSENTNNSSSGNSNNNTHGNN
TPKLSTQRLTNNRNQLSLWINQPSIAPSNNVVPWVEQQQQQTLDSENNTKTDDSSNDASATNNNNVN
VNVNANANVNANANIAHQTHVNTNVNANTTASINASTILNTTPSINDTNDNAKKINVSMISNNNN
NNNNNNNNNNNNSSSGSSNIANMLPSVNNATTNNNSNNINSTNNNTINEADDDDELIPTAIVIKNI
PFAIKKEQLLDVMTKLNPLPYAFNYHFDNGVFRGLAFANFTSTDETSAVVNQLNGREIGGRKLVR
EYKMLPAQERERIEREKREKRGQLEEQRHSASNASLASLLSAASTTAATKNLSVAGTNPSHTTER
MFLNLPFNNSSFNAPPVEINFNDLEVLLEYTLQLVLYRDDITKSTFELAISSIFEFYSTENHINLC
NYLNLELFDNGLLIRKKPGSIAQCITQKSIIPNSQVSGPTHPHHHQKNQLHQQQQQHTSTSTS
LTLFIIDDESSIGWYISCSSAP

ATAAAAAAAAAGAAATACAATTAAAAAAATTTTCTTCTGTGAAAAGGCAATTTTCGGGTCTAGTAGTA
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CAGTTTCTTTTCTTTTATATATTTTTTCTTACTTTTCTTCTTCTTCTTCTTCTCTCTCTGACAGTATATTAATA
AATATTTCTTTTAACTTATTTTTTCAATCAAGAAGGTACTGAAGATATCAATTAACCTCTCAGTTAAA
TCCATATTACCAGTTGTGGAATAATCAGAAGAAAAAAGAGAGAAAAATCACGGGAATTAC
GTTCTCAACAGAAAATAACAATAATTTTTTTTTTATTCATTCCAAGGTATAACAAGAACGTTAGGAA
TAATATAAAATTATCACCAGCTGCCATCAACGTGTGTCGACAACCAATCGACTCCTCCCTTAAC
TAGAACCATAGAACCTCAACATTTGTTTCTATAGAAAAATGAAGTTTGAAAAAGGTAAAGTGAGAA
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AACACAATTTGAACCAAGCTTTTCGCAACGACCAACAAGTGTCTGGATTGCAATCTCAACAACAACATC
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CATCCTTAATTAACAATTAGCAATTGAAACATGTTGGATTAAACACCAAGATCAACTCATGTTA
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ATTTGAACATGGTGTGTATATAATTATCCTGAAATATTTTAAATGATCTGGAAAATGAGGATTCAA
GTATTATCACCAGAATGAGGTCACATTTGACAGCATCTTTATTCTATGATTTGGTTTGGTGTGTAC
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TGCCCTTGCCATTTTACAACCAAATCACTAAGGATGATTTCAAGACAATTACCACGACATCACCTA
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AGTTTCAACAATCACCACCACCGCAATTTTCAATGATTTCTTCAACGCCGCCCTTCAGCAACCAC
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CACCAGAAGTAAACAAGAAAACCTCTGTTGCTTCCATTTGCATCTCAAATCACCACCTTTTTTGATC
AACAAACAAGTGGATGGTTTAATAATGATAACCAAGATGACGACTTTTTGGGTTGGTTTGATGTTA
ATATGATGCAAGAGAAATAA

YBL066C_homolog 917aa (SEQ ID NO 290)

MKFEKGKVRILPKPSPTPTNPQTPLPLPAQTKPVNSKRKSAASTPGNESKSRKSNSTASTPNSA
TPTSVGTPPPQKTSKPTGHRPVTSCTFCRQHKIKCNASDNYPNPCERCKMGLKCEIDPEFRPRKGS
QIQSLKSDVDELKAKIEMLTKNESLLTQALNQHNLNHASQQQQSSGSQSQQQHPPNPQRALSYS
NNSPPQVAFSNASPIPSVTSIQQNAPLTHENSNDSPYALNTPENIEELQPISEFILGDVTLPLNRAN
ELHDKFMTTHLPFLPIIISRSATELYHKSQLLFWAVILTASLSEPEPKLYMSLASLIKQLAIETCW
IKTPRSTHVIQALIILSIWPLPNEKVLDDCSYRFVGLAKNLSLQGLHRGGEFIEFSRNQVSLGP
DAERWRTRSWLAVFFCEQFWSSLLGLPPSINTTDYLLNARVDKSLPKNFRCLISLSIFQCKLVNI
MGISVTRPDGELLEPSNRAGSLSLDRELERLRFKLQFEEGGPIEVVYLYIKLMICCF AFLPGTPIE
DQVKYVSFAYL SATRIVTIVSKMVNDISLIELPIYIRQAVTYSVFMFLKHLHSRYLIDKYVDSARQ
SIVTVHRLFRNTLSSWKDLQNDISRTAKVLENLNMVLYNYPEIFLNDSENESSIIITMRSHLTAS
LFYDLVWCVHEARRRSVLDKGKRAQPNKKILPLPFYNQITKDDFKTITTTSPNGTTITTLVPTDQ
AMNQAKSKSFDSKPLEINGIPLPMLEATGSTREVLDSLPSQLPSQAPTLQQYPMQDDQQQEPS
QQQQQKHSQQSQYQQQQQSNQQQPHLQHQRFQSQSPPPQFSMISSTPPLQQPPFILANSPLPQTY
LPKIDEMNMSPEVKQENS VAPFASQITNFDQQTSGWFNNDNQDDDFLGWFDVNMMEK

YBL078C_homolog 908bp public: 1..908; exon 1: 417..449, intron 1:
450..533, exon 2: 534..908 (SEQ ID NO 291)

TTATTATTACTATGACACACACTTACTCTCTTCTATGTCTCCGCTTACATCACACATCATACGTTT
GAAAACACCCACCCCTTTTCTTATCTACAAAAAATAACAACTCACTATACTACTAAAC
CTTTTTTTTTTATTTATTTATTTTGTATTTTGTATATTAATCAAATATTATCATTCATCTATATA
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TATTATTACCAAGGTCTCAATGATTAGTGTGGCTAGCGTCTGTTACTACTTACCCCGTGTGTGTAG
ATAATTGCCACTCAATCTTTAATTGACCATCGACCACAAAATAATATGGAAATAATACTAACAGA
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TGATTTTTTAGTCTCTGAATCTTCTTCCGATCATATATACTAACATTTTCGTGGGTGTATTCTT
TAATAGAAAAGAGACAAGCCGAGGCAGCCAGAAATTGCTCAGAGGTTCAAGGATAGAGTACCAGTCA
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TTTTCATCTTTGTCAATGACATATTACCCCAACCGCTGCATTAATCAGTACAATCTACGAAGAAC
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CAATTGACATTTTCATCATTAGATTTTCAGTGATATCCCTGATTATGTTTAA

YBL078C_homolog 135aa (SEQ ID NO 292)

MRSQFKDEHPFEKRQAEAARIAQRFKDRVPVICKVENSIDIPEIDKRKYLVPVDLTVGQFVYVIRK
RIKLPSEKAIFIFVNDILPPTAALISTIEEHKDEDGFLYVLYSGENTFGEKLAIDISSLDFSDIP
DYV

YBR073W_homolog 2891bp PathoSeq: 1..2891; CDS: 501..2888 (SEQ ID NO 293)

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TGTTTGCCTTATTGGTTGCCATATGGGATCTACGCTTATTGCTTCAAGTATCATGTTTGCATCT
CCAGAGCATACTATTATGTTTTTGGCATGGATATTAGTACCATCAACGGTTATGCAAAGTAGCGCT
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GCTCGACTAAAAAAGAATTTTGTCAAACGCGTATCAGAAATGTTTACCCTTTTTTTTTTACCACAG
ATCAAATGAATGTTTCGACCTAATGCTCCGTTTCCGCTCCTAGACCAATAAAGGGGGGTGTTGCGG
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CTACCGATCCCAGCTCAACAAAATACGTGATCCAATGGAGAAAGAACTTCAAAGAAGAACAAAA
CATGGGACGGTATGGGTATGCCGTGATTAAACAGCTTGAGAAATGGGGCATGCGAGATATCTATCA
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ATGACGACTGTGCCGATGCCATCGCGTTGCCCTCCTCCTCCAAAAGCCAAAGATTATGTCAAAGTAA
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TTTCGAGATTAGATGGGTGACCCCCAACAAATGTGCGTAGCAAGTTGGTTAATCAGTTTAAACACGA
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CTTCGAGGTTGATTTTGTGTTGACAATGACTGGAACCCAGCGACCGATTGCAATCGATGTCGCGAA
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TTGACGATGGTGGGCGCTAAAGAGGACGGCTGTAAATTTGCTTGAACGATTATCGACACTACA
ATCCAGAGGTGAACCGTAATTTGGATTTTGAATCTGCGCTACACCGAATTGCTAACAATTCAAGCT
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YBR073W_homolog 796aa (SEQ ID NO 294)

MFTLFFFTTDQMNVRPNAPFRPPRIKGGVAVVQKVVRKLPPTTNPKPAILTTDPGSTKYVIQW
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VGSNSTPQTVTRVTHQFKKVAPPTASSRKPLYDDCADAIALPPPPKAKDYVKVNIDPHLAKVLRPH

QVEGVKFMYECLMGYRGFGGHGCLLADEMGLGKTLMTITTTIWTLKQNPFMKEGAVVNKVLVVCV
TLISNWRQEFRKWLKANKLVNLTNNPMSNEKQDILNFGKLVYQVLVVNYEKLVAHFDELSAVKF
DLLVCDEGHRLKNSANKVLNLIKLNIPKKIVLTGTPIQNELVEFHTLISFLNPGVLPKLFQRN
FITPISRARDINCFDPEVKKRGEEISQQLIELTQSFILRRQAILANYLTQKTDILLFVPPTSLQL
KLFDYITNLKFFNQFEAFTMINLFKKICNSPSSLADDELFPKIVEEKFNLMASGKINILVPLLE
IASLGEKIVLISNYTKTLDLLEQVLKVSLEFSLDGSFPNNVRSKLVNQFNTNPDINVFLSSKS
GGMGINLVGASRLILFDNDWNPATDLQSMSRIHRDQGLKPCFIYRLFTTGCIIDEKIFQRQLVKNKL
SSKFLDNDATSKSDVFDNDLKNIFEIDTSTISNTHDLECVCEGDGSMLSOPTIEESEPPPKQAW
VTALELKKKIDDEALKRTAVKFALNDYRHYNPEVNRNLDFFDSALHRIANNSSYENKQLPITFIMS
RVTN

YBR086C_homolog 2643bp PathoSeq: 1..2643; CDS: 501..>2643 (SEQ ID NO 295)

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TTGTTTGAATAATTTATTACTTATTCAATATATTTTTTTCTTCTTCCCTTCTTCAACTTCTTC
TTTATACATTTCAATCAACCTTCCAACAATCCTATAATTACTTACTTACCTTCTTCAATTGGATTA
ATTGGATTTGAATTGTTACAATTGAATCTTCAACGAGATGACTTTACCAATTCAGGATTTAGAAC
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AATCATTTGAAAACATTAATTGATTTATTATACGATAAAGGGTTTGCCGCCCAAATTAGACCTGGTG
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ATTTAATTAATAATTTATGAATTTGGTGTACGGGTAAAGATGACGTGTAGCTTCTAACTTAGAA
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ATTTAAAAATTAATGTTACTCAACCAAATTTATCAATTGCCACTATCAAAAAGACATATGGAGTTG
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CTGGTTATGTTCCATTAATCATCACTTCATTCATATATTTACCATTGCTCATTTGGTGCAACCTC
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AGTTTACCCCAATCAACTTTGAATTTCACTGGTCTTAAACCAACCGCAGAACTGATGATAAAG
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CTT

YBR086C_homolog 714aa (SEQ ID NO 296)

MTLP IQDLEPDYIISVNYPTDNGSPTPQAEKSLKTLIDLLYDKGFAAQIRPGDLHLVFKLSS
YKFSEEAEDLIKNYEFGVTGKDDVLASKLRIIYQYLTPQSVGGCGITPNSGDWKFVTSIVPITN
AFNETTLVEDLKINVTQPNLSIATIKKTYGVEVALYFEYIKHYTFWLLLLLSIIGLVSHFRKDKRFS
LTFAFINLLWGVFLASWHRREQHLVNVWGVQNSHLIEEHNSSELAKVNEREYEEKSTYFHANNNGF
RFLKQLAFIPIALVFVGVLSYQLSCFCIEIFLTDIYDGPGLSLTLLPTVLISVFPILTIVYNA
VTDIIKWHNDNQYSKNNLSLVKTFVLNFLTGYVPLIITSFIYLPFAHLVQPHLGDIKTTIATYA
GENRFYTKYLLKLKSQEEFKINQGRDLAQFFYFIVTNQVIQLVLKYILPLGLRFVFNFIETKIQKK
PQLQTKDDNPDESIWLHNVRSLKLPENVDNDDFRGLVLQFGYLIMFGPVWPLAPLVCIIIFNLIFF
KLDNFKLLNGKYFKPPVPRRVDLSIHPWNLALFLLAWIGSII SPVVTAFYRHGTAPPKSMGQFALDK
ASVHVSSSVFLVLLMFVSEHGFLILSYLLFEFSSLFKSQVEWENDFVDNDIKLRHDYYSKVKPTY
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YBR093C_homolog_1 1784bp public: 1..607, PathoSeq: 608..1784; CDS:
399.1781 (SEQ ID NO 297)

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GGGCTCTGTTTAGTTTAACTTCTTGTAGTTTATTATTCCGATTGGGTTAGCTCAATAACTGCATT
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GGAGAGATTTTTCAAAACTTCTATTATAAATAGAACCCCTATAAGTCCATAATAATTCAATTGAAGG
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AAATCAATTGTTATTCAAGACATGGTGAAAGATACCCCAAGTAAAAGTAATGGTAAAAGTTTAGAAG
CAATTTATGCTAAATTTGAAAACACAAAGGTACTTTTAAAGGTGATTGTGATTCTTAAATGATT
ACACTTATTTTGTCAAAGACCAGAGTAACTATGCTAAGGAACTAGCCCAAAAAATTCTGAAGGAA
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AAATCAACGTCAGAGGAAGTTCACCAATCTGTGATTTATTCACCAATGAAGAATTCATTAAGAAGT
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ATGCTGTGCTGCCAATTCAAAATGTGCTACTGGTCCAGGGTTCTCTTGTAAGTGTGATGATTTG
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YBR093C_homolog_1 461aa (SEQ ID NO 298)

MVSVSKLINNGLLLTSQSVFQDVATPQQASVQQYNILNFLGGSAPYIQRNGYGISTDIPAGCEIAQ
IQLYSRHGERYPKSNKGSLEAIYAKFENYKGTFGDLSFLNDYTYFVKDQSNYAKETSPKNSEGT
YAGTTNALRHGAFAFRAYGSLYKENSTLPFTSNRNVRHETSKYFARGFLGDDYEEGKTVKFNIIS
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INVRGSSPFCDLFTNEEFIKNSYGNLDSKYYSNGAGNNYTRIIGSVILNSSLLELLKDTKNSNQVWL
SFAHDTDL EIFHSALGLLEPAEDLPTSYIPFPNPYVHSSIVPQGARIYTEKLQCGNDAYVRYIIND
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YBR093C_homolog_2 1871bp public: 1..1752, PathoSeq: 1753..1871;

CDS: 501..1868 (SEQ ID NO 299)

GAGTTTATGGGATTGGGTTTTTCAATTAAAGACTCTTCGTGATAATGCAATACCAAAACCAAAAT
TTATTTAACGATGCAATAATTATTTCAATGTGAGCTATCCATGAATCAGTGAGAATCTTTATTATG

GAAGAAATTGGTCAAAATTTGACAATGTTTAGTAACTTTATATCTTGGTGTGGGATGGTGCCACA
AATGGAGATTGTTGAGTGATACATGAAAAATACGTAGTTAAATTTTGTCTTGTCTTTATTTATTTA
GCCACTTTTTTATCCGATTCCTCATATTACCTTTGGTAAAGTGATAAGATTAAATATCATATTAGTA
AAACACCCCCAATGATGAATGTTTGTATTTATAGCCAGACTATAAAAAATTACGGGGATTTAATTCG
CGACTCACCCACGTTCTCACACAGTATGTGCTTTTTTTCATAAGTATGATTTGAACCCTAAATATC
AACTTTTCATAATAAACATAATTCTTTCCAGACAATAAATGGTTGGTTTATCACGAGTACTTAATG
CTGGGTTTATCTAAGTGACAATCTGTTTCCAGGATGTTGCTGCCCCACATCAAGCATCAATTG
AACAAATATAATATTGTCAAGTACCTTGGTGGCAGCGGTCCATATATTCAAAATTCAGGGTATGGGA
TTTCTACTGATATACCAGAAAAATGCACATATTGAACAAGTTCAAATGATTAGTAGACATGGTGAGC
GATTTCCTAGTAAAGGAGATGGGAAATACTTTAATTCAGTGATGGAAGTTTTCAAGAGATATGGTG
AATTTTCATGGAGATTTATCTTTTTTAAATGACTATGAGTATTTTCGTTACTAATCCAGATTATTATG
AAAAGGAGACTACTCTTAAAAACTCAAAGGTCCATATTTTGGAACTACAAATTTATTACGACATG
GAGCTTATTTTAGAAAAAGATATCAATCACTATTTGACCAAAAGGAGAAGCTTGTGTGTTTACTA
GTAAITCTGGAAGGTGTTATCAAAGTGGTGTCTATTTCCGCTCGAGGATTTTATAGGAGATGATTACT
CAGAAGATACAGTTGAATTTGTTGTTGTTGATGAAGACAAAAAAATGGGTGGTAATTCATTGACAC
CAAGATACGCTTGTAAAACTTTGAATCAAGATTTACACAAAGATTTGGTGAATCAGTACGATAAGA
CTTATTTGGACGATATTTTATCTAGATGGCTAGTAGACAATCCTGGATTAGATTTAAGTGCAGATC
AGGTCTCGTCATTTATTTCTTTGGTGTGCCTTTGAGATTAACGTTAGGGGGTATTCTCCATTTCTGCA
ATCTATTTACAAAAGATGAATTTATCAGAAGTGGGTACCGAAACGATGTTGGTAATTACTATCAAA
CTGGTCCAGGTAATAATATGACAAAGGTAATTTGGCTCACCTATGGTGGAAGCGTCGTTGAAAATGC
TTCAAGAAGATTCAAAAAATTTGGTTGACATTTACCCATGATACTGATATTGAGATGTATTTGACAT
CTTTGGGATTGATTGTTCCACCAGGGGATTTGCCCGTTGATCGAGTACCATTTCCCAATCCATATA
ATGCAGCAGAATTTTCCCTCAAGGTGCTAGAACTTACACTGAAAAATTGAAATGTGGTGAAAAGC
AATATGTTAGATTTATTTGTAATGATGCAGTTTATCCATATCCGGATTGTAGTGGAGGTCCTGGGT
TTACTTGTGAATGAAATGATTTTATCAAATTAGTTAAAAGTCGTTTACATGATGTTGACTATAAGC
TTCAATGTGAAGTGGACGGACCGGAATTGACATTTTATTGGGATTATAAAGACAGAAAGTATA
ATGCGCCGTTAATAGATCAGTAA

YBR093C_homolog_2 456aa (SEQ ID NO 300)

MVGLSRVLNAGFILSGQSVFQDVAAPHQASIEQYNIVKYLGGSGPYIQNSGYGISTDIPEKCTIEQ
VQMI SRHGERFPSKGDGKYFNSVMEVFKRYGEFHGDL SFLNDYEFVTNP DYEEKETTPKNSKGPY
FGTTNLLRHGAYFRKRYQSLFDQKEKLVVFTS NSGRCYQSGVYFARGFLGDDY SEDTVEFVVDED
KKMGNSLTPRYACKTLNQDLHKDLVNQYDKTYLDDILSRWLVDPGLDLSADQVSSLFLWCAFEI
NVRGYSFP CNLF TKDEFIRSGYRNDVGNYYQTGPGNNMTKVIGSPMVEASL KMLQEDSKIWLTFTH
DTD IEMYLTSLGLIVPPGDL PVD RVPFPNPYNAAEFFPQGARTYTEKLKCGEKQYVRFIVNDAVYP
YPDCSGGPFTCELNDFIKLVKSRLHDVDYKLCQCEVDGPAELTFYWDYKDRKYNAPLIDQ

YBR093C_homolog_3 1888bp PathoSeq: 1..1656, public: 1657..1888;
CDS: 500..1885 (SEQ ID NO 301)

TGTAGTATAAATAAGGGTATGAAATACCAACATCCCAGAATATCAACGAGATAGAAGAGAGGAGTT
TCAATATATATCTTGTGAATAATAACTTCGTTCTAATTCACATACACAAC TAGACGTGTACACGC
TCAATCTCAGGTAAAGAAAGTTTATATTCCATCACTATATAACAACAATCAGGCTTTGCAAAAAA
CATTTAAAACTAATACTGGTAATATGGAAATATAACGCCTCGTAGTTCTACGCACGTGGCATCCTT
TATCTATTTATTTCAATTTACCCCTAATTTATGAATTAGCTTAATAAGAGCAGTCAAATTAACACGG
CTCAATTAATAGTACTTAATAATATGAAGCCGATCAATTAACCGATCCTTTGAATAATTTGAAAAAT
AAAAATAAGTAATATAAATAGGTATGCATTTTCCCTACATTTATTTCTCTTTCTATTTTAATTTG
TTTCTTAAACAGCAACAACAACAATTGAAATTCAAAAATGGTTTCTGTTTCTAAATTATTGAACAA
TGGATTGTTATTAGCTGGTCAAAGTGTCTTCCAAGATGTTGCTACTCCACAGCAAGCTTCTGTGCA
ACAATATAACATCGTCAATTTCTTTGGCGGTAGTGCCCCCTTATATTCAAAGAAACGGATATGGGAT
TTCTACTGATATCCCTGCTGGTTGTGAAATTGCTCAAATTC AATTGTATTCAAGACATGGTGAAAG
ATACCCAAGTAAAGTAATGGTAAAGTTTAGAAGCAATTTATGCTAAATTTGAAAACTACAAAGG
TACTTTTAAAGGTGATTTGGCTTTCTTAAATGATTACTTATTTTGTACTGATAAAAAACAATTA
CGAAAAGGAAACTAGCCCAAAAAATCTGAAGGAACCTATGCCGGTACAACCAATGDCCTTGCGTCA
CGGTGCTGCGTTTAGAGCCAAATATGGATCCTTATACAAGGAAAATTCACATTACCAGTTTCTC
TTCCAATTCAGGTAGATGTTACCAAACTTCAAGATATTTTGCTAGAGGATTTTTAGGTGATGACTT
TAAAGAAGGTAAACTGTCAAGTTTAACATCATTTCTGAAGATGCTGATGTTGGTGCCAATAGTTT

GACTCCAAGAAGTGCATGTTCCAAGAACAAAGAACGGAGCAGTAGTACTGCCAAAAAATATAACAC
AACATATTTAAATGCTATCACTGAAAGATTAGTTAAACCAAACCCAGGTTTGAATTTGACTACAAG
TGATGTCAACAATTTATTCAGTTGGTGTGCTTATGAAATCAACGTCAGAGGAAGTTCACCATTTCTG
TGATTTATTCACCAATGAAGAGTTTATCAAATATTCTTATGGTAATGACCTTTCCAACATTATTTC
TAATGGTGTCTGGTAACAAATTACACCAGAATCATTTGGTTCAGTGATTTTAAATTCTTCTTTAGAACT
TTTAAAGACACTAAAAACTCTAATCAAGTATGGTTATCATTTGCTCATGATACTGATTTAGAAAT
TTTCCATTCTGCTTTTAGGATTATTGGAACCAGCTGAAGATTTACCAACATCTTACATCCCATTCCC
TAACCCATACGTCCATTCTTCTATTGTTCCACAAGGTGCCAGAATATACACAGAAAAACTTCAATG
TGGAAACGATGCTTATGTTAGATACATTATCAACGATGCTGTCTGCGCCAATTCCAAAATGTGCTAC
TGGTCCAGGGTTCTCTTGTAACCTTGATGATTTTGAAAATTTTCGTTAAAGAAAGAATTGGAGATGT
TGACTTTGTATAACAATGTGGTGTCAATAGTACCTACCCATCTGAGCTTACTTTCTACTGGGATTA
TAAAAATGTCACTTACAATGCTCCTTTAGGTGATTTTAA

YBR093C_homolog_3 462aa (SEQ ID NO 302)

MVSVSKLLNNGLLLAGQSVFQDVATPQQASVQYQYNIIVNSLGGSAPIYIQRNGYGISTDIPAGCEIAQ
IQLYSRHERYPSKSNKSLKLEIYAKFENYKGTFGDLAFLNDYTFVTDKNNYEKETSPKNSEGT
YAGTTNALRHGAFAFRKYGSLYKENSTLPVSSNSGRYQTSRYFARGFLGDDFKEGKTVKFNIIIS
EDADVANSITPRASKNKERSSTAKKYNITLNAITERLVKPNPGLNLTTSDVNNLFSWCAYE
INVRGSSPFCDLFTNEEFIKYSYGNLDSNYVSNAGNNYTRIIGSVILNSSLELLKDTKNSNQVWL
SFAHDTDLLEIFHSALGLLEPAEDLPTSYIPFPNPVHSSIVPQGARIYTEKLQCGNDAYVRYIIND
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVFVKQCGVNSTYPSSELTFFWYDKNVITYNAPLGDF

YBR093C_homolog_4 1886bp PathoSeq: 1..102/1038..1062/1078..1886,
public: 103..1037/1063..1077; CDS: 501..1883 (SEQ ID NO 303)

ACTACTTAAATTGGCATATCCAAACAAACTTGAAGTAGGAGTTTCCTTATTTTTATTTTGTATTTA
TATATTTGATTGCGATTAAATGTCATAAAATTTAGTTCGGTAATTATGTCACAAAAACAAACAATCA
ACATATTTAAATCGTTATCCCAACTTTTGTCACTTTACTAACACCTTTTATTTTGTGTTATACAAAT
TGCACAATCAATTACTATAACTTTTTTTTGAACGTTGGCTCTGTTTAGTTTAACTTCTTGATGTT
TTATTATTCGATTGGGTAGCTCAATAACTGCATTTTCGTACAATAATGTTAATTCAATTCTAAAT
TCCGATGAACCGAACACACAAAAACATCCAGTTCCTGGAGAGATTTTTCAAAACCTTCTATTATAAA
TAGAACCTTATAAGTCCATAATAATTCAATTGAAGGATTATTTTCTTTTCCCTTTTCTGATTACTT
TCACCAATTTTCTTCTCTCCAAAAAACACCTTCTTCATGGTTTCTGTTTCTAAATTAATCAATA
ACGGGTGTTGTTATTAAGTAGTCAAAGTGTTTTCCAAGATGTTGCTACTCCGCAACAAGCTTCTGTGC
AACAATACAATATACTCAATTTTCTTGGCGGTAGTGCCTTATATTCAAAGAAACGGATATGGGA
TTTCTACTGATATCCCTGCTGGTTGTGAAATGCTCAAAATTCATTGTAATCAAGACATGGTGAAA
GATTCCCAACAGCAAGTAGTGGGAAAGATTATGAGAAAAATTTATGCTAAATTTAAAACTACAATG
GTACATTCAAAGGTGATTTGTCAATCTTAAATGATTACACTTATTTTGTCAAAGACCAGAGTAACT
ATGCTAAGGAACTAGCCCCAAAAATTTCTGAAGGAACCTATGCCGGTACAACCAATGCCTTGCCTC
ATGGTGTCTGCGTTTAGAGCCAAATATGGATCCTTATACAAGGAAACTCAACTTTACCAATCTTCA
CATCCAATTTCAACAGAGTACATGAACTTCAAAGTATTTTCGCTAGAGGGTTTTTAGGTGATGATT
ATGAAGAAGGTAAACTGTCAAGTTTAAACATCATCTCTGAAGATGCTGATCTTGGTGCCAATAGTT
TGACTCCTAGAAGTGCATGTTCCAAGAACAAGAACTGAGCAGTAGTACTGCCAAAAAATATAACA
CAACATATTTAAATGCTATTGCTGAAAGATTAGTTAAACCAAACCCAGGTTTGAATTTGACTACAA
GTGATGTCAACAATTTATTCAGTTGGTGTGCTTATGAAATCAACGTCAGAGGAAGTTCACCATTTCT
GTGATTTATTCACCAATGAAGAATTCATTAAAGAACTCTTATGGTAATGATCTTTCCAAATATTATT
CTAATGGTGTCTGGTAATAATTACACCAGAATCATTTGGTTCAGTGATTTTGAATTCATCCTTGGAAC
TTTTAAAAGACACCGAGAACTCTAATCAAGTATGGTTATCATTTGCTCATGATACTGATTTAGAAA
TTTTCCATTCTGCTTTAGGATTATTGGAACCAGCTGAAGATTTACCAACATCTTACATCCCATTCC
CTAACCCATACGTCCATTCTTCTATTGTTCCACAAGGTGCCAGAATATACACAGAAAAACTTCAAT
GTGGAAACGATGCTTATGTTAGATACATTATCAACGATGCTGTCTGCGCCAATTCCAAAATGTGCTA
CTGGTCCAGGGTTCTCTTGTAACCTTGATGATTTTGAAAATTTTCGTTAAAGAAAGAATTGGAGATG
TTGACTTTTATTAACAATGTGGTGTCAATAGTACCTACCCATCTGAGCTTACTTTCTACTGGGATT
ATAAAAATGTCACTTACAATGCTCCTTTAGAAATTGTAA

YBR093C_homolog_4 461aa (SEQ ID NO 304)

MVSVSKLINNGLLLTSQSVFQDVATPQQASVQQYNILNFLGGSAPYIQRNGYGISTDIPAGCEIAQ
IQLYSRHERFPTASSGKDYEKIYAKFKYNGTTFKGDLSFLNDYTYFVKDQSNYAKETSPKNSEGT
YAGTTNALRHGAAFRAKYGSLYKENSTLPIFTSNRNVRHETSKYFARGFLGDDYEEGKTVKFNIIS
EDADLGANSLTPRSACSKNKESSSSTAKKYNTTYLNAIAERLVKPNPGLNLTTSDVNNLFSWCAYE
INVRGSSPFCDLFTNEEFIKNSYGNLDSKYYSNGAGNNYTRIIGSVILNSSLELLKDTENSNQVWL
SFAHDTDL EIFHSALGLLEPAEDLPTS YIPFPNPVYHSSIVPQGARIYTEKLQCGNDAYVRYIIND
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVFIFKQCGVNSTYPSSELTFFYWDYKNVTYNAPLEL

YBR181C_YPL090C_homolog 1635bp public: 1..938, PathoSeq:
939..1635; exon 1: 500..505, intron 1: 506..930, exon 2: 931..1632
(SEQ ID NO 305)

ATATATATATATTTATGTATTTTTTTTATTGTTGTTTCAGGAATTTTAAACATGTTTCATGAATAATGA
TAATCTATGAACAAATTAAAGAACTCTTTGGTTTCATTTGCAACCAATGTGCGTGACTTAGGGCTA
TAGCCCTACTTTTTACTTTGTACGATACCTGCATATTTTGTGTTGTGCGAATAGTTAGCGTAATAATC
TTTTTTTTTGTGTGTGTGCGGTTTACTTACTCTTCTTCTTCTCGCACATATTTTATTAGAGCTTAC
AGTTGTTTGTATAGTGAGAGTTTCACTAACACAAAGCTTCAACAATACTAACAAATTTTCGCACGC
TGTGGAAGGAGAACTTACACTGTACACTACACTACACTGTACACTATACACCACCAACAGAAAAA
AAAAATTATCAAATTTTCAACCTTGAGAGAAAAAAGTGGAAAAAACTTCTTCTTACATTT
AGTTAATTTTCAGACAGGCACAAAGGAATTAATCACCATGAAGGTATGTGATTGAATATAACCTAT
ATCAGTGATTATAATTAGAGTCTTTATTTGGATATTGCAATAATTGGATAATAAAGAAAGAGCATA
AGAGTAGGAGTTTTAAACAGGATAATTGGATTCAATAAGAGGAAAAATTTTTATCGTCGTGATTA
TAACAAATACAAAGAAATTAAGCAATGAAGTATATAAGCAAATGAAGGACTAGTTTATTAGGGGT
GACATTTTGTAGACTACGTAAAAGTACTTTTCGATTCAAGGAAAAACCAATTTTAGTATCTATCAACA
AACTACAAATCAATTTAGTTAACTTCAATAATGACAATAATTTAATCACTGAAAAACAATAAACAT
GCAAAACAAGCAAAACTAGTCAAGCTTTACGAATCAGTCAATACTAACAATACTTTTTTTTGTTC
TTTTAGTTAAACATCTCATATCCAGCCAACGGTACTCAAAAATCTATGGATATCGATGATGACACA
AAATTACGTGTTTCTACGGAAGAAAGAAATGGGTCAAGAAGTTGAAGGTGACTCAGTTGGAGATGAA
TTCAAAGGTTACATCTTCAAATCACTGGTGGTAACGATAAACAAGGTGTCCCAATGAAACAAGGT
GTTATGCACCCAACAGAGTTAGATTATTATTATCTAAAGGTCACCTTGTGTACAGACCAAGAAGA
ACTGGTGAAAGAAAAAGAAATCCGTTAGAGGTTGTATTGTTGCTCAAGATTGTTCAGTTTTGGCT
TTGTCTATTGTTAAACAAGGTGACAATGAAATGAAGGATTAAGTACACCACTGTTTCAAAAAGA
TTAGGTCCAAAGAGAGCTAACCACATTAGAAAATCTTTGGTTTAACTAAAGAAGATGATGTTAGA
GATTTTCGTTGTTAGAAGAGAAGTTACTAAAGGTGACAAAACCTTACACCAAAGCTCCAAAGATTCAA
AGATTAGTTACTCCACAACTTTTACAAAGAAAGAGAGCTTTGAAAGCTAAAAAGTCAAGAATGCT
CAACAACAAGAGATGCTGCTGCTGAATACGCTCAATTGTTGGCTAAGAGATTGCATGAAAGAAAA
GAAGAAAGAGCTGAAATTAAGAAGAGAGCTGAATCTTTAAAGAACTAA

YBR181C_YPL090C_homolog 236aa (SEQ ID NO 306)

MKLNISYPANGTQKSMIDDDTKLRVSTEKRMGQVEGDSVGEFVKGYIFKITGGNDKQGVPMKQG
VMHPTRVRLLLSKGHSCYRPRRTGERKRKSVRGCIQAQDLVSLALSIVKQGDNEIEGLTDTTVPKR
LGPKRANHIRKFFGLTKEDDVRDFVVRREVTGDKTYTKAPKIQRLVTPQTLQKRKALKAKKVKNA
QQORDAAEYQQLLAKRLHERKEERAETIKKRAESLKN

YCL016C_homolog 1520bp public: 1..1079/1081..1520, PathoSeq: 1080;
CDS 501..1517 (SEQ ID NO 307)

GTGACGAGAACTTCTGTCATCTCGAGTCTGCCAACTGCCTCTAACAGCAACAACAATAAGAACAAT
GATAACGGAGGAGGATTATCCCATACAAACAGAATAGTTGTTGGTGTAGTTGTTGGGGTTGGTGGT
TCTATATTAATTGGTTTGTGGCCGTTTTATTTTACTTGAGAAAGAGAAACAACCGTGATTATGAA
GGTGGATGGACTTTCTGGAGAAAGAATGAGAAATGGGAAGTGATGAGTTCTTCAATGGTGAATTG
GGTGTCTAGAGACAGAAATATTAATCAAGGATCAAATTTTAAACAAGGCTTATTTTGGATGAGGGT
GGTTTTTTTTATAAGTATTTTGTAGTTGAATTTAAATTTTGTACCTTAAAGTCTTTTAATTTAAT
TTTAATAAAAAGTGGTGATTGCGCAAACTTCAAGGATATATTTGGTGAAAAAATAAATAAATTTG
GAACTGAACGCGTCTAACATCTTATACCTCTAAGCAAAATGTCAGAGTACTCTGTGTATCAACAGT
TGAATGAAGATACAAACGCAACTAAATATACTTATAAATTAATACAGCTACCATCAAAGATACTAA
ATCAACTTGAATCCAAGTCAACTAATTTGTATATAAATCTGATATCAATTCCTTAGCATTATGCA
CTGATTACAGAACTTTCAAGTTACGACAAATGAACCATCCAATACAGTCTTGCTATTGAACAAAG

AACCTGACAACAAGTTAATTGGGTTTCAGAAAACCAGTTATGAATATGAGTTGACAGAAATCAAAG
GTTTCGATCGATACGTCCGATATCCCTATTTTCAACGGACAAAACAGCACAGCAACCTATTGATTTGA
TAGCATTGGAAGATAATTTCGATTTGTTACATCAAGAGTTTTATCGAATTGGTATGAGTTGGGAG
GTTGTGAAATTGATAATGGAGCATATATAATGAGTGCAGATATTATTACTGAACTATTATATCTAT
TAATCACCAAATTGATGAGTTTACAAGTGCACGAGTTTTCTCCGGAAGATGTTTCATCCATCATCA
CGCCCCCTTATAATGACTCAATGGTAACATCAATCATACACAAATTTTGCCTATAGAAAGTGAGA
AATATCAATTGAATGATTTAAAAATTACACAGTGGTTTGGCATTGTTGAGATGTCAAAAATCAATC
ATAAAATGACCGATATTTTCAGAGTCTTATTGAATTGGAAAAGTAGTTGCCGTCAATTCTATAACC
CTCCATTGGACATCAGTCAATTGGCAGGCTATTACTGCTCCCAATCGAAAACAAAATATTGTATG
TCGACCCAGAACTTTTATCAGAAAATTTGAGTCAACGATTCAAAGAATTGTTTGAATTGGATAAAA
GTTGGAACATGATGAGTTTATTCATTCAATTAAGTTTGTCTCCGGTAAAAAGGTCGACT
CAATTATTTTAAAGTATGGCAAGAAGAAGAAAGTTGGTAGAGATAGATTTATAGTCTGCTCCTAGAT
AA

YCL016C_homolog 339aa (SEQ ID NO 308)

MSEYSVYQQLNEDTNATKYTYKLLQLPSKILNQLESKSTNLYIKSDINSLALCTDSETFKLRQMNH
SNTVLLLNKEPDNKLIGFQKTSYEYELTEIKGSIDTSDIPIFNGQTAQQPIDLIAEDNSICSHQE
FLSNWYELGGCEIDNGAYIMSADIITELLYLLITKLSLQVHEFSPEDVSSIITPPYNDMSVTSII
HKFCTIESEKYQLNDLKITQWFGIVEMSKINHKTMDISEFLLNWKTSLPSFYNPPLDISQLAGYYC
SPIENKILYVDPESLSENLSQRFKELFELDKSWNYDEFIPFIKKFVPAGKKVDSIILKYGKKKKVG
RDRFIVCPR

YCR073WA_homolog 710bp PathoSeq: 1..710; CDS: 315..707 (SEQ ID NO 309)

GGTGGGGTCCCATTTTAATTTAAAAAATTTTTTACCATCCAAAGGATTTTATTTACCCAAAGAC
CAAAAAATTTATTTTGAATGGGGATTTAAATGGGGATAATTTTATTTTGCCTGATGAAAAGATT
AGTACCCGTTTGAAAGTCTTGATTCAAATTTATGGTCAAGCTAAAAGAGAAATATTTGATTTAATTA
CTGGTGATAAAAAACCAAGAATTTTCCATGTTGATGAATCATTAATTGATGATTCTCAAGAAGCTG
CTGATGAATATGAAAAACAATTGATTAATAATTTTGGCTAAAAAAGATTCCGGTGAAATTACCTTTAT
TTGATTTATTTTATTAGGTTGTGCACCGGATGGTCATATTGCTTCATTATTTCTTAATCATGGTG
AACAATTGAGAGAAAAATTAGCTTGGGTTTACCAGTATCAAATGCTCCTCTGGGACCAGAAAATA
GAATAACTTTATCTATCCCAGTTATATGTCAATCCGCAAGAGTGACATTTGTTGTTGAAGGGTTAA
CTAAGGCACCAATTATTTAAACCATTATGGAAAGACCAGAAAAAGGTTTACCAAGTTCAATTGTTA
ATGAAGGTGCTGCTGGTAGAGTGAGTTGGTTTGTGATGATGATGCATTGAATGATTGTTTGATA
TAATAAAAAAGAAATACAAATATTTATCTATACCTGAACCAAGTCATTAA

YCR073WA_homolog 131aa (SEQ ID NO 310)

VKLPLFDLFLGCAPDGHIALSFPNHGEQLREKLAWVLPVSNAPSGPENRITLSIPVICH SARVTF
VVEGLTKAPIIKTIMERPEKGLPSSIVNEGAAGRVSWFVDDDALNDLFDITKKKYKYL SIPEPSH

YDL010W_homolog 1190bp PathoSeq: 1..1190; CDS: 501..1187 (SEQ ID NO 311)

TGTTACAAAACATTCTGTTGGAGAGATAATTGAATTCAAAATTAACGTGTTGAATCCAACATTGAA
CAATGAATACACGTCCAAGAAAAATTTGACATGATTAGAATCGCGGTCAATTACATTCCCGGAACG
TCTTGGACTACTTGGATACAACAATGGAAAAATGAGGAAAAATGAGGAAAAATGAGGAAAAACGAGGAAA
ACGAGGAAAAATTTTACCGAAGAGTAATTATATTACAAGCATTGAAAGAGGAGAAGTGAACGCCCC
AAACAGAAACAATACCGAACATCACAAAAAAGACAACAGCTAAAATTTTTTGGTCAGAA
CACAACCTTGGAAAGAAAGAAAAAACCAGAAAAAAGAAATTCATCTAAAACACATACACAATATAT
ATATATATATATAAATATATCCATATACATATGCTTTAATTTAACCTTCCCGCCTTTCTTTTCTTC
TTTTTGAATTATATCGATTTTAAAACTACACTTCATCATGGCTGGAGTTAGACAATTAAGAATAA
TAGCATTAACGGCCTTTGTCTTGGTTTAAATTTTACTTTACATAAAGTTGGATCCAACGCTGCAT
CCTTGGTTTCATGCACAAGCATCAGACCAACAACCAAAACATAACACCAAAAGTACTACATATA
CCGCCACTAATGACGAATCAGTTGCCAATCTCATTGATTCTAAAAATGATCCTCAAACCTGATGACA
AAATAAATCAAAAAATATCACAGATCAAGATGAAGCCATCAATGGTAATAAAGACACTAATAAAG
ACACCACCAAGTCAAACCAGATAATGGTGAATATGATCCAATATCTGATTTGATAAAAAATTAGAT
CATTATACCAATGACAAATTTTCAGTAAATCATATTGTCCATATTCAAAAAAGATTAAACAATTGT

108/161

TATTAGAAAAATATGATATAACACCAGCACCAATGTTGTTGAATTAGATCGATATGAATATGGAG
CTGAATTACAAAGTTATTTGACAGAGAAGAGTGGGAGAAGAACTGTGCCAAACGTATTGGTTGGTA
AATCATTTGAAAGTAGGGGTGGTTGTGATGAATTTGAAAAACTTCATAAAGATAATGATTTGATTA
AATTGTTAGTTGAATGGGGTCTGGTCGTTTACAAGTTGCAAAGAAGAATACCCCATCAAATGCCT
AA

YDL010W_homolog 229aa (SEQ ID NO 312)

MAGVRQLRIIALTAFVLGLIFTLHKVGSNAASLVHAQASDQQPNKHNTKSTTYTATNDESVANLID
SKNDPQTDDKINQKISQDQDEAINGNKDTNKDTTKVKPDNGEYDPIISDLIKIRSLSPMTIFSKEYC
PYSKKIKQLLLEKYDITPAPNVVELDRYEYGAELQSYLTEKSGRRTVPPNVLVGKSFESRGGCDEFE
KLHKDNDLIKLLVEWGSRLQVAKNTPSNA

YDL083C_YMR143W_homolog 1256bp PathoSeq: 1..1256; exon 1:

501..521, intron 1: 522..848, exon 2: 849..1253 (SEQ ID NO 313)
AGTGGTTGTTCAATAATGGTAAGTTCCTGGAAATAGCCATTGTTGCTTTCTGGTGGTTAGACTTGT
AGGAAGTAGAACTGTTTTCCAATGAAAAGTAGTTTAAATTAGAAAAATTTTCAAAGTCCGTGAAGC
CCAGTCTGAATGTGCGAGGAAGCCCAGTCAGTTAGTAGTGTCTTCCCTCCACTGTCTGTAATACA
AAATTTCCCTTAGTGAATGCGAAATATATCTGTACTGGGAACCCCCGGAAAAAAAACCTA
TGCTCAAAACTATATGTACTGTACACAATCTAGGGCTATAGCCCTAATATTGTACAGGAAGAAGCTT
TAATATGGTGCAGAGAGCGTTTCCAATTTTTTTTTTTCAGGTGTAGTCTGTTCTATGGCAATAC
TGTTGTTAGTAGAGAGTGTCTCGCACTAACAGAACATTTTTTTCAGAACAGGAAAATTTTTGAAAT
CTAACATCTTTTACTGAAAGCCAAGCATCAACACAATAATGTCAACCCAATCTGTTCAAGTATGTA
AACGAATTGAAATAAAGAGATAGAGAGATGTTTTATTATCAAAATACGAAAGGAAAGGCAATTTAA
AAAGGAAATCAAAAAGTCCCAACCTTGCAAGTAGAAGAATTGAGGTATATGAATTTGATAGATAGCC
AGAACGGTGTACATAAATGGGATATAGAACAAAACCTATACGAGGAGTTTGTTCACGATCATTC
AATAACCAGAAAACGATAATATTTTAGCGACCATTAATGACACTTGAAGGCTCACTGGGCCAATA
GAATATCTCCATATACACTTTTGAACATTTTACTAACAATTTACTTTTGTCTTAGACTTTTGGTA
AAAAGAAGACTGCCACTGCCGTTGCTCATGTTAAAGCCGGTAAAGGTTAATTAAAATTAACGGTT
CCCCAATCACCTTGGTCCAACCAGAAATCTTAAGATTCAAAGTTTACGAACCATTGACTTTGGTTG
GTTTAGATAAATTTCAAGGTATCGACATCAGAGTTAAAGTCACTGGTGGTGGTCACGTTTCTCAAG
TCTACGCCATCAGACAAGCTATTGCTAAAGGTTTGGTTGCTTACCACCAAAAATACGTTGACGAAG
CTTCTAAGAACGAATTAAAGAAAATTTTCGCTTCTTACGATAAGACCTTGTTAGTTGCCGACTCAA
GAAGAATGGAACCAAAGAAATTCGGTGGTCTGGTGCCAGAGCAAGATTCCAAAAATCTTACCGTT
AA

YDL083C_YMR143W_homolog 142aa (SEQ ID NO 314)

MSTQSVQTFGKKKTATAVAHVKAGKGLIKINGSPITLVQPEILRFKVEPLTLVGLDKFQIDIRV
KVTGGGHVSQVYAIRQAIKGLVAYHQKYVDEASKNELKKIFASYDKTLLVADSRRMEPKKFGGRG
ARARFQKSYR

YDL125C_homolog 959bp public: 1..959; CDS: 501..956 (SEQ ID NO 315)

GTGGTAAGATATAGAAAGCTTACCACTTTGACAAAGTTTGAAATAGGATGGGTGAAAATTTGGACAT
CTTGAATACTTAAATTTCTGAACCTTGATCACCAGATCCTTTTCTTTTACATAATTAGATATGATGG
ATAGGTTAGAATCGTCTTTAAAGAGAAGGTATAATATCTAACTGATTTGGCGAGGTGTTGGAAAAG
TCACTCCACTGTATATATTCTCGGAGTTTAAAGTACTACAGTTCACTGGGGTGAATACCTAAATAG
GGGGGTAGAATACGAACCTCTACAAATTTTAAGGAGACTATGACCCGAAAAGAGAAGAAAAATTTA
TTACTCTAAGAAGTTTATATACCTCCACAACCTCACTTTTCTTTAGTTTCACTCTGCTTTTTTTTTT
CTTACACATCTTAAGGTCAAACAATTTAACTTATAGCTTGTGAAAATCTCACTTCAATTCAAGTT
CTCTTTCAATTGACATTATAGTATTTCCCAATTCAATTATGGCTTCTCATGCTTCTGTATATTCT
GTAAAATTATCAAAGGTGAAATTCCTTCTTCAAGTTAATTGAAAGTCAAGAACTTATTCCTTCT
TGGACATTCAACCAATTGCTGAAGCCCACGTTTAAATTATCCCTAAACACCATGGGGGCAAGTTGC
ACAACATTCCAGACGACTACCTTAGTGACATTTTACCAGTTGTCAAAAAATTGACAAAAGTCTTGA
AATTGGACGAAAATAATCTCCAGAAGGTGAAGTTTATAACGTTTACAGAACAACGGAAGAATTG
CTCATCAAGTTGTTGATCAGTTCACTTCCATTTGATTCTTAAAGGATGAGGCTACAGGTTTGA

GTGTTGGTTGGCCTGCTGAAGCCACTGATTTTGATAAAATTAGGAAAATTGCATGAGAAATTAAAGG
AAGAATTGGCTAAGGTAGATAATGAAAAATTATAA

YDL125C_homolog 152aa (SEQ ID NO 316)

MASHASCIFCKIIKGEIPSKLIETAKTYSFLDIQPIAEAHVLIIPKHHGAKLHNIPDDYLSDILP
VVKKLTKVLKLDENNTPEGEGYNVLQNNGRIAHQVVDHVHFHLIPKDEATGLGVGWPAEATDFDK
LGKLHEKLKEELAKVDNEKL

YDL133CA_YDL184C_homolog 297bp PathoSeq: 1..297; CDS: 220..294
(SEQ ID NO 317)

CATAATTATTACATATAAACTCGCACTATAATTTTTTTTTTCTATTCTGTGTGTGTGTGTGTGT
GAGAGCCAGAGAAACCAACTGACTGAGTGATCGTCTCTCAACAATTTATTTCTCCTCGTCTTATT
TTTTTTCTTTCTTTCTTTCT
CCTTTTCAACATGAGAGATAAAGTGGAGAAAAAAGAGAGTTAGAAGATTAAAGAGA
AAGAGACGGAAGGTTAGAGCTAGATCCAAGTAA

YDL133CA_YDL184C_homolog 25aa (SEQ ID NO 318)

MRDKWRKKRVRLKRRKRRKVRARSK

YDL136W_YDL191W_homolog 1303bp PathoSeq: 1..1303; exon 1:

501..503, intron 1: 504..943, exon 2: 944..1300 (SEQ ID NO 319)
TATTGTCTGATGCTATACGGAATGGGCGTTACAAATATACAACTTATATTTGAAAGTAAATTCTA
TTATTTTCTTCTATCGTATGCATACCGATTATTATCACAAGGACAATTGCCTATTGTTGTGTGGAA
TAAATTTAAATCCCTTCTTATTGGTGTCTAGACTTTGCTTTTTGTGGTGATTAGGGCTTTAGCCCT
ATCACGTGAAATACGTATATATAAAAAATCTTTATAGCGCGATAAAACATATTTTTTTCCGTATT
AACAAATATGTGTGAAGTTTTGTCTGCTGTTTCTCACTGTTTTCTCTTTTTTTCTGGTAGTAT
CAATTAACGCTTAGATCCAATACAGTTTGGTAACCTGTACACGAACAAAATCTCAAATTTGTTAC
TGTGTGAACCAACAAGGAAGAGAAAAAAAACCCATACAAAAATTTTTTCAGTATCAAGGAATTAGA
AGAGACGTTTAAATCAACAAAGTTCAAATCTATCAACAATGGTATGTTTAAATATCGATATTATCCA
TAGATGTACATGTATCCTAATGGGTTTCATTATTTGGAAAGTTATGTTTATGGGAGTTCTATTTAT
TAAGATATGGGATAAGAATTAAAGTATTGGATGAGTAGTACAAGACCAACAAAGAGAAATAGCCCC
CTTTCCCTCCACTATTCAATATACTCAACAACATTATCAAGTTAAAAGTTCAGAAGATACACGTAA
ATGAAAAGTTAATACCAAGAAGATACAAATTACCAGTCCATACCGTGTGGGTTTAGATTACTA
TATTTTACAAGAAACATATTATATGAAATGATACCAATCCACAGCGACTTTTCAGATAGCCAAAT
AACTAAGCAACTCAAGATAACATAGGATCATGCATCAATCACAATGAAACATTAACTACTAATAA
CTTTTTTTTTTATTATTAGGCCGGTGTAAAACTTTTCAATTAAGAACTAAATCTAAGGAACAATT
AGAATCTCAATTGGTTGAATTGAAACAAGAATTGGCCACTTTAAAAGTTCAAAAATTACAAAGACC
AAGTTTACCAAGAATTCACACTGTTTCGTAAAAACATTGCTAGAGTATTGACTGTTATTAACTTGAA
TCAAAGAGAAAATGTTTCGTGCCTTTACGCTGGTAAAAAATACATTCCAAAAGATTTAAGAGCTAA
AAAGACTAGAGCTTTAAGAAGAAAATGACTAAATTTGAAGCTTCTCAAGAAACTGAAAAAGCTAG
AAAACAAAGAATTGCTTTTCCACAAAGAAAATTTGCTATTAAAGCTTAA

YDL136W_YDL191W_homolog 120aa (SEQ ID NO 320)

MAGVKTFLRRTKSKEQLESQVLKQELATLKVQKLQRPSPRIHTVRKNIARVLTVINLNQRENV
RAFYAGKKYIPKDLRAKKTALRRRLTKFEASQETEKARKQRIAFPQRKFAIKA

YDL167C_homolog 2690bp PathoSeq: 1..1640, public: 1641..2690; CDS:
501..2687 (SEQ ID NO 321)

CTCTGTGTAAATTGATGAAATCCACACAATAAAAAATTTCTTTCTTTCTTTTAAAGAACCTAAAAACA
GAATCAACATTATTTGCCCCATACATATCCAAGAATTAAATACTTATTAGTTCTAAGTGGAAATAGA
AGAGAATCAAACCTTAACATTACTGTTACGCAACGTCAAGAGGGCATTTTTTTTAGTTTTTAATTTGT
TTCAATTTCAATTGAATCTTTAAGAATCACCGAGTATACATACTTTCTTTTGTATTTTATCAGGGA
GCCACATCCAACCACCAGTTACATCCCAAAAATCCCTTAATCTTGTCTTAGTTGTATTATTAAT
CTATTGAATTTAAGTTTGATATGCGAGAGAATATTGTGGATTGTATAAGTTTTGAACTGGACTTGA
ATACTTTGAGGGGCTTAATCATATATTGCATTTTATACCCTACTCGCGGTGTTGCTTACCACACTG
ACTAGTATGATCTTTCTGAGATTTCTAGCCAATAAATTATGAGTGATATTTATATTATTATTCATA

TTTCTACTACCTGTGATGACTCGCCGACATTTGTCTACTAAGGATTCTTCCGAGTTAATTGAATTTG
CTTGGGAAACAGTCGATAGTGTCTACTTTGGAAACTTTATACAAAGGATCAAACCTGGTTCGTCCAA
CCAACACACCTATCACACCTTACTGCTCGAAGATTATAGAATAACATGGGACAATGTCAAAAATG
CTGGGTGCTTCAAAGACGCCATCACAACTTTGATCAATACGTACAAGAACACATAATTTCCAAGA
AAAAGGAGTTTTCAAATTGTGATGTTTGACATTTCCAAATTGAGAGTTTCAAGTTGGTTCGTGAAGCTA
GAGACAAATCCGTGGTFTTTACCCCTCGTATCTACAACATCCAAGGATTTTGTATTTACCAAGAGAAT
ATTTAAATTGGCAATCTAGCCACCCTGAAACATTATCATACCCCCCAACTTCTTAACTAATATTA
TTACTGCATTAGAAGTTGAGGTTGAGAATATATCTGAATATGTGCACTTGCCAACTTTTCTTCCA
CACCATCACCATCAAAAGCTTCAGCAACAACGACGACGACAACCTGCAAATGTCACAGCCATTGACG
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AATTGATCAAAAAATCCATCCCTGTTGAGAATCACCTAATGTATTTACAAGACCTTTTGATTCCG
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ACACCACACAATCAGAGTTGGAAATCATGGTTCACTCAGTATGGTGGAAGACCAGGTGGGTTTGGGA
CTTTTAAGTCTGCAGATGATAACAATAATAAACAACAACATAGCAATGGCGGGAAAGGATATC
AGAATGCGAGAAAATATGGTATTTTCAAGGTTTGTGGCCTTTAATACTCATGAGGAAGCAGTTGATT
GTTTAGCTTTGAAATGGGAGAGTGTGAATGATCGTCCTATTGAAGTTCAAGCGTCTTCTAGTAAAG
TGTTTGATATGGCCATGGATAAATGTTGTTGACTCTGTTCCCACTCTCAAAGAACAGACCTAGAC
CCGGGGATTGGACTTGTATTCTTGTGGGTTTCCAATTTCCAGAGAAGAACACACTGTTTCAGGT
GCTCTTTTGCGGCAGTGGCGTTTCAGGATGTTTAAACAGTAATACAGGCAATGCCAACGGTAATG
GCAATGTTAGCGGCAACCACAACCACAACCAATAGTGGAGCTCGCCGTGGCATGAATTTACAGC
CTGCTCAAGCTAATGAGAAAATGGAACAGGCAATATTAGTATTCTTCTTACAACGATCCAATCA
AGGGTCCAACAGGTAATGTCATAATCACCTCAACAATTTCTGAGACCAATTTACTGAACAACACTA
ATCTTAACAACAACAATCATCATAGTAATAATTATCACAATAACTACCATCACCACAACAATA
ATAACAATCATGGGAATAGCAATGGTAACACCATAACATGGTCGTTCCCATTAACAATAGTGTTC
CATTTAGAGCAGGTGACTGGAAATGTGAAAATTCATGTATCACAATTTCCGCAAAAATTTGTGTT
GTTTAAATGTTGGTGTGCGCAAACCTGCTATTAACAATCAACAAAATAATAACAATTCATTGCGTGA
ATTCAACGGCCGCTGCCATAGTGTGAGCAACAGCCAGTGGTCAACCTTTAAACTTGAATAATAATG
CATTTTGAACCTTCAGCAACAACAGTCTCAGTCACAACCCCAAGGTCAGCACCATTACAACCAAC
ATTCCTCGTAACAACAATGCTTCTGGGGCATCAAAGTTCAACAATGGCTACAACCCAAAGAATCAGT
ATTACAATAATAATAGCAAGAATCTTAGCAACAATTTTGGTCTTAATGGTATGCATCAGCAAAACC
AAAATCAAATTTTGATGTATTACACAATTTGCAACAACAACAGCAACAACAACAGCAACAACAGC
AACACAGCAACAACAGCAACAACAGCAACAACAGCAACAACAGCAACAACATGATTTAA
ATGGAAGTAGCTCTTCCCATCAACTGAACTTCAATTGAATAATACTTGA

YDL167C_homolog 729aa (SEQ ID NO 322)

MSDIYIIHISTTCDDSPFTVKDSSELIEFAWETVDSVTLETLYKGSNLVRPTNTPITPYCSKIH
RITWDNVKNAGSFKDAITNFDQYVQEHII SKKKEFSIVMFDISKLRVQLVREARDKSVVLPSYLQH
PRIFDLPREYLNWQSSHPETLSYPPTSLTNIITALEVEVENISEYVDLPNFSSTPSPSKASATTTT
TTANVTAIDVLSSETEPNGKVIANLHAKIAKQLIKKSI PVENHPNVFTRPFDSAQDITAFTSERSK
VLYLSNLPNDTTOSELESWFTQYGGRPGGFWTFKSADDNNNNNNNNNSGGKGYNARKYGISGFVA
FNTHEEAVDCLALNGRVLNDRPIEVQASSSKVFDMAKDLLLLTSFPLSKNRPRPGDWTCLSCGFSN
FQRRTHCFRCSFAAVAFQDVFNSTGNANGNGNVSGNHNHNHNSGARRGMNLQPAQANEKIGTGNI
SIPSYNDPIKGPTGNVTNHLNSETNLNNNTNLNNNNNHHSNNYHNNYHHNNNNNNHNGNSNGNTIH
GRSHYNNVFPFRAGDWKCENCMYHNFKNLCLCKGVAKPAINNQQNNTIHSVNSTAAIAAATAS
GQPLNLNNNAFLNLQQQSQSQPQQQHHYNQHSRNNNASGASKFNNGYNPKNQYYNNNSKNLSNNF
GLNGMHQQNQNLILMYSQQLQQQQQQQQQQQQQQQQQQQQQQQQQQQQQHDNLNGSSSSSHQSKLQL
NNT

YDR238C_homolog 3359bp public: 1..1467/1469..3040/3042..3359,

PathoSeq: 1468/3041; CDS: 501..3356 (SEQ ID NO 323)

AATAGCATTTGAACAAGAAGAAGAGGACAACGATAGACCAAGGTTGGTTTTAGCCAATCCTGATTAT
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AGGACTTGTTTTTTTTAGTAAGTGTGATCTCTTTTCTGGGTGTACATTTCCGATAGCCAACCA
GGTTATATTTTAGCAGTTTATAGACAGTGTATCGATGGGTAATATAAATAAAAGCTCATTGAATA
CTATCTAGTGAAAAGTCGTGTGTAATTCGATTTGAAAAATATAAAACCATACACGTAAATGAAATG
TGTGTGAAAGTACAACCAACAACGAAAAAGAACAAAAAATGTTGTCCGCCAAAAAAGG

AGAACAACAAATCAAAGTTTCAAGACTATCTCAAATCTTGTGTGTCACCATAACTATCAATTGTTCA
CCTCTTGAACCAACATCAAATTGAATAAAGCATAGGATCATGAGTGACAGTGGTTATACATTAATCT
ATGAGCCTAATACGGCTACGAAAGTATCTGTCAATGAATTTAAAAATTTGTTGGAAAAGGGTAAAG
ATGATGTGAAAGTAGATACCATGAAGAAGATTTTGATTACCATATTAATGGAGACCCCTTACCTG
ACTTGTGTGATGCATATAATCAGATTTGTTCATGCCCTCCAGAAATAAAGAATTGAAAAAGTTGTTGT
ATCATTATTGGGAGGTTTGTCCAAAAATGGATGAATCAGGTAAAAATGAGACATGAAATGATTCTTG
TGTGTAATGCCATCCAACGTGATTTACAGCATCCAAATGAATATATTCGAGGCAATACTTTGAGAT
ATTTGACGAAATTGAAAGAGCCAGAATTATTGGAAACTTTAGTTCCCTAATGTCCGTCAATGTTTAG
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AGGACTCTATTCAAAATCCAGCTTTAAAGCAACAATATGCCCCAATTAATGACAGAAATTATTGAAA
GCTCTTCAAATGTTGTTATGTATGAAGCTGCTAACACGTTGACTGTTTTGACTTCAAACCCACAAT
CAATTTTGTGTTGGCAGGAAACAAGTTTGTGTAATTGGCTACTAGAGAGTCTGATAATAACGTTAAAA
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TAGAAATTTTACGAGGTTTATCTTCCCAAGATTTGGATGTTAAAAAGAAAGCTCTTGATGTTACTT
TACAATTTTATCACCACCAGAAATGTTGAAGATGTTGTTAAGTTATTGAAGAAAGAATTGCAAGTCTA
CAGCTTTATCCAATGATGACAAGAATGCAGATTTATAGACAGTTGTTAATTAATGCCATCCATCAAT
TGGCTATTAAATTTGTGGAGGTTGCTGCCAATGTCATTGATTTATTGTTGGATTCTATAGCCGATT
TGAATACCCTGCGCCCTACGAGGTTATCACATTTGTTAAAGAAGTTGTTGAGAAATTTCCAGATT
TAAGGGACGCTATTTTGAAGAAGATTGATTTTGGCTTTGCCACATGTGAAAAGTGGTAAAGTTTCC
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ATACTGAGGAATCACAAGAGGAAGAAACCGAGTATGATGGTAAACCTCGCAGAAAGGTTCCAGTTG
TATTGCCAGATGGTACCTACGCTACTGAGTCAGCATTGACAAGCGAAACAACCTGACTCTTTGGA
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ACGGATTAAAAGCAGAGCATTGTTGATTGTTGCTGATTTTGAAGATTGGGGAATCTAGCTTGG
TTTCTAAGAAAATTGATGAGGATTCTGCTGACAGAAATTTGTCTTACATCAAGATTTTGAACGATG
AAGAAGACCTTCAGGAAATCAAGACAAGCTTCCCTTGAAGATACTAAAGATGCATTTAAAGCACAAA
TTAATAATGCTGAATTGAAGAAAGCAGAGCAATTGGCTAAGGATTTGCATGATAACGCTGAACAAA
TTGACGATGCAATTGTTTATGACAGTTGGATAAAGATAACAAAAAGAGTAAAGCTTCTGTGGATG
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TTATACAAATTGACTGGGTTTTCCGATCCTATTTCAGCAGAGGCATTGTCAAAGTTTCAATACG
ATGTTGTGTTAGATGCTTGTCTAGTGAATCAAACCACAACCTACTTTAAGAAACTTATCAGTTGAAT
TTGCTACATTGGGTGATTTGAAAGTGGTTGATAAACCAACTACCGCAAATATTGGACCTCATGGTT
TCTACAAAGTTCAAACAACATTTAAAGTTACTTCGCTGATACTGGTGTTCATCTTTGGTAACATAG
TGTATGACGGTCAACACTCGGACGATTCACGTATAGTTATTTGAATGACGTTTACGTTGACATTA
TGGATTACATTAAGCCAGCCACTTGTTCAGAAAGTCAATTCCGTAATAATGTGGAACGAATTTGAAT
GGGAGAATAAGATAACCATTAATCACCTATTGAAACATTGAAAGAGTACTTGGATGAATTAATGA
AGGGTACAAATATGCAATGCTTGACACCGGGTGGGTAATTGGAGAAGAATGTCAATTTTTATCAG
CAAACCTGTACTCAAGGTCAAGCTTTGGTGAAGATGCATTTGGCTAATTTATGTATAGAGAAACAGA
GTGATGGACCAATAATTGGTTCATGTGCAATAAGATCAAAAGGTCAAGGTTTGGCTTTGTCAATTGG
GTGATAGAGTAGCTTCCATTTCAAGAAAAGGTAAGAAGGCAACTATTGCTCGTGTAA

YDR238C_homolog 952aa (SEQ ID NO 324)

MSDSGYTLIYEPNTATKVSVNEFKNLEKGDVVDTKMKILITILNGDPLPDLMLHIIRFVMP
RNKELKKLLHYWEVCPKMDSESGKMRHEMILVCNAIQRDLOHPNEYIRGNTLRYLTKLKEPELLET
LVPNVRQCLEHRHAYVRKNVAFALWSIHKVSDDLAPDADELIYRFLYEENDSVCKSRNAFVCLGDLN
REAALQYIQDNISVIETLDPLIQAFIEFIKKDSIQNPALKQQAQLMTEIIESSSNVVMYEGANT
LTVLTSNPQSILLAGNKFVELATRESNNDVKIITLERINQLHKQHPGVLQDLSLEILRGLSSQDLD
VKKKALDVTLLQFITTRNVEDVVKLLKKELQSTALSNDKNDYRQLLINAIHQLAIKFVEVAANVI
DLLLLDSIADLNTTAAVEVITFVKEVVEKFPDLRDAILRLILALPHVKSGKVFRGALWVIGEYALE
ESLIQESWKYIRGSIGEVPIIASELKSKRRDTEESQEEETEYDGKPRRKGPVVLDPDGYATESAL
TSETTDSLESDSKTPIRKQILAGDFYLGAVLASTLVKLILRLQSLKQTQEKILNGLKAEALLIMVS

ILRVGESSLVSKKIDEDSADRILSYIKILNDEEDLQEIKTSFLEDTKDAFKAQINNAELKKAELA
KDLHDNAEQIDDAIVFRQLDKDNKSKASVDDVAAAAGSNELKKENLSSRLNKIIQLTGFSDPIYA
EAFVKVHQYDVVLDVLLVNQT'TTTLRNLSVEFATLGD LKVVDPKPTTANIGPHGFYKVQTTIKVTS
DTGVIFGNIVYDQHSDDSRIVILNDVHVDIMDYIKPATCSESQFRKMWNEFEWENKITIKSPIET
LKEYLDELKMGNTMQCLTPGAVIGEECQFLSANLYSRSSFGEALANLCIEKQSDGPIIGHVRIRS
KQGLLALSLGDRVASISRKGKATIARV

YDR294C_homolog 2270bp public: 1..278/280..2270, PathoSeq: 279;
CDS: 501..2267 (SEQ ID NO 325)

GTTTGATCACATGTGTTGTGAACACTCGGGTAATACAAAATAGTGAGAGAGAAGAAGGGGAAAAAA
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AGCAAAGTTAACAAGCACAAATTGTCATTTAACTTAATTGGTGGATTAATCGGGATCAATCTGAAT
TGTTTCCCGTATTGTTTAAAACCAAAGAAAAGGATAATCAAAACTAAATCTTTCATATTAACACT
ACCATTTTGTAGTGGTCAGTTTATATAATTATCCACTGTTCTCTTCACAATTAACAAAAA
AAAGAAAAAAGAAAGCTCTCTCTCCCCCAAAGAAAAGCAAAGGTAATTCCTTCATACACACCTT
TGATATCTTCTCTTAGACTTTTCTTTTAATACTTGCATCAATGGAATATTACTTGTTCATACT
GGAGTTTTCATTGAACATAATATTATTAATATTTATGCTTGAATTGAATTCAATTACGATTC
CTCGGAATTTCACTGAATTTCAACTCACAGCATTAAAGATCTACTATCAACTTAAGATTTTATTT
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TAGATTCTATTGCAAGGTTATACCTATATGTTAGTTCTACGGTGTCTCAATCTTTTCACTAC
CATTATTATAAATCCAAAATTGACAAGGAATTGCAAGCGACTATTGGCAAAGTAGAAGAAGAGATTA
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GATTACCAGGTGTACGTCATCTCATGTGATCTACAAATATGGGTTTGTCTCCCAAGGGGTGAT
CAATAATTATGTACCGTTGCGCAAAATTACGTGAGTGTCAATACTATATTGCAAGTGATGGACGG
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CTACATTAATCAATATTGGGAAACAAGGATACACCAAGTTTTGTTACGATATTGTGCTGGCGTCAA
TGAAAGTTAAACGAGCAATTGAAACTGACCCGATATCTCAAACATTTACAAATTATTGGTGATC
CAATTGGGTGCGTAATTTCTGTTCAACTTGCACCTCAGCAATCGGGAAATTTAAGTATTTACGAGA
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AAGAAGCGGTGGCAATTGCCGAGGAACACAAAAGAATGGAGTGACCAAGCTCCAGGTGATACTG
CTGCGTTATATGGTATAGCTGGCAGTGATACATACAGCAGGTTGGCTGATAGATTAATTGTTGCAT
TTTTAGATACCTTATACAAAATTTGA

YDR294C_homolog 589aa (SEQ ID NO 326)

MLELNSITIPRNFTEFQLTALKIYYQLKILFLATYCAQGSFGLNGSVCLARDIFVGYVVYTQLLKL
YRVLRGYGIVDSIRRLYLVSSTVSSQIFSLPFIKSKIDKELQATIGKVEEEIMKNDPQLLQFPEL
PEQGIDADNVSLDKLQNLKHSWDWINGRVSGAVYHGGENLLSLQVEAYKKYSVANQLHPDVFPVGV
RKMEAEEVVMVLDIFNAPSDGCGSTTSGGTESLLLGLSAREYKGYRGITEPEVIAPVTIHAGIE
KACFYFGMKLHKVDLPVTFQVDVKKVERLINSNTVLICGSAPNYPHGIIDDIESLSKLAVKYNIP
LHVDACLGSFIVSFLEKSKVHGDRKLPIDFRLPGVTSISCDTHKYGFAPKGSSIIIMYRSPKLREC
QYYIASDWTGGMYSPTLAGSRPGALVVGWATLINIGKQGYTKFCYDIVSASMVKRAIETDPIL
SKHLQIIGDPIGSVISFQLAPQSGNLSIYEISDLLTKKQWHFATLQNPALHFAFTRLTVPVVD
LIADLVEATKEAVIAEEHKKNGVTAPGDTAALYGIAGSVHTAGLADRLIVAFDLTYKI

YDR430C_homolog 3605bp PathoSeq: 1..330/1927, public:
331..1926/1928..3605; CDS: 501..3602 (SEQ ID NO 327)
TTCAATTTTTTTTAAAAAATAGCAAAAAGGTATTTCTTAGAAATTGAAAAAAAAAATCACAAAA
AATTTATAAAACCGGATAGGGCCGTTATCGCAGGACGTGTCCCATGATCAATCTACAATGAAATGA
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AAAACCTTCCTTTTCCCTGGTGATAAAATTTTGACTTTGAAGCATAAAGAAGACAGAGCTAAAAA
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ACCCAGTTGGTCTAAAATTCGATGGTTACGAAGTTACCCAAACATCACCTATCCCAGAATTTTCCC
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CCAACAGGTCTGTTGAGTAACTTTATGAATGCAATGACAGGCCATGATTACACATTTTATCCATTTG
CTACCACCAATTCAAAGGATTTTGAAAACCTTAATGGATGTGTATTTATCGTCAGTGTTTGAACCGC
AATTAACCATACCGATTTCTTGCAAGAAGGATGGAGAGAATAAGAAAATCAAATGTTTCATGACATAT
CGTCCAAGCTTGAATTCAGGGAGTTGTATATAATGAAATGAAGGGCCAGTATTCGAACTCTGCAT
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TTAAATGGAAAATATTGAGCTCATTTATGTTTGTATGGACACAACCTCTCCTTTCTATCAAGAGTTAA
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AGATATTGTCGCATTTTAAAGAAGATTATAAACAAAATGGTTTAAGGATCTTTAAAGAATTATTAG
AAAAGACATTGTGTAACCTCATTCGCAAAAATTTAAATTCACCATGGAGCCAAGAGAAGATTTTA
CCAAACAATTTGGTAAAAGATGAGAATTTGATGATCGAGAAAAGAGTAAGTGAACCTCACAGAAGATA
ACAAGAAGGCAATCTATGAGCAAACTTGAATTAGCTAAATTACAATTGGAGGATCAAATACAG
AAGTTTTACCCACATTGACTATTGATGACATTCCAAAGAGAGGTGATTTTTATGCCATTGATTTGG
GCCAAGTAAATAAGAAAGTTGTACATGAAAGGGTAGTTGATACCAATGGCTTGGTTTATGCCAACG
CTTTAAAGATATTTCTTATTTACCCACCAAACCTTTACAAGTACCTTCCATTGTTTAAACAATGTT
TGACGAACCTTGCTGGAACAGAAAACACACCCATTACGGAGTTGGAACATAAATACAAATGTTAA
CTGGCGGGATAACATTTAGTTCTAAAATATCGACTGACCCCTATAATATTGAGCAACTAAAATTAC
AGTATGTGTTAAGTGAATGGCTTTGAAAGAAAAGTCATCCTCAGTTTATGATTTATGGTTGGAGA
TTTTAACTACTACCAAATTCGACACCAGTGATGAGGTATTAGAAAAGTTGTCAAGTTTGTATTTAAA
ACATGGGACAAAACCAAATCAATAATATTGCTGATCGCGGTCACTTCTTATGCGGCTGCTGTGAGCT
CACTGAAATTGACACCGCTGAAATACATCAGTGACATCGTTTCAGGTTTGAGTCAAGTTCAATTTG
TAATGGAGTTGAACCTCCAAATTAGAATCAGAAGGGAAAGAGTACTTGGCCAAAGAGATTATTCCGA
TATTGCAAGAAATACAAAAGTATGTATTGCAAGGTGAATTCAGGTATAGACTAGTTGGAATCAAG
AGATTATTGTTGAAAACGAAAAGCTTATTGAGAAATTTGATAAGGATATTTCTTCGAACAGACCAA
CTTTATCGTTAACAGTAACAGATGGTTTACTGGCATTGTTGAACTCATTCAATTACAATCATACAA
GTGAAAATGCTTAGTTAACTTACCATTTCAAGTGGGATACTCTTCATTAGGTAAGATTGGCTCTT
CGTATTTCATCAAAGGATGGTGTCTTTTACAATATTATCTCAGTTATATTCTTTAAAAATCTAC
ATTCCAAAATAAGAGAAAGCAATGGTGCATATGGAGGTGGTTTGACATATGATGGGTGAAACGGGA
CATTAACCTTTTATTCGTATCGTATCCTAATCCTGTAAAGTCGATTCAAACCTTTTAGAGATTCCT
TACTGTATGGACTTGATGCTAATTGGAACGATAAGGATTTACAAGAGGCTAAGTTGCGGGTTTTCC
AAAGCGTCGATGCTCCAATTAATATCTCTTCTCAGGGTCTAGTGCCTTCTTTGAAAATATAGATG
ATTACTTGAGACAGGAAAGAAGAGAAAACCTTTTGGGTACCACTTTAAAGGATCTCAGAGATGTGA

CTGAAAAGTATCTTGTGATAACCAAAACAACCTTGTCAGTGTATTGGTGACAATGAAATTTTAA
ATGTCGATAATAAATGGCAAATTAGAAATTTTCAAGTATAG

YDR430C_homolog 1034aa (SEQ ID NO 328)

MLKTRLKQSR AISRVRRYACSHPI SPNLDKYPVGLKLHG YEVTQTSP IPEFSLTAVSLKH TESGA
THLHLDSPNDSNNVFSIAFKTNPPDNTGVPHILEHTTLCGSKKFPVRDPFFKMTNRSLSNFMNAMT
GHDYTFYPFATTNSKDFENLMDVYLSSVFEPQLNHTDFLQEGWRIENQNVHDISSKLEFKGVVYNE
MKGQYSNSAYYFYIKFLESITYPSLNNSGGDPKKIVDLSYEGLLLEFHSKNYHPSNAKTFYTKLPLE
DSL SKISKYYESFEKKVSSVDVKQPIFSTDKSEIFDVTIPGPVDTMNGKETSEQYCTSI TWNLGNP
LDPNMQYDIFKWKILSSLLFDGHNSPFYQELIESGYGDDFSANTGLDSTTALLSFTVGLNYLTKQK
VDNFNEKVMEIINNKKIPELSNEESSSYHGRIDAILHQIEIGFKRHKPDFGGLSSIVPSWVNGV
DPIDTLQVEKILSHFKEDYKQNGLRIFKELLEKTL CNPHSQKF KFTMEPREDFTKQLVKDENLMIE
KRVSELTEDNKKAIYEQNLELAKLQLEDQNT EVLPTLTIDDI PKRGDFY AIDLQVNNKKVVHERVV
DTNGLVYANALKD ISYLP TKLYKYLPLENNCLTNLAGTENTPITELETKIQMLTGGITFSSKISTD
PYNIEQLKLQYVLSGMALKEKSSSVYDLWLEILT TTKFDTSD EVLEKLSVL IKNMQNQINNIADR
GHSYAAAVSSSKLTPSKYISDIVSGLSQVQFVME LNSKLESEGEKEYLAKEIIPILQEIQKYVLQGE
FRYRLVGNQEI IIVENEK LIEKFDKDISSNRPTLSLT VTDGLSALLNSFNYNHTSENVLVNLPFQVG
YSSLGKIGSSYSSKDGASLQILSQLYSFKNLH SKIRESNGAYGGGLTYDGLNGTLNFYSYRDPNPV
KSIQTFRDLSYGLDANWNDKDLQEA KLRVFSVDAPINISSQ GASAFFENIDDYLRQERRENFLG
TTLKDLRDVTEKYLV DNQNNLVTVIGDNEILNV DNKWKQIRNFQV

YDR450W_YML026C_homolog 1366bp public: 1..1366; exon 1: 501..548,
intron 1: 549..976, exon 2: 977..1363 (SEQ ID NO 329)

TTAAGAACTAGCAGATG TAAAAATG TTTTATGTCATTATATAATTTGTTAATACATGTATATAGATT
TTTTAATGAATGTATTCCCTAAATAGAACAGAAATATGATGCTGTTACAGCAAAAACCTGGTTTGAG
TATTGGAGAATGTTATAAACTGAAATTTGATTTACAACCAAAACCCGTGTACAGTGTAAAGTAATTA
GGGCTTTTAGGGCTTTCTATATACAGGCACCAAGAATTTTTTTTTATGGGCGATAGAAATAATGTAT
GCGCGCGATTCTTCTCTGCTAGAGGTTTTCTTTTGTATGTCTGTAAACAGTGC GACTCACATAGTT
AAGTAATTTTAAAGCCAGAGATTGTGTACAGTCGCACGCCCCCTAATCACATAGTTAATTTCTCAA
CTTTCTCTCTTTCTCTCTTTCTCTTTCTCCTTAAGGAAAAAAAATTTATTTCATTTGTTGAAAAT
TTTTGTATAGTTTCAAGTTTAAACACACAGTAATCAAACATGCCATTAGTTGTCCAAGAACCAAGGTT
CATTCCAACACATTTTACGGTATGTGAGTGTATTATAAGATTATTTGAATGAGATAGAAAAGGGTT
AAGGAAGGAAAGAAATTTATCCAAC TACTGTTTGGGAAAGATTAAATCAGAAATTTGAATGCAATGA
AAAACTTTTCAAGAGATGGATATGGAACAAGATTGATTGTTATCAACAAATATAAAGAAAAGC
AATGATTTACTACTGTTTGGGAAAGATT TGGATATGTGTATCAACAATACTACTATTTACTTTGG
AGTAATATGTTTCAATATTTATCAGAGACTTATCAAAATTTATGAGTTTATTATTATTGAAGTTCA
ATACCATCAAGCCTTTT TTTTAAACCATCACTCTATTCAACAATCATTTAAATATTAAGTCTTTTT
TTTCCCTGTTTAAAGTATTCGATT TACTAACATTATGAATTATTATTATAGTTTGTAAACACCAA
CATTTGATGGTAGAATCAAGATCATGTACGCCTTGACCAAGATCAGAGGTGTCGGTAGAAGATATGC
CAACTTGGTTTGTAAAAAAGCCGATGTTGAATTAACCAAAAGAGCTGGTGAATTGACCCAAGAAGA
ATTGGAAAGAATTGTCACCAATTATGCAAAACCCAACCAACTATAAAATCCAGCTTGGTTCTTGAA
CAGACAAAAGATCAAGTTGATGGTAAAGATTACCATGTTT TAGCTAACAACCTTGAATCTAAATT
GAGAGATGATTTGGAAAGATTGAAGAAAATCAGATCTCACAGAGGTATTAGACACTTCTGGGGATT
GAAAGTTAGAGGTCAACATACTAAAACTACTTCTCGTGGTCTGTAA

YDR450W_YML026C_homolog 145aa (SEQ ID NO 330)

MPLVVQEQQSFQHILRLNLTNIDGRIKIMYALTKIRGVGRRYANLVCKKADVELTKRAGELTQEEL
ERIVTIMQNPTNYKIPAWFLNRQKDQVDGKDYHVLANNLESKLRDDLERLKKIRSHRGIRHFWGLK
VRGQHTKTTSRGR

YDR471W_YHR010W_homolog 1327bp PathoSeq: 1..1327; exon 1:

501..530, intron 1: 531..946, exon 2: 947..1324 (SEQ ID NO 331)
ATAGTTATTACAATATAATAAAGCAAATAAAATAAAGAAATGATAAAGAACCATATTAACAAAGTT
TGAACGTGCTGTAAGTAAATCTTGATACGAGAATATTCATCTTGAATATTTCTAAACGATACTG
GTAATACCTAATTCATTTGGTGTGGTGCATCACGTGCTAGGGCTATAGCCCTAATAGTATATGCA
GTCGCATACATTAATTGGTCATCTCATAAGTAAATTATATAATGTATAGTGTGCGCGCACTGTAAT

YDR486C_homolog 1157bp PathoSeq: 1..1157; CDS: 501..1154 (SEQ ID NO 333)

TTCCAGTCATTCCGAAATGCATAAGCAAGACGTTAGTTGTATTGTGGTTGTTTAGTCTAATCCAAA
AATACTTGCCATGACGACCCACTGAAGTAAACAACCTGCATTTGTTAAGGCTTTTCTCATCTTATTC
ATTCTTTTTCAGCATCATCTCGTATCTTTAAGCAACGGGAATAGCAATGGATCATGTAAACAAATTCA
CTTTCGTGATTGAAAGCCCCAAAATGTTTCGTTTAAACAACGCACACATATGTAAACCTTAAACCG
AGTTAGTCGTCAAGAAAATAATTCAGTGTTTAAAGTCTGTACCTTTAAGCGTCAAACGTACTTCTGCA
ACCTCTGGCATTGAGTGTAATTTAAATATTCATGATAATCTGGAACACAAGCTACGAAAAAAAAA
GAAAAAGAAAAATAGTACGAGTTCCTGGTGAGATAAATAATGGAGAACACTTTTTTTTTTCTCTTT
GGAGGTTTTAGAAGGCAAAACCAAATCTAGACAAGGAGATGAACAGATTATTCGGAACGAAAAGCA
CTGCGCCCAAAACCATCTTTGAATGATGCAATCAAGGGAATCGATGAAAAGAGTGGGGTCTTTGGATG
TTAAATTAAAGCAAGATCAACTCGGAATTATGCCACATACCAACAAAAGATAAGCAGAATGAGAGACG
GACCCGGGAAGTCGGCATAAAACAAAAGCAACATCAAGTTACTAAGACAGAGGAAGCAGATAGAAG
CTCAAAAAGGATCAGTTAGAGAATCAATCTTGGAAATATGACACAAGCTTCCATGACAACAGATAA
TACAAAATACCATGGTCAACAATAAATGCAATGAAAACAGCCAATAAACTGTTGAAACAAACTTATG
GAAAAATTAAATATCGATGAATTGGAAGATCTTCAAGATGAAATGTTGGATTGATTGATAAATCAA
ATGAACTACAGGAGGCACTTCTGACGAGCTATGATGTACCCGATGACATCAGTGAGCTGGAGTTGG
ATGCTGAATTAGAAGCTCTTGGCGAAGAAATTTGAAATGAAATGGCAGAGAGTGGGATAG
GTGCACCTAGTTACTTAATGATACAGAACCTCAGCAGCAGATAAATTGCCTACATTTATTGACG
AACCAACCAAGAAGAGCTCAAAAAATCGCAAACTAG

YDR507C_homolog 4550bp PathoSeq: 1..1424, public: 1524..4550; CDS: 501..4547 (SEQ ID NO 335)

GAATGAGATTTTTTTTTTACTAAGGGTGCACCTACTACTAGTTATTTGTTTTGTTGTTGACGATCA
TTAAAGAAAAAATTTACAGTATACACAAAAACCTTTACTCTGCTGTTTTTTTTTATTTTATGTTT
TTGGTTTCAAAATTTATTAAGAAAGCAAAATATTTAGAAATTTATATTTTTTGTTTTTT
TTTCTTTTGGTTTCTTTGAATTTTGAACCAATCCAAATTTTTTTTGAAAAATTTTCTTCTTCT

TCATTTGTTGACTTTTGAAGTTTATTCATCCATATTTCTTCAAGTTAAAATAGTGTTCATATCT
GTCCAACCAAGAAGAAAACCAATAAACAACATCAATTTCCAACTTTGTTTACATCAAAACAGAAACAA
AAAACAGATAATTTATAGACACCTTCATTCATTCGTTATTTTTTTTCCAAGTACTACACGTCTTTAT
TTTTAATACATTTATCATAAACAAAATTTATATCAATAATGCCACATTCAAGACAACCTTCGATAT
CGTCATCGATTATGTCCCAATCAAATCATAATCATCCACAGAAGATCGGACCTTGGAAATTAGGTA
AAACTTTAGGAAGAGGTGCCACCGGTAGAGTCTTATAGCTACTCATCAAACCTACTGGTCAAAAAG
CTGCCGTTAAAGTAGTTTCCAAATCCGAATTACAAGACGAAGAAACCGAGAAAAATGGAGATGGAT
TACCATATGGTATAGAAAGAGAAAATTATTATAATGAAATTATTAACATCATCCTAATGTTTTGAGAT
TATATGATGTATGGGAAACATCTAAGGCTCTTTATCTTGTCTAGAATACGTTGAAGGTGGAGAAT
TATTTGATTTATTGGTGGAAACGTGGTCCATTACCTGAAGTCGAGGCTATCAAGTATTTCCGTCAAA
TCATATTGGGTACGGCTTATTGTCTATGCTCTTGGTATATGTACAGAGATTTAAAACAGAGAATT
TGTTACTAGATTCTCAATTGAATGTAAAATTAGCCGATTTTGAATGGCAGCTTTAGAAAGTAACG
GCAAATTATTAGAGACTTCTTGTGGTTCACCTCATTATGCTGCTCCAGAAATCGTTAGTGGATTGA
AATATCATGGAGCTGCTTCTGATGTTTTGGTCTTGTGGGGTTATATTATTTGCCTTGTGACAGGTA
GATTACCCTTTGATGATGAAAATATTAGAAATTTACTTCTTAAAGTCCAGGCTGGTAACTTTGAAA
TGCCCCGTTGATGAAGTTAGCAGAGAAGCTAGAGATTTAATTGCTAGAATGTTAGAGGTTGATCCTA
TGAGAAGAATATCTACTGAAAAATCTTAAGACACCCATTGTTAACCAAATACCCAATGTCAAACG
AAGATTTAATCAGTGAAAAATCATTACCACATCCACATACTGGTTACAAATCTTTAGGGTCAGTTA
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TTGTTGATTGTCTTTTGAAGATGGATCCAATCCAGAAAAACATTCTATGCATTATTGATGAGAT
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AAGTGGTACGCAGTGGGTCCAAATACAGTCTTAATGGAACCCCTAGAAGAAAAAGAGCCAGTCACA
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GAAACTCCGTTGCCAGACATCTGTGGCTTCCTCGGCCAACAAATCTCCTCGTAAATCACCATAACA
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AATCCCCAACTAAATCTCCTTACGGAAGAAGATCAAATTCACAAAGACAATTTGAAAATGAACCAT
TAAAGGCAAAGCCAAGAAATATTTACAATGAGATTGTTGATGCACAAAGCAACTTTTCTCTACCTC
CATCGCTTCCACCTTCTTACCTTCAAAAGATTCTCGTTATATGATCGATGAACCCAATCAACCCC
AGTTGCAACAACCTGCTTTAAGTCAAGTCCCTGAAAATCCTATTGTTGATGAATCCCCTGATTTAA
TGCAGTCAGCAAAAATTTCTAGTGGAAAGAGAAATTTCAATAATAGGAAAGAAACAACAACAGCA
ACAGCAACAAGAGAATGTC TAAGAGAAAATCAATTCGTGCATCTATGACCACGGGATTGAAAAGAA
ATTCCATAACCATGAAATTGTTATCTACTTATGCTAAATATCAGGTGATGACGACTGGGAATACA
TGGATAAACAACAAAAGAACATCGGCTACTTTTGCAGCATTGTGTGACAAAATATTTAATCAAG
AAGACTATGACGAAGAAGACGAACAATTAGTTGATCCTGAAGAAAAGGAAGCCAAGGAATATGAAA
GGTTAATGGAATTGGAAAGAAAGAAACATGAAGCTGAGTTGAAAGCTAGAAGAGAATTAGAAAAGA
AGAAAAGAAGACAAAAGAGACGTTCCATTTTGAGTTCTAAGAAATTAAGTATTATTGTCAAGAATG
ATGCTGATCCAAATAATAGTGAACAAGAGTTGGTTCGATGAAGGTATAAAACAACCAAAACGTCAT
CCAAAACTTGACCGCTTTAAGAGCATTATCTGAAGGAAATCATGCATCTGAAGAATTGACATTGG
AAGACGTTGAGAATTTGAAGAGACGATCAGCATCACAGCCGTTCCAAAAAGAAGACAAACTCCGG
TTTTGACAAGAAGACCTGTATCAAGATTAGATCCATTATGGCAAGCACACGAGAATGAACAGTTAG
ATAGAGCAAAAGATGCCCTTGGAAACAAGATGGAGGGATTACAAAAAGAGAAGTTCTACTGTTAGTC
GTA AAAAAGTCAACAGAGAGTCGATGATATCAGTTATGGATGATATTGTTGAAGAGGACCAAGGCC
GTGTCAACAGGAGATCAACACGAAACACTTACTATGAAAGGGAAAGAGACTATGAATTACCAGAAC
CAACTGTGGAAGATTCCAACCTTGACTGATGACTACATGACAGAAATCAGAAAATCAAGACTTTTGA
ACAGTCAGTTAAATGTTAGGGATCCACTTAATGAAAAAGAAAATCTGAACCCAAGACTCTTATTA
GCAATGTTCAAATACCGAGTGT TACTAGAAAATCAAGAAATTTCACTACTTCCAACAAAAGGTTGT
CGGTATTGTCTATGTATTCAACAAAGGAATCATACCGTGATTTGAATTCTATAATTAACCTACCAG
ATGAAAACCCCGAACAGCATCAAAACATGAACAAGCCAGCGTTACGAACCAAGTATTGCTGATCGTT
TGGATAAAGCTGGATTGGCTGAACCAGAATATGAAACTGAGACTGATGGTGAAGATAAAGTGTCTG
TTATTGATTGATGATCATTTAGCTGATAGAAGGACTTCCTATTATGATGGATCTGGAAGAGAG
CATCTGAGCTTTCAACAACATAACGTTACAATGTTCAATTCAGTTTCAAAAAAGACCAAAATCCA
AAGTTCCTGATTTGCCAAAGAATGATTATGATGACACATTTGTTCAGTAATAGTGATGAAGTTCATA
AGCGTCAGTATAAATCGATGGTTTTCTGATGAGTCTAGTGCATCTGATGATGATTTTGATAAGATTA
AATTACCAGATGGTAAATCAACTAAATCTTCCATTGATGAATTGGCTAACGGCACGCTTACAAGTG
GTCATAGAAAACCAAAGATAAGACATTTCTCAACCGGGCCAGAAATGTTGATTCTCATTTGAATG
GAGGTATTGAGTCGTCTCAACCAATGTCTAAAGTTTCGTGGTAACAATTCAGTGGTCATGATGATA

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GTGTTCCACCACCACCGCCAGCTCACAAGGTGAATAAAAAACCATTTGGATGATAAGACGAATTTCC
CTCCACCAGAAGTGGATCCAAAAAGAAAAGGTTTATTTTTAGAAAACTTTCTTGGGGATCCAAAA
AAACCATTTGAAAATAATACAAACGCCGCCACTAATACCACGACTCAACAACAATTACCAAGTCCTG
CTGAATCAAAAAGAGGAGAAAACCAAAAAGTTTATTTTTAGATGGTTTTTCGTCATCTAATACTCCAT
CTGCTGCTGAAATTAGAAAATTCAACACCATTTTACCTAAACATGAAATGTCTACTGCTTTATTTG
CTTTATTGAATTTCTTGGTCTAATTTTGGTTTGAAGATTACGGAATGATCAAGTTGGATATTATA
TTACTGGTGTCTATTTCTAAACATAATTCTTTTAAATTTAAAGAGTTGTAAATTTAGAAATTAAGATTA
ATCAAAGAGATTTTAAATCAAAAATCAGAAATTGTTTGTGTTAGAGTGAAAGGATCTAAAGTTACAA
CTGATACTTTATTTTGTGAAATTGAAAAGGTCTTACTCAAAGAAGGTGGTTTAGATAAATAA

YDR507C_homolog 1349aa (SEQ ID NO 336)

MPHSRQPSISSIMSQSNHNHPQKIGPWKLGLKTLGRGATGRVLLATHQTGQKAAVKVSVKSELQD
EETKNGDGLPYGIEREIIIMKLLTHPNVLRDYDVWETSKALYLVLEYVEGGELFDLLVERGPLPE
VEAIKYFRQIILGTAYCHALGICHRLDKPENLLLDSQLNVKLADFGMAALESNGKLLTSCGSPHY
AAPEIVSGLKYHGAASDVWSCGVILFALLTGRLPFDDENIRNLLLKVQAGNFEMPVDEVREARDL
IARMLEVDPMRRISTEKILRHPLLTYPMSNEDLISEKSLPHPTGYKSLGSVRNIDKQILSNLTI
LWNRDPEEEIVDCLLDGSGNPEKTFYALLMRYKHNQDDNTNNNSPKKSTSFNNKVVRSGSKYSLNG
TPRRKRASHISVSRPTSFQYKSNPGAGATANRNSVARHSVASSANNSPRKSPYKSPYRSPYK
SPSKRYSYNQSPTKSPYGRRSNSQRFENEPLKAKPRNIYNEIVDAQSNFSLPPLPSLPKSDSR
YMIDEPNQPOLQOPALSQVPENPIVDESPLMQSAKISSGKRNSIIGKNNNNNSNKRMSKRKSIR
ASMTTGLKRNSITMKLLSTYAKLSGDDDDWEYMDKQTKRTSATFAALCDKIFNQEDYDEEDEQLVDP
EEKEAKEYERLMELERKKHEAELKARRELEKKRRQKRRSILSSKLSIIVKNDADPNNSEQELVD
EGIKQPKRQSKNLTALRALSEGHNASEELTLEDVENLKRRSASQVPVPRRQTPVLTRRPVSRDPL
WQAHENEQLDRAKDALEQEWDRDSQKRSSTVSRKKVNRESMISVMDDIVEEDQGRVNRRTNRNTYYE
RERDYELPEPTVEDSNLTDYMTIEIRKSRLNSQLNVRDPLNEKRKSEPKTILSNVQIPSVTRKSR
NFTTSNKRSLSVLSMYSTKESYRDLNSIINSPDENPEQHQNMPKALRTSIADRLDKAGLAEPEYET
ETDGEDKVSVIDLDDHLADRRTSYDGSGRASRASTTKRYNVHSSSEKRPKSKVPDLPKNDYDDT
FVSNSEVHKRQYKSMVDESSASDDVFDKIKLPDGKSTKSSIDELANGTSTSGHRKPKIRHSQPG
PEMLIPHLNGGIESSQPMKVRGNSSGHDDSVPPPPAHKVNKKPLDDKTNFPPEVDPKRGKSF
FRKLSWGSKKTIENTNNAATNTTTQQQLPSAESKEEKPSSFFRWFSSSNTPSAAEIRKFNITILP
KHEMSTALFALLNSWSNFGKDLRNDQVGYITGAISKHNSFNLKSCFKRIKINQDFNQKSEIVC
VRVKGSKVTTDTLFCIEKVLLKEGGLDK

YER102W_YBL072W_homolog 1121bp public: 1..1121; CDS: 501..1118
(SEQ ID NO 337)

ACAATACTAGGCACTGTTGAGTGAGTGAGCATTTTTTCTGTTTCTCACTCAGTTAACAAAATAAAA
AAAATTTTCATAATTTAGAAGTTTCATTTACAGTCTTTTTCAATTAACAGTGATACAAGAGTGTA
TGTAAGACAAACATGTACTAGCAACTATAATATGATTTACCAATGATTGGGATCACAATAAATGTG
TTAATATGAATGAGAGAAGGATAGTGAATAAGAGATTACGAAAGAATAGATTCAACAAGTTCAGAA
TGGTATACAATAAAATGGAATTATTTTCAAATATGCAACTATCATTATGACTACTACGACAACAA
TTTAAATCGAGAGAAGATCATTAGATCAAGAGTTGGGAAACTAATACCAAGGAAATATCATTAAGA
ATTAATAGCTTTGCAAAAATTGGTTTTACTCATATTATTTGTTTTAGTTGGAAAGCGATTACATCA
TGGAACAAAGTTTACTAACAACATTGTTATAGGTAAAAATGGGTATTTCTAGAGATTACGTCACA
AAAGATCCGCCACTGGTGCCAAAAGAGCCCAATTCAGAAAGAAGAGAAAGTTTGAATTAGGTAGAC
AACCAGCCAACACCAAGATTGGTCCAAAAGAATTCACTCTGTCAGAACCAGAGGTGGTAACCAAA
AATTCAGAGCTTTGAGAGTTGAAACCGGTAACCTCTCTTGGGGTTCCGAAGGTGTTTCCAGAAAAA
CCAGAATTGCTGGTGTCTGTTTACCATCCATCTAATAACGAATTGGTTAGAACCAACACCTTGACCA
AATCTGCTGTGTTCAAATTGATGCTACTCCATTAGACAAATGGTACGAAAACCACTACGGTGCTA
CTTTAGGTAAAAAGAAGGGTGGTGTCTCATGCTGCTCAGCTGCTGAAGTTGCCGATGCCAAGAGAT
CAAGAAAAGTCGAAAGAAAATTGGCTGCTAGATCTGGTGTCTGCCATTGAATCCGCTGTTGACT
CTCAATTCGGTCTGGTAGATTACGCTGTCAATTTCTTCAAGACCAGGTCAATCTGGTAGATTG
ATGGTTACATCTTGGAAGGTGAAGAATTAGCCTTCTACTTGAGAAGATTAAGTCTAAGAAATAA

YER102W_YBL072W_homolog 206aa (SEQ ID NO 338)

MGISRDSRHKRSATGAKRAQFRKKRKFELGRQPANTKIGPKRIHSVTRGGNQKFRALRVETGNFS
WGSEGVSRKTRIAGVVYHPSNNELVRTNTLTSAVVQIDATPFRQWYENHYGATLGKKKGGAHAAH

AAEVADAKRSRKVERKLAARSGAAAIESAVDSQFGSGRLYAVISSRPGQSGRCDGYILEGEELAFY
LRRRLTAKK

YFL014W_homolog_1 819bp PathoSeq: 1..819; CDS: 419..816 (SEQ ID NO 339)

TTCTCCTGTGAAAAGTTTCGAGATGTAACGTTTCGCAGTAATAGAGAGCCAGAATCCATTTTTGTG
TACTACAGACAAATTCAGAAGTTTCAACTGCTGCATATCGCCTTAAATGACTGTAGCATTCGTCCA
AATTGAGACCCCTCAATTACATTTTGTCAAAAAAATTTGGTCCCTAGTGTGCTATCGATAACGAAG
TGAAGGCAGTTTAGCTTGGAGACATTTAGAGAACCTTAGTTACATCTCATCTTCCGTTTCGAGAAAT
CGTTGATTTACCGTGCAGCGCTTATATTGATTGCTACTTGTTCACGACCACAGCAATATAGCAA
TCATAAATAAATTGCCCCGCGGTTGACAGTGTATATCTTCGAGGAATGGCAACCTTTGCCCCCTC
TCGAAAAACAATATAAATAGAGTCAATTTCTCTAGTAGAGGTAAATTCCTTGAATCTTGTTTTTT
TCGACATACACCATAAATCCCATAGAAAACGCAAAATGTCTGACGCCGGAAGAAAAAACATTTCT
ACTAAAATCAACGAAGCTATAACCCCCGAATCCGAAAAGTCTACCTTGGAAGGGCAAGGAACAA
GTCACCAGTACCCTTGACAAAGCTGTTGGCTCAAATGTTCCAGATAACCAAAAATCTTTCACTCAA
ACTGTTGCAGACAGCGTGCAACAAGGTTCCGATAATGCTAAAGCTGATTTGAAGAAACAATCCGAA
CAAGCAGAGGGCGAACAAGACCCCTTGCTGAAACAGCTCAAGAATATGTCGAGGTTGCCAAAACCTG
AAATTGGAAGGCTGCTGAATACGTGA

YFL014W_homolog_1 106aa (SEQ ID NO 340)

MSDAGRKNISTKINEAITPESEKSTLEKGKEQVSTLTKAVGSNVPDNQKSFTQTVADSVQQGSDN
AKADLKKQSEQAEGEQRPLSKQLKNMSRLPKSKLERSNT

YFL014W_homolog_2 884bp public: 1..884; CDS: 501..881 (SEQ ID NO 341)

CCTTCTCCTGTGAAAAGTTTCGAGATGTAACGTTTCGCAGTAATAGAGAGCCAGAATCCATTTTTG
TGTAATACAGACAAATTCAGAAGTTTCAACTGCTGCATATCGCCTTAAATGACTGTAGCATTCGTG
CAAATTGAGACCCCTCAATTACATTTTGTCAAAAAAATTTGGTCCCTAGTGTGCTATCGATAACGAA
GGTGAAGGCAGTTTAGCTTGGAGGCATTTAGAGAACCTTAGTTACATCTCATCTTCCGTTTCGAGAA
ATCGTTGATTTACCGTGCAGCGCTTATATTGATTGCTACTTGTTCACGACCACAGCAATATAGC
AATCATAAATAAATTGCCCCGCGGTTGACAGTGTATATCTTCGAGGAATGGCAACCTTTGCCCCC
TCTCGAAAAACAATATAAATAGAGTCAATTTCTCTAGTAGAGGTAAATTCCTTGAATCTTGTTTTT
TTTCGACAAACACCATAAATCCCATAGAAAACGCAAAATGTCTGACGCCGGAAGAAAAAACATTT
CTACTAAAATCAACGAAGCTATAACCCCCGAATCCGAAAAGTCTACCTTGGAAGGGCAAGGAAC
AAGTCACAGTACCCTTGACAAAGCTGTTGGCTCAAATGTTCCAGATAACCAAAAATCTTTCACTC
AAACTGTTGCAGACAACGTGCAACAAGGTTCCGATAATGCTAAAGCTGATTTGAAGAAACAATCCG
AACAAGCAGAGGGCGAAGCAAGACCCCTTGCTGAAACAGCTCAAGAATATGTCGAGGTTGCCAAAA
CTGAAATTGGAAGGCTGCTGAATACGTGAGTGGAGTTGTCACCGGTGCTACCGAAGGTGCCAAAA
CCGGCGCTGATAGTACTAAAAAATAG

YFL014W_homolog_2 127aa (SEQ ID NO 342)

MSDAGRKNISTKINEAITPESEKSTLEKGKEQVSTLTKAVGSNVPDNQKSFTQTVADNVQQGSDN
AKADLKKQSEQAEGEAKTLAETAQEYVEVAKTEIGKAAEYVSGVVTGATEGAKTGADSTKK

YGL011C_homolog 1244bp PathoSeq: 1..1244; CDS: 501..1241 (SEQ ID NO 343)

GAAGGGCACCATAATGAAATCGACTCACTTCAGGATTATAATGGTATGAAACATTGTACTTGTAT
TAGTGCCAGGATGATTAGGATCATATATTGGGGTGTCTTCGAGTCTTGGTATCGGTTGTAAACG
TATCTGTTTCACTTATCAGTATCGTCATTTATATTAACTACTTTTCTCCTATGGTTATATATTGGT
AAACAAAGAAACAAAACAACAAAAAGAAGTAGTAGTTTGAATAATGTCATAAAGAAACAAAG
AATGAAAGAATGATTGAATGAAAGAAAAAATATGAAAGTGAGTGCACATAATGTAGAAAAA
TGTCGAATGTCTTGAACCTTACCCATTGAGTAGTTGTTGTTAGTTAGGAGGAAGAAACAACAGAA
AGAAAGAGAGAAAGAAAAATTTGCCCACTACAAATATTCAACAAGTTTCATATAGTAATATAATCC
CAATTGATCATTACTTTATTCCACACAATTCATAAACAATGTCCAATTCAGCAGGTTTGTATAGAC
ATATCACTATTTTTTCTCCTGAAGGTAGATTATACCAAGTAGAATATGCTTTTAAAGCTATCAATT
CAGCAATATCACCAGTTTAGGAATCACAGGTCAAGATTCTGCCGTTATTATATCACAAAAGAAGA

TCCAGATAAGTTATTAGATCCTAAACCGTGCATATATTTTTTAAATCACTCCTAGTATAGGAA
TGGTTGCCACTGGATCAATTGCTGATGCTAGAGCTCAAGCCATGAGAGCAAGATCTGAAGCTACAG
AATTTAGATATAAATATGGTTACGAAATGCCGGTGGAAAGTTTATCAAGAAGAATGGCGAATATAT
CTCAATTGTATACTCAAAGAGCTTATATGAGACCATTGGGTGTTGCTTTAACTTTTTATTCAAGTTG
ATTTTGCCTGATGAAGGTAGAGGTCCACAAATTTTAAATGTGATCCTGCTGGATATTTCACTGGGG
TGAAAGCCGTGGCCACTGGTCCAAAACAACAAGAAGCAACGACTTATTTAGAGAAAAAATTCAAAA
AAACCGATGCTGTTAAAGGAGATTGGCAAAAAACTGTTGAATTTGCAATAATTGCCTTGAGTTCTG
TGATTGGAACCTGAATTCAGAAAAAATGATATTGAAATTTGGTGTGGCCACTGAAGGAGAATTTAGAA
TTTTGACACCAGAAGAATAGACGAAAGATTGATTTCAATAGCTGAACAAGATTAG

YGL011C_homolog 247aa (SEQ ID NO 344)

MSNSAGFDRHITIFSPEGRLYQVEYAFKAINSANITSLGITGQDSAVIISQKKIPDKLLDPKTVSY
IFKITPSIGMVATGSIADARAQAMRARSEATEFRKYGYEMPVESLSRRMANISQLYQRAYMRPL
GVALTFIQVDFADEGRGPQIFKCDPAGYFTGVKAVATGPKQOEATTYLEKKFKKTDVKGDWQKTV
EFAIIALSSVIGTEFRKNDIEIGVATEGEFRILTPEEIDERLISIAEQD

YGL031C_YGR148C_homolog 968bp PathoSeq: 1..968; CDS: 501..965 (SEQ ID NO 345)

CATTGTAGGTACACCTGTTTTTGTCTCAATGTACACACACACGACCAGCAGTAGGAAAAAACA
AATTAAATGAAAAATCATTTTCGTTCAATATTAAGCTTCTTAAGATAACCAACCAATTAATATGTA
TGTGACATACCATATAAATAAAGCTACAAATGGGGATAACTATGTATTTAATGATAAATGAATGGA
AGACCAGAATGTATAATGTTATAAGATAGTGATTTATATTGAAAACACCCTTAAAAAATCAACCA
CCCATCTAACCGTCGAATTGGAATGTCAATTTAGTTAGCATCGAAAATCAACAAAGACATGGGGA
ATCATTTACATATAAAAAATAGAGAGAGAAATACAAACTGCTACGTTATGTTTTGTTTCATTATGTC
TTGTTTCATTATGCTTTGTTTCATTATGTCAAAAAATCTATAGTTACCTACCTCTACATCAATTTATG
GTCTGAAATACTAACATTTTTTTTTTATTTATAGTGAAAAATGAAGATTGAAGTTGACTCCTTTTCAG
GTTCTAAAATCTACCCAGGTAGAGGTACTTTATTTGTCTAGAGGTGACTCTAAAATTTTTAGATTCC
AATCCTCAAAATCTGCTTCTTTATTTCCAAACAAAGAAAGAACCCAAAGAAGAATTTCTTGACTGTTT
TGTACAGAAGACACCACAAAAAGGTATTTCTGAAGAAGCTGCTAAAAAGAGAACCAGAAAGACCG
TCAAGCACCAAGAGCTATTGTCTGGTGCTTCTTTGGAAATTGATCAAAGAAAGAAGAGTCAAAAAC
CATCTGACAGAAAAGCTGCTAGAGACTCTAAATTAGCTAAAGACAAAGAAGCTAAAAAGCTGCTA
AAGCTGCCAGAAAAGCTGAAAAGGCTAAGGCTGTTGCTTCTGGTGCTTCTGTTGTTTCTAAACAAC
AAGCTAAAGGTTCTTTCCAAAAAGTTAAAGCTACCTCCCGTTAA

YGL031C_YGR148C_homolog 155aa (SEQ ID NO 346)

MKIEVDSFSGSKIYPGRGTLFVRGDSKIFRFQSSKSASLQQRKNPRRISWTVLYRRHHKKGISEE
AAKKRTRKTVKHQRAIVGASLELIKERRSQKPSDRKAARDSKLAKDKEAKKAARKAEKAKAVA
SGASVVSQQAAGSFQKVKATSR

YGL043W_homolog 1418bp public: 1..436, PathoSeq: 437..1418; CDS: 501..1415 (SEQ ID NO 347)

AATCTACCATTAGGCAATGTCATATAATTTAGATTACGAACAGCTGATGACGCAGTTTCATTATCT
CCATAATTTATAATGGCATACCCTTTGGATTTACCTGTTAATTCATCAAATAATAACTTCACATCT
AATACTGGTCCAACCTGATCTTGCAATATCCCGCACCTGTTCTTCAGTGTAATCAAATGGAAATTTA
CCTATTGAAACACAAGTGCTTTTACTATCCATATTTAGTTTGAGCTGCCTAGTTTTCCTGATTCTT
GGTAACAAAAAATATAATTTATTTAACAAATTTATCGATAGAATCTCTTCCAAAGTACAACCAATTT
CGATACATTTTTTTCTATGAGATGTTTTTTTCCCCTTTGTCTTTAACTAATGTATTTGGGTACACT
ACCTGAACCTACCAGTTCAGTTCAGTCTAAAAAATTTTTATTATTGTGTTTGTATTACTACCC
TTTGCATATATTACTAATATTTATCTTACCCTTTCATCATGGATACAAAGGAAATAAGATCTACCG
TATCTAATCTTGAAAAAGCAGTAGATGACACCACCATTTTAAAGTTGTTGAATATCTTGAATGATG
GGGTTAAACCATCCGAAAACTCTTGAGAGAAACCAAGTAGGTGTAGCTGTCAACAAATTCAGAA
GTCACGACAGTGCCGAAATCAACGGTTTAGTTAAAAAATGATCAGAAATTTGGAGAGATGCCGTGC
AAGCCGAAAAGAACAACAAAAAGAAGTTAGCAATAGCAGCTGGAACAGGAACAGGAACACCTTCAA
GCTCAGCAATTTGCCCATCATCATCGGGTTCTGGAAGTACAACACCAAAACCATCAGAGTCAACCA
CACCATCGGCTGCCCGTAAAGGTCCAAGAAATCCAAAAACTGACGGTGTAATACTCAATTATACG
AAAATGATACCAGAAATGCATCGGTTAGTGCTTTATACACGTCGTTAGCAGTTGATCGTGACGATT

CACCAAAACACATTTTGAAGATAGCTATTGAAATCGAGGCTGAAGTATACAAGAGCGAATACCTGA
AAGTAAGTGACAGTTATAGAAATAGGTTAAGAAGCTTTACCATGAATCTTCGAAATAAGAAAAACC
CAGAATTAAGAGAAAGAATCTTATCGAAACAAATTTTACCTGCTGCGTTCATTAAAATGACCCCTA
ATGAAATGGCTCCTGAGGCATTGAAAAAGGAAATGAAAAATTGCACAAACAAACTTGTGTTGATG
CTCAAGGTGCTACTGAAAAGAGAGCAGTGACCGATAGATTCACTTGTGGCAAGTGTAAGCACAAGA
AGGTCAGTTATTATCAAATGCAAACCAGATCAGCGGATGAGCCTTTAACTACATTTTGTACTTGTG
AAAATTGTGGCAATAGATGGAAGTTTTCATAA

YGL043W_homolog 305aa (SEQ ID NO 348)

MDTKEIRSTVSNLEKAVDDTTILKLLNINLNDGVKPKSEKLLRETKVGVAVNKFRRSHDSAEINGLVKK
MIRNWRDAVQAEKNNKKLAIAAGTGTGTPSSSAISPSSSGSGSTTPPKPSESTTPSAARKGPRNPK
TDGVNTQLYENDTRNASVSALYTSIAVDRDDSPKHILRIAIEIEAEVYKSEYSKVSYSYRNLRSF
TMNLRNKKNPELRERILSKQILPAAFIKMTPNEMAPEALKKEIEKLHKQNLFDAQGATEKRAVTR
FTCGKCKHKKVSYYQMQRSADEPLTTFCTCENCGNRWKFS

YGL103W_homolog 1301bp public: 1..688, PathoSeq: 689..1301; exon
1: 501..548, intron 1: 549..899, exon 2: 900..1298 (SEQ ID NO 349)
ACATTTATTGTTGGCTATACTTTCCAGTTTAAAGGAATGGTTAGGCGGGTCAGTCTACTTTATT
TTTACTGTAATGTGTTGTGCCAGTGTATGGTTTATCAAGACTAAAGTTCCTGAGACAAAGGGTAAG
CATTCGTACCAGGAAGTCTGGAATTAACGGTAGTTACTTCCAGTATATATGGTGTTCATTGTGTT
TTGTGTCTAAAGTTGCGTTAGGGCTAAAGCCCTAATCAATAGTAGTGTACTTTGTTTGAaaaaaAT
AATACATGCAAAATACTGCATATTAGAAATATAAGGGAATGAAAATGAAAAAAGAATAATTT
TGTAGATCGCATAGTGTGAGCGCGCACACACACAACTTTGTAGTGTCTACAGTTTCTCTCTTTC
CCATACACTCTCGCAGTCGCACGCTTGACAAAAGTTAATTAGAAATAGAAAAATTTCTCATTCCCTT
TTGAGTTTTCACCATAATCAACTAGTAATAACCAACAATGCCTACTAGATTAATAAAACCAGAA
AACACAGAGGTAATGTTTCTGGTATGTACAATTTCACTAAAGTTTAAACGGATGAAAGAGTATTGA
ATGTTCAAGGACATATGGAGATTTAGAGAAAACATGGAAAATAATCGAAAATGAATAATGAATGG
AAAATTTTTTAACTGAATATCAGAATAGACACAACACAACAGATCCAGAGTCATTATCACATTGA
TCATACAACCAAGCAATGAATATGAGTAGTTTGGGAAACCACAACATACGAGTTATTTTTTCAGAA
CAATCAAGTTTATCATTTCAGAAAGACAGTTTCCATCAATATGTCCAAAATACTCTTTGAAGTCAAT
TAAAGTCAAATGAACGAATTACTAACTTATTTTTTTCTTTAGCCGGTAAGGGTAGAATTGGTAAAC
ACAGAAAGCACCCGGGTGGTAGAGGTAAAGCTGGTGGTCAACATCATCACAGAACCAACTTGGATA
AATACCATCCAGGTACTTCCGGTAAAGTTGGTATGAGATACTTCCACAAACAACAAAACCACTTCT
GGAGACCAGAAATCAACTTGGACAAATTTGTGGACTTTGGTTGATTCTGAAAAGAAAGACGAATACT
TGAGCAAATCATCTGCTTCTGCTGCTCCAGTCATCGACACCTTGGCTCACGGTTACGGTAAAGTTT
TGGGTAAAGGTAGATTACCAGAAGTTCCAGTCATTGTCAAAGCCAGATTTGTTTCTAAATTAGCTG
AAGAAAAAATCAGAGCTGTTGGTGGTGTGTCGAATTAGTTGCTTAA

YGL103W_homolog 149aa (SEQ ID NO 350)

MPTRLTKTRKHRGNVSAGKGRIGKHKRHPGGRGKAGGQHHHRTNLDKYHPCYFGKVGMRYPFHKQON
HFWRPEINLDKLWTLVDSEKKDEYLSKSSASAPVIDTLAHGYGKVLGKGRLEPVPVIVKARFVSK
LAEEKIRAVGGVVELVA

YGL147C_homolog 423bp PathoSeq: 1..423; CDS: <1..420 (SEQ ID NO
351)

GCTATCAAAATCACTGTTTACAAATGGTGACAGAAAACACGTTGCTGCTTTAAGAACTGTCAAATCT
TTGATTGCTAACTTGATCACTGGTGTCACTAAAGGTTACAAATACAAGATGAGATTTGTTTATGCG
CATTTCCCAATTAACGTTAACATTATTAAAAAAGATGGTCAAGATTACGTTGAAATTAGAAATTTT
TTGGGTGAAAAAGAGTTAGAGAAAGTTAAATCCATGAAGGTGTCAACATGGAAATTTCTTCTACT
CAAAAGGATGAATTGATTGTTTCTGGTAACTCCTTGAAGCTGTTTCTCAAAATGCTGCTGATATT
CAACAAATCTGCTGCTGTCAGAAACAAGGATATCCGTAAATCTTGGATGGTATTTATGTTTCTGAA
AGAGGTACCATTGTTGAAGAAATCTAA

YGL147C_homolog 140aa (SEQ ID NO 352)

AIKITVHNGDRKHVAALRTVKSILIANLITGVTKGYKYKMRVYAHFPINVNIIKKDQDYVEIRNF
LGEKRVREVKIHEGVIMEISSQKDELIVSGNSLEAVSQNAADIQQICRVNRNKDIRKFLDGIYVSE
RGITVEEI

YGL213C_homolog 1655bp PathoSeq: 1..1655; CDS: 501..1652 (SEQ ID NO 353)

GATGATCGCTAACAAGGTACCCGATTTATTCATCAACAAAGAAGCTACTTCATAGAATTGATTCTC
AACCTTAAATAGCTTGTAGTTTTTATGATTGGGACTAATTGTGCAGCATCGAACAATATTGCCAGT
TGCATAGAATAAATCGGTATTATTACGGCATACCAATCGATTGTAGGGGGTTGAAGCTGGTGCTAA
TTCTGGGGTTGTTGCATTTCCAGTCCATAAACGTTGAAACACAAATTGCTGTGTAATTTGGTGAAT
GAATTGATCAGATGATCCTATGGGTGGCATTGTTAAGGTTGTTTCGCTACGATGTATTTCTAGGATA
ATGAAGGTAAGTACGAACCTTATGAGTTTTGATTTCTTCTGATGTTTTTTTTCTTGTCTTTCTT
TTGTCGTTGTAGCAAGAAGAAAAAAGTGTCTTCACAAGTCTTGGACTCAATTTTCACCCCT
CCACAACTCAATTTCAATTAACATCAATAATCCAATATGGGTAAACAGTATATATCTACCGTCA
GTGCATCTCAGGCTCATAAGCTGGATATTCTTGGTGTAGCTATTACCAATAAGTTCACTGTATCCG
TGTCTAGTGATGGATATGCGAAATTTTGGGACACAAGCAAGACGAAGTTCATCTGCCTAAAGAAT
TTGTCCAACCTGGTATTTATAGATAAAAGCGGAATCCATGCGGTGGCTGCTTACGAAAATGTTTTGC
CAAGCTCTACATTTGAAAGTGACATTATTAGCATTTCATGTTTCAATGGATCTATCATCTTCAGAT
ATTATGATCAATGATGACTTTTCAACTATCGAAAGTCTAACTGATGATATAAAATCATTTTGAAAGCA
ATTGTTGGACCCCTGGCTTTTATCGCGATCCAGAATCCAAACAAGACTATTTTATTACAACCAAGA
CCAATGGCACTACAGAGGTTTCAATTTATTGAATATTGTTGATGAAAATGAGAAGGCTGTAATCACAT
TTGAAAAGTTTGGGCAATTTAAAGGAACTCTTCTTCTTCCCAAATCTTTGGCTATATGTCCAA
CAGAGAATAAAAAATGTGCTGTGGGGTACATCAATGGTGTATGTTGTTATATGACTTTGTTAGCT
TGAAATTGATATACACATTTTCGTTTCGAGTGATTTGGTGACCAGTAGAAATCCCAATCGACGCTTA
TACCTAGGGTGTGGCATTTTCCCTGGTGGAACTTGTGGCTGTGGCAAGAGACAATCAAGCTG
CTGGGTCAATTACATTATACGACGTTGAGCATGGTGAGAATGTGGGGTCTTTGGCCACACCCTCAC
ACTCGGCCAAATCTGTTGTTGGTGGGTTTGCACATCAAGGCTGGATTTTGGGGTTGAGTTTGTATG
AGGAAGGTAAGCACTTGGCTAGTTGTGGATTTGACAAATGCATAAGAGTCTGGAATTTAGAAACAA
CCGAAAGGGAAGCAACAATTAGTATATCTATATCAGACTTAGATGATACTACACATAATGATCAAG
GCGAGAGTGTGCGCTTCTGGTGTGCTTTTATTAAAAAGGGGTTAGAGGTGGCTCTGGTGGTGACA
GCAATGAAGGATTATGTGTCGTGAGTTTCGATAGAGGAATAAGATGGTACCGAGAGGCAGGAGGAA
TATAG

YGL213C_homolog 384aa (SEQ ID NO 354)

MGKQYISTVSASQAHKSDILGVAITNKFTVSVDGYAKFWDNKQDEVHSPKEFVQSVFIDKSGIH
AVAAYENVLPSSTLKVTLLAFACFNGSIIFRYIINDDFSTIESLTDDIKSFESNCWTPGFYRDPES
KQDYFITTKTNGTTEVHLLNIVDENEKAVITFEKFGQLKGNSSSFNSLAICPTENKKCAVGYING
DVLLYDFVSLKLIYTFRSDLVTSRNSQSTSIPLVLAFFSPGTTLLAVARDNQAAGSITLYDVEHGE
NVGSLATPSHSKSVVGGFAHQGWILGLSFDEEGKHLASCDFDKCIRVWNLETSEREATISISISD
LDDTTTHNDQDESVASGVAFIKKGVRRGSGGDSNEGLCVVSFDRGIRWYREAGGI

YGR085C_YPR102C_homolog 1418bp public: 1..1418; exon 1: 501..503,
intron 1: 504..896, exon 2: 897..1415 (SEQ ID NO 355)

ATAGAGATGCTTATTCCTGGTGGTTCAGTTAATTTATATCATGTCACTGAACAAGGTTGGACTTATC
ATGGTAATTTCAATGTTGGTGATCTCTTTTGGGAAGTTAAAGAAAAGGAACAATCATTTGTAAATG
TAGATGGATAAAGTAAGTTGATTGTATAAAAAAAGAAATGGATTTCATTAATATAAAATTTACAAATCT
GATAATAAACTACAGTAACATTTATGCAACAATTGAAAGTATCCTGTGTACCGTGATTAGGGCTCA
AAAGCCCTAACAGGTTGCACGTGATGTTGATTTATTTATCCCTGCACACATTGAGTTTTTTTTCTA
TGGTGAAAATTATTAGTGAGACGATGTTGTTTCGCATTTTACCACACACTCTCACACTGAGTGTAGT
CATACTAACAATCTTCTCACACTATACAAAAAAATCTTTTCGTTTGAAGGTTTGAAGGTTTC
GTTTTCTCAATAGTATATCCATCAATAACTGCCAAAGATGGTATGTTCAAGTGTTTAAAGATGATC
GAAATGTTTTGTTTTAATTGGAAGTGATATCATAATGAGAAAATATGGGAAATAGAGATAGGACCG
AATTAATTGAAAGAGTTTTCTTTTGGGGAAATGGGTTCAATAAGATTTTCAAGATTGGAATCAAA
TTATGTCAGATGTGAAGAAGAGTAAATATAACAAGAAGTTCAAATCATTAATAAATTTTATGTAAAT
ACAACGATTATCAATTACAGTCAACGAATAGAATAAAACAAAAGCCAGCATATAACAGATACCAGT
GATTCATCCCAGTGATATAAATAATGATATTCAATTAATAAACAATATTAAGACATTTTTTATTAT

GTATCAACAAAATACTAACTTATCTTTCTTTTAATTAGTCTGACAAATCCCAAAATGTTATGCGTG
AATTACGTATTGAAAAATTAGTTTTAAACATTTGTGTGGTGAATCCGGTGATAGATTAACCAGAG
CCGCCAAAGTTTTAGAACAAATTATCTGGTCAAACCCCAAGTTCAATCTAAAGCTAGATACACTGTCA
GAACTTTTCGGTATTAGAAGAAATGAAAAAATTGCCGTCCACGTTACTGTGAGAGGTCCAAAAGCTG
AAGAAATCTTGAAAGAGGTTTGAAGTTAAAGAATATCAATTAAGATCTAAAAACTTCTCTGCTA
CCGGTAACTTTGGTTTCGGTATTGATGAACATATTGATTTAGGTATCAAATATGATCCATCTATTG
GTATTTACGGTATGGATTTCTACGTTGTTATGGGTAGAGCCGGTGCTAGAGTCACCAGAAGAAAGA
GAGCTAGATCCACTATTGGTAACTCTCACAAACCAACAAAGAAGATACCATCCAATGGTTCAAGA
CCAGATACGATGCTGAAGTTTTGGATAAATAA

YGR085C_YPR102C_homolog 174aa (SEQ ID NO 356)

MSDKSQNVRELRIEKLVLNICVGESGDRLTAAKVLQSLSGQTPVQSKARYTVRTFGIRRNEKIA
VHVTVRGPKAEIILERGLKVKEYQLRSKNFSATGNFGGIDHIDLGIKYDPSIGIYGMDFYVVMG
RAGARVTRRRKRARSTIGNSHKTNKEDTIQWFKTRYDAEVLDK

YGR118W_YPR132W_homolog 919bp PathoSeq: 1..919; CDS: 482..916 (SEQ ID NO 357)

TATTGCGTAATCGTTATCAATGTTTGGATTGTTGCAACGCTGGGTTGTGTGTATATGCGAGAAATG
AGTAATTGTTTAAAAATAATCGATGCAGCAGTCTGCCACTAAATAAAATAAAATGTCATATTGACAT
GATAAGGATTTATCAATACTGTTAGGTCTATAGCCCTAACTTTAATCATTTACACGTGATACAAAA
AAGTTGTTTGATCCCGCAGCAGTATGAGTACGCACTCACTAATTATAGCCTGAAAAAATAATTTT
CACATAGTAAGGGGATTTTGTATGGTGGTGCGCTCGCCTAAGACGCTCTGCATACATTTTCTAAAGT
CACACTGATATAGGGATGTTGTGGTAGTGATTGTGTGTGTTCCACCAAATAACTTTGCGGACACTCT
CATATACTCAATTTTTTTCTTACAAAAATTTTTTTCTTCTACTTTTTTCAAGAATTCTTCTTTTA
CAATTCACAACATCAATCATGGGTAAAGGTAAACCAAGAGGGCTTAACTCTGCTAGAAAATTAAG
AGTTCACAGAAGAAACAACAGATGGGCTGATCAAGCTTATAAAGCTAGATTATTAGGTACCGCTTT
CAAATCTTCTCCATTTGGTGGTTCATCTCACGCCAAAGGTATCGTTTGGAAAAAATTGGTATTGA
ATCTAAACAACCAAACCTCTGCTATCAGAAAATGTGTCAGAGTCCAATTAATCAAAAACGGTAAGAA
AGTCACTGCTTTTCGTTCCAAACGATGGTTGTTTGAACCTTGTGACGAAAAATGACGAAGTCTTGT
GGCTGGTTTTCGGTAGAAGAGGTAAAGCTAAGGGGGATATTCCAGGGGTAGATTCAAGGTTGTAA
AGTTTCCGGTGTCTCTTTATTAGCTTTATGGAAGAAAAGAAAAGAAAAGCCAAGATCATAG

YGR118W_YPR132W_homolog 145aa (SEQ ID NO 358)

MGKGKPRGLNSARKLRVHRRNNRWADQAYKARLLGTAFKSSPFGGSSHAKGIVLEKIGIESKQPN
AIRKCVRVQLIKNGKKVTAFFVNDGCLNFVDENDEVLLAGFGRRGKAKGDIPGVRFKVVKVSGVSL
LALWKEKKEKPRS

YGR277C_homolog 1164bp PathoSeq: 1..724, public: 724..1164; CDS: 196..1161 (SEQ ID NO 359)

AATTCATTTGATCTCTAAGAAGATGAACAGGCCCTTGAATGGGAGGGGTTGGTTTCGACTTCCACGAA
ATGTGGTTGGAAAACTTGAGTCCTCAAAAAGGTTCTCTCGTAAAAGGCCAGAGAAAGAAAAACC
ACCAAACCCCAACCAACCTAACCTTTTCTTCCATCCATTCTCTTCTTACTTTGCAAAATG
TTGAATCCAGTTATATTCATTAAAGATCCTATAAAATACGATTATTCACAATTTATTATATCTTTA
CTCCCGAAATTCATTAATTGTAATCGTATTGATTTAGTTATACTTTGTCAAATCACCGAATCAAAT
CAATTGAATGAAATTTTATGTTTTTATTATCAATTAATTCGTAATCATAAGAATAATGGAGATACT
GATGGAGATACCGACAGTTTGCCTATGTTTGATTATCGATTGAAATTAATATATATTATTAATTTA
TCAACAAAAAATGAATCAATTATGTTTAAATAATTGGAATCATGGATATATTGCGGAAGGTGAT
AATGATAACAGTACTAATTTGTCATCTTTGCCATTGTCAATAACACAAATATCAAAACATTGAAATT
CCAACAATCCAATCAAGAGCAAATAGTAGTAGTGCTTATAATGATGAGGATGATAAAATTACTACT
AGTCCGCAATATCAACAATTTAAACTACTGCTGTAGGTGGAACATTTGATCATTTACATGATGGT
CATAAAATTTTATTATCAATGGCAATTTTTTTAACTTCAAATAAATTAATTTATGGTATAAATGGT
TCTAATTTATTAATTAATAAAAAATTTAAATCTCAATTACAACTTTTAATCAAAGACAAAATTTA
GTTATTCAATTCATAAATTTATTATTATTGAGTGAAACCAAGTGTATTTTTTTTGAATTTATGAA
ATTAATGATGTTTGTGGTCCAACCTGGTTATATTAAATGATATTGATAATTTAATAATATCTCAAGAA
ACTAAATCTGGTGGTGAATTTGTTAACAATTTTCGTAAAGATCATGGATTTAAATTTATTAGATATT
ACAATAATTAAGTGATTGGTGGGAATATTGAAGAAAATTCATGGAAGGTAAATTAAGTTCAA

CTGATATTAGAGAACAAGAATATAATCGATTATTAAATCAATAA

YGR277C_homolog 322aa (SEQ ID NO 360)

MLNPFVIFIKDPIKYDYSQFIIISLLPKFINCNRIDLVILCQITESNQLNEILCFYYQLIRNHKNNGD
TDGDTDSLPMFDYRFEINILFNLSTKKNLQCLNWNHGYIAEGDNDNSTNLSSLPLSITQISNIE
IPTIQSRANSSSAYNDEDDKITTSRQYQQFKTAVGGTFDHLHDGHKILLSMAIFLTSNKLIIGIT
GSNLLINKKFKSQLQTFNQRLVLIQFINLLLLSETSVIFFEIEINDVCGPTGYINDIDNLIISQ
ETKSGGEFVNKFRKDHGFKLLDITIIKVIIGNIEENSWKGKLSSTDIREQEYNRLLNQ

YGR284C_homolog 1427bp public: 1..1427; CDS: 501..1424 (SEQ ID NO 361)

CAAGAGTAAATCTAAATCGTTCCAATGATTTTGGACAGCTCATAGGTTAAGAGGTCTACATGTGT
TGGTGGCAGTAGTATTGGTATTAAGTGGGTGGCTCATGGTATTAGAGAGTGGGTGTTATAAAGAA
GGTTGTGATTTTTTTTTTCCACTGGTGGTGGTGGTCTGATTGTACTGCTGTTCACTTTATTGTTT
CGTTTCGTTTTTTCCTTTGTTTTGTTGACGTTGACATTTTTTTTGTCTGTTGTTGTTGTATGGGAATT
TTTGTATTAGTTGTTCTTTTTTGTTTTTTTTACTTGTTCAAAGTTTCATATAATAATAATATTCT
TGTTTTCATATTTTTTTTTTTCAGAACAAAGAACAAATACAACCTATATAATTTGATCTTACTCTTAT
CCCCAGGTTTTTCTATTTGTTTTTGGGTTTGCCATTCATATATATATATCTATTATTCAAATCAAT
TTGAGGAGTATCATTAATTTAAATTTATATCAGTTAACAATGTCGTATCGTGGTCCTAATCAATTTG
GTAATCAACCTCCACATCATGGAATACCTTCTCAACCTCAACCACATATTGGTCCAATATCTTCCA
GCAAAAGTCCTTTAGAACAAATTTGAAGATGTTGCTAAAAAAGTTGAAGATTGGATCGATGATTATT
TTAAAGTCTTGAACCATACGTCCTCCAGCAATTGGTAGAGCATTTTTTGGTGGCCACTTTCTATGAGG
ATACTTTTAAGAATCTTCACTCAATGGAATGAACAAGTTTATTACTTGCACAACATAGACACTATT
GGCGTTGGTTGACCGTTTTATCTTGATCAATAATATATGTTGGTTATGACAGTTGCATCCACTTTAG
TAATTGCCAGAAAAAGAATAACATTGCTACTATTGCATTGATCGTTGTTGTTATTATACAAGGTA
TTGGGTATGGTTTTATTGTTTGATGCTCAATTTGTTTGGAGAACTTGTCCGTTGTTGGAGGGTTAG
TATTAGCATTTTCCGATAGTATTGTTAGAGATAAAAGATCCTTAAACATGCCAGGTTTACCGATGT
TGAACAATCAAGACAACAAAAAGTATTTCTTTTAGCTGGTAGAATTTTGTAGTATTATTATTTT
TGGGATTGCTCTTTTCTCTGATTGGTCAATTGGGTAGAGTTTTCATTATTATAATCGGGTTAACTT
CTTGCTGCTTCAATTGTTGTTGGTTACAAGACAAAGTTTTCAGCTGCTATCATGCTTATTGTTTTAT
TCTTATACAATGTGTTCACTAACCAATTCTGGGCTTATGCATCTCAAGATGCTAGACGTGACTTTT
TGAGATATGAATCTTCCAAGTTTGTCAATTGTGGGAGGATTATTGTTAGTGGTTAATGCAGGTG
CTGGTGAATTCTCCATCGATGAAAAGAAAAAGATTTATTAA

YGR284C_homolog 308aa (SEQ ID NO 362)

MSYRGPNQFGNQPPHHGIPSPQPHIGPISSKSPLEQFEDVAKKVEDWIDDYFKVLKPYVPAIGR
AFLVATFYEDTLRIFTQWNEQVYVYLNHYRHYRWLTVLFLINNMVMTVASTLVIAARKNNIATIA
LIVVVIIQIGIGYGLLFDAQFVLRNLSVVGGLVLAFSDSIVRDKRSLNMPGLPMLNNQDNKKYFLLA
GRILLVLLFLGFVFSDDWSLGRVFIIIIGLTSCASIVVGKTKFSAAIMLIVFLYNVFTNQFWAY
ASQDARRDFLRYEFFQVLSIVGGLLLVNVNAGAGEFSIDEKKKIY

YGR285C_homolog 1876bp PathoSeq: 1..1215, public: 1216..1876; CDS: 501..1781 (SEQ ID NO 363)

AATTATTAGTTGAAAAACAAATCATACCTATTGCCAGAGCTCAAATGAAAGTGAGAATTACGTTAT
CTAAAAAAGCATACTTAAAGACTTTTCAAGATGAAATAAAACCTGTTATTGATCAAATTGTGGAGG
AAGATAACAATGGGAAACAATATGAGATTGTTGGGATTATAGATCCTATAAATTATAGAGTCTTGG
TCACATTAATTGAAAATACAGATGGAAGCAACAAAGTCGCTAAAGGAGAAGGGTCTATAGAAGTAT
TAGATATGCTCTGCCATAAAAGAATAAACTAAACTAGACAAAGTGATAGAATCTTTTTTATTAATA
GATGCTTATCTTAGTTATGTTCCAGAACAATTCATGTTAGGAGAGAGAGAAACGCAATCACTCAAT
TTTTGCACAAACAAAAACGAGAAGATGAAGAAGCAAAAAAGAAAATTTTTTTTCTCAACCATCT
TAAATCCTCTTACAATTAATTTTCAACCAATAAAGAACATGCTATTGTATTACCATCAGGAACCTA
CTGACGGATTTAAAGCCGCTCTCCAAATACTCTGCCCCAGTGGCTCGTCCAATTGAACCAGTTGGTC
GTTACTTCTTAGCCACGCCTCAAGAACTTTGCGTGGACACACTGGTCTGAATTTGAAAAATTGG
AAGCTGAAAAGAATGTTAAACAAATCGAAGTCAACGAAGATGAGGATTGGGAGATGAAGAACAAA
GTGAAGAGTTATTAGAACACGATCCAAGAGAATGGAAGACTGCCAATTTATATGCTGTTTTAGGTT
TATCTCATTTGAGAAGTAAAGCCACTGAAGATCAAATCAGAAGAGCCACAGAAAACAAGTTTGA

AACATCATCCAGATAAAAAATCCGCTAGTGGTGGATTAGAAAACGATGGATTTTTCAAATTATTC
AAAAAGCCTTGAAGTTATGTTGGACCCAGTCAAGAGAAGACAATACGATTCTATTGATGTTGAAA
ATGATCCAAAACCAGCTCCAAAATCAAATACGATTTCTTTGAAGCTTGGGGTCCAGTATTTG
AAAGTGAAGCAAGATTTTCTACTAAACAACAGTTCCATTGTTGGGAAATTTAGAAAAGCACCAAAAG
AAGAAGTTGATGCTTTCTACAGTTTCTGGGGAAGATTTGACTCTTGAAGACTTTTGAATTCAAAG
ATGAAGATGTTCCAGATGACACTGCCAACAGAGATCACAAACGTTATATTGAACGTAAGAATATTG
CCCAACAGAAAAGAAATTGAAGCAAGAAGATCACAAAGAGATTATCGAATTGGTCGAAAGAGCTCATG
CTGAAGATCCAAGAATTAAATTGTTCAAAGAAAAAGCCAAGAAAGAAAAGGCTGCTAAGAAATGGG
AAAAAGAATCTGGATCAAGAAAAGCTGCTGAAGAGGCTGCTGCCAAAAGGCTGCTGAAGAGGCCG
CTGCTAAGAAAGCCGCCGAAGAAGCCGCCGCTTTGAAAGCCAACCTCTAAAAAGCTAAAGAAGCTG
CTAAAGCTGCTAAAAAGAAAAACAAGAGAAACATCAGAGCTGCTGTTAAAGACAATAATTACTTTG
GTGACTCAGCTAAATCTGCCGACATTGATGCTGATGCTGATTGTTAATCGAAAAATTCGACGATG
TCAAATTAGGTGAAGTTGCTGATAAAGTTAAAGATGCTGATGCTGCTTCAGTGAAATCTACTTTTG
TTGAAGTTGCAAAGGAATTGGTTGGAGCTGGTTCTTTAGATGCTTCTATTGAAATATTTTAACT
AGATTTTTTTTTTTGTAGGAAAATAATATATATAGAATGTAACTATCAAAAACAATTATACAGAAG
CTGAACTCAAACAAGACTAAACAGCAAG

YGR285C_homolog 427aa (SEQ ID NO 364)

MSIVLPSGTTDGFKAISKYSAPVRRPIEPVGRYFLAHASRTLGRHTWSEFEKLEAEKNVKQIEVNE
DEDLGDEEQSEELLEHPREWKTANLYAVLGLSHLRSKATEDQIRRAHRKQVLKHPDKKSASGGL
ENDGFFKIIQKAFFVMLDPVKRRQYDSIDVENDPKPPAPKSKYDFFEAWGPFVFESEARFSTKQVPV
LLGNLESTKEEVDAFYFSGFRFDSWKTFFKDEDDVDDTANRDHKRYIERKNIAQQKEIEARRSQE
IIELVVERAHAEDPRIKLFKEKAKKEKAACKWEKESGSRKAAEEAAAKKAAEEAAAKKAAEEAAALK
ANSKKAKEAAKAAKKKNKRNIRAAVKDMNYFGDSAKSADIDADVDLLIEKFDDVKLGEVADKVKDA
DAASVKSTFVEVAKELVGAGSLDASYLYFN

YHR021C_homolog 1178bp public: 1..537/917..1178, PathoSeq:
538..916; exon 1: 501..503, intron 1: 504..932, exon 2: 933..1175
(SEQ ID NO 365)

TTTCATTTGTAGGCATTGTGTAGAATGTGGACTGTAGGAAGGTGCAAAATATATATCCAATAAGTC
ACATCTCAAATTGGTAGTAGAAGAATTCACCTTGGGACAGTATTCTCTGCTTAAATGAGTTTAC
TGATCAAATAAAATATTGCGTCAACCATTGAAAAGCTATTCTTGACACTTTTTGCAGTTTTAGTTT
TGGTTGTTTCACAATTGAAAAAATGTTGAGCCCTAATAGCCCTAATTGTTTGCACGTGATGT
ATTGCTTTGAGTGAAAAGTGATACATTTGTACACACACAAAAAATACTAATTCTTCCCCCA
ATATGCTGCGTATAGTGAGAAATCTTCTTCTCTTGCCTACTATCGCATTTTTTTTTTGGTAA
CTCACGAAACCTAATTGGAAGAAGAAAAGAGAAAAAATTTTCAGTTTTCAATAGATTTTC
AGTTTTTGAAATTATACATATTAGAGAAACAAGTTAACAATGGTATGTTTCATTAGATTTACCATGAG
TTATGGAGGGATATTCCTGGATGATCAGAATATCATAATATAGGAGTATACTATTTTACTGGAATC
AAGATATAATTGAATTGAAATAAAATGAATAAGAGGAAGCATAGAATACGGAATGATGATTAAAC
AAATCAGAAAACATTGTACTACCGAATAATGAATTAGGATCAACATATTAATATCAACTACTACTT
TAAAAGAACAGGAAATGAGAAAGAGAAATCAGCATGAAAGTTACCACCTCAGAAAACGTCAAAGAAA
TATACTTTTGGTGTGGATCCATGTGTATTACTGAAATCATCGAAACGAATATAACCTCCTTTTC
CCACATTGACATAACTCAGACACAATCTTTCAAATAAAACATGTAATACTAATACTATTATTTTTTT
TCGTATAGGTTTTAGTTCAAGATTTATTACATCCATCTCCAGCCACTGAAGCTAAACAACACAAT
TGAAAACTTTAGTTCAACAACCAAGATCTTTCTTTATGGACGTTAAATGTCAAGGATGTCTTAATA
TCACCACTGTTTTTCAGTCACGCTCAAACCTGCTGTCACTTGTGACTCTTGTCTACTGTTTTGTGTA
CCCCAAGTGGTAAAGCTAAATTGACTGAAGGTTGTTTCATTGAGAAGAAAGTAA

YHR021C_homolog 82aa (SEQ ID NO 366)

MVLVQDLLHPSATEAKQHKLKTLVQQPRSFMDVKCQGLNITTVFSHAQTAVTCDSCSTVLCTP
TGGKAKLTEGCSFRK

YHR141C_YNL162W_homolog 1179bp PathoSeq: 1..1179; exon 1: 501..503, intron 1: 504..861, exon 2: 862..1176 (SEQ ID NO 367)
TTTATATTGTTTTTTGTTTCTATGTATAGTAATTAATTTGATGTTCCATTATTCATGTAATT
GTGATGTATTTTTTTGTTGGTCCCTTTTGTGTTTGTATATTTGTCAGCTGGTCCGGATCATACAA
ATTTGGAAGGAGCTACCAAAGCAGAAATGATAGCAAAAAAACAGGAGACTTTTGAATTTCTTG
GTTTAGGGCTCTAGCCCCAATGCCGTGATATAATTGATTGATGCTTTAAAATTTGTGCGGTGAAAA
ACAGAAGCGAAAAAAGAGCTGGAAAGTGTGATTAAACAACAACGAGGGAAGAAAAAAACTTAA
TTAGGTGAACAAAAATTAATGTGTGAGCGGTGACATGCACAATTTTCAATTGGTTATTCTCACGCA
CTAACAACTCAACCTCCATTGTGAGAAAAGAGATTTTCTTTGAAAAAAATTTACATACATATC
TTAGTTCACTAGTAAC'TTTCGAAGACAACATAGACAAGATGGGTATGTTCCAGTATAGCAATATTC
AACAATGAGATACAAGATATTCCTCCAATACAAAGAGATTAATGGTGT'TTTTGATAGAGTGTAAG
CCATGTGT'TTAAATAAGAATGATT'TGTCAAGGGATAAGATGAAAAGTGGAAATTGTC'CAAACAACAT
TGAAACGAAT'TTCT'GGGATAGCGT'TCAAACAATCAAACCTATCCAGGT'TTCTTATGACAATTAAG
AAAACAAGTCAATATTATCAAAGATGGAGT'TTTATAAGGAGAGATATTGAAACATCAAATTGTTGA
AAGAAATAGCCAAC'TATTTGGCACCATTTCCTGTGATCATAGAAATACTAACAATCCTCTTGTGTT
ATAGTTAACGT'TCCAAAACTAGAAAGACCTACTGTAAAGGTAAAGAATGCCGTAAACATACCCAA
CACAAAGTTACCCAATACAAAGCTGGTAAAGCTTCTTTGTTTCGCTCAAGGTAAAAGAAGATATGAC
AGAAAACAATCCGGT'TATGGTGGTCAAACCAAACAATTTTCCACAAGAAAGCCAAGACTACCAAA
AAAGTTGTTTGTAGATTGGAATGTGTGTTGCTGTAAAACCAAGGCTCAATTACCATTGAAAAGATGT
AAACATTTTGAATTTGGGTGGTGACAAAAACAAAAGGTCAAGCTTTACAATTTTAA

YHR141C_YNL162W_homolog 106aa (SEQ ID NO 368)
MVNVPKTRKTYCKGKECRKHTQHKVTVQYKAGKASLFAQGKRRYDRKQSGYGGQTKQIFHKKAKTTK
KVVLRLECVCKTKAQLPLKRCXHFELGGDKKQKGQALQF

YIL112W_homolog 3583bp PathoSeq: 1..3583; CDS: 365..3580 (SEQ ID NO 369)
GTGCGAATAATACAAGCGATCGTTTGAATAATCCAATGATTAGCTCTGATCAACGAATTCAAAATT
TTCCCCCTCAAGGACGTAGTACAACAAGAGATGAGAAGGGGTTTGAAGTGT'TTGATTTCAGAGGAGA
TGACGGTGCAAAAAGATCTACCACCAAAGAAGCACATAATTTTTTGAATGATTACAGAAAGAGTTC
CATTAGTGATATCTCAAGCCAAAAATTTTCAAGGGAAAAGTTCCCGTAATGTTTACGGGAAAGCAG
CAGGCGAAGTTCAATAATAAAAAATTTGATCATCTACTAATGTGGACGTGTCAACGAAACCGGAAAA
TATAATAGCAGAGATAACAAAACCTGAGAAGAATATGACTTTGAGTTCAGAGTCAACCAATCCGAG
TGTCGAAGAAGTTAGTAAATCTTTGAAACCAACAATTTACCAAGAAAACCTTCACTTACTTACTT
AAAATCTGCCAAAACTAAGGCTAAAGAAGAAAAGGTAAACAATCGAAAAAGTGACAAAACGATTAA
TTCAGAAGAACGAAAAACGGAACCAATTCAACAAAGCGAGCAACTTTTAACGGACAAAAAGGATAA
TAAACTGGAACCCAATAGTGAAGTAAATTTGAAAGACAATAATGACGACCTGAAAGCTACAGCTGG
CTGTGCCCTTAGGACCTGATAAGAATACTGGAAAAACGATTCAAGATAAATCAGAAACGACTCAACC
AAAACCTTGCCCGCTCAGAATCATT'TGCCGATACATCATTATTGTCTCCAGTTAATGAAAGTGATAC
TGATT'TCAAT'TTCAATGAGTTAGCAGAGATACCGGAAGCAAAGGATGGTTCAAGTTGTGGCAGCAA
TGTGCTGGAGAACATTGATGAGAATGAAAATATTTTCAAGCTGAAACTGTTATAGCAGATGACCT
TCCACGTCTCGATGAAGGAAAGAACTTTTACGTGAACAAACAGCAGATGTAAAGAGACATAAATT
GAAGAAAACAAAATTGAATACTATTTTGTAGTTCCGATGAAGAGGAGGAGGAGATTCAAGAACCAGA
TTTCAAACCTCAAGAACCAGAAAACTACCAGAAGATGACCAACATCCTGATTTTCAAATTCAAA
AGCAACAACAGAAATCAGTAACGATAAAACAGAAAGTAAATAAGCCAGAAGTGAAAGAGGTTGGCGA
GAAAGAGAGAAATCACCAACTAGAAGATAGATTACCAATTAAGAAAGAGAAAATGCGGTGCGAGAA
TGCAAAGACATCTGAAAACGGTGTCAAGTTCAAATCAGAATCTAAGATTTCAAAGTCAAGAAACT
ACCTTACAAAGTTAAACGTGATTCAAGTGGTTCGATCATTATTACAACGAGCTTGCAAGAAGGGTAA
TTTTGCAGATGTCCAAGATTACATAGAGAGGGGTGCTAGTGCCAATGAAAAGGATTTCTGTGGATT
CACATGCTTGTGATGAGCGAGCATTTGGAAGGTATACACAAATTTGTGAAATATCTCATCGAAAAATGG
TGCTAATGTAAATGCGAAAGCTGATGAAGCTGGTGAATCCGAGACACCATTGATCGATGCAGCTGA
AAACAAACATCTTGATTGTGTTAAAGTGTACTAGAAAATGATGCTGATCCTACTATTTTCAATAT
TGATGGATTACCGCTTTTAACTAAGATTTTATAATGAACATGAAGGAGAAGAAGGATATGATGAAAT
TATTCAAGTTCTAGAAGAAGCAACTGCAAACTATAACAGTCGTTTACCAAGAGAAGTTCAAGTTTGT

ATCAGATGCTCCTATTGGTAGTGGACCAATCATGGAGGATCCAAATGACAACTATTTTGCAGAGCT
AATTAAAGGTAAGGGAATATATAAATACGCTGCAGAGAATTCAAAGAGAAAAACAGCAGAATATTT
TGTTGCTGGTCATAATTTAGAAGGAAAACAGATATTTTAATTTTAGCTGCTAGAAACGGCCACAC
AGAACTTGTTGATATTATACTAGGGCTAAACCCTACACCTTTTAATATTGATACCGAGTCAAGTTG
TGGTGTTACTGCATTATTGGCCAGTATTGGACGCGGTCATTTTGAAGTTGTCGATTCTTGTGTGTC
CAAAGGTGCTGATCCATTCAAGACAAGAAAAAAGATGGGTTGAATGCTTTAGAAATTGCACAACA
CTCGCCACATTTTGGATTACGCGGAAGTTAGTGTAATAATGAAATTCATGGAGAAGAAGAGTGGAAC
CAAATTTTGTCTGGTATTCCGTCAGGGTAGTATCTCGTGCAACATCTCGTGACCTTCTGTTCC
CGTATCATCAGACGAAGATGACGTAGTGAAGAAAAAGAAATTACAGCACACACAGAAAATAAAAG
TGCTGAAAAGAAGCTGGAGGATAAAATCACGAAAACAGTTAATGAGCATGTCAGCAATCGGAAACC
CCACGAGTCTACAGGTCGAAAACCTTGAAGAACTCATAGCAATGAGGAAAGAAAGCGGAAACGTGA
ATGGTCAGACATGAACCTAAAGAACCACATCTTTTGAAGAAGTCAAAGTCTGATTGAAATTTGAA
ATCACTACATAGAGAATTCATTCTGATGATCACCACACCAGTGAAAGCCATTTCGATTCTTTTGC
AGAAAAAAGAAAACATTTATCGGCAACGCCACCTGCTCCTCCGCCACCACCACCACCACCTTC
TCAAGCAGTTATCAAGGCACAAGAAGAACAAAAATCAAAGATGCTGAAGAAGCTAGATTGTGGCA
AGAAAAGGTGCAAGCTAAAAAGAGGGCTCGAAGAGAAATGTTTTTAAAGTCCGAGAAAGAGAAAGA
GCAGAAACCGGAAAGAAGAAGAAGAAATTGCGAGCACAGAAGAAAAACGAATTGCCAAAGCAAAACA
GGAAGAACAGGAGAGACTTGCTAGAGAAGCAGAAGAGAAATCGAAAGAACTAGAAGAAAAAGAAAGT
GGGGTTGCGACAACAGTTGACATTAGATCATTATCCGGTTGGATTGCGTTATTGCAAGTTTGATGG
AAACCCAAATATCTCGGCTGTTGATAAATTTTGCCTTTCTATGTATTGTAAATCGACGATAAAAA
GTATGCTGTTGATTGCAAGTCTCCTTGATCACGTCACCGGTTGTCAGCAAGGTTATCAATACTGT
ACAACCTCATCAGAAGAGAGAAATAAATGCAACTGAAAAAAGCAAATTTGTGGAAGCTCTTTTTCAA
GTTTATTGGTATTGATCCTAGGAATCCAAATTTGATCAAAGAAGCTCAATAACAAATGGTCAAAA
ACAGTTTCAAATTTGTTGCTTCATTTTGTGGAGGTAGATTTAGCTGAAGAATTTTAAAGGAATT
TCCAGAAGTACACTCAAAGCAAAAGATAACCAAATTTGATGTTAGTTTAGAGTCTTTGAGTGGGTT
TTCTGATTGCGTCAAGGATGATATAATAGTTGATCGAAATCTTGAAATTTGATATTGATTCCAAGAA
AATCGAAAAGTTTATCTCCTCATTTGAATACTAGGAAAGACATTATTAGGACTGTCAGTACTTT
AGCACACCCACTATGGTGA

YIL112W_homolog 1072aa (SEQ ID NO 370)

MTLSSESTKPSVEEVSKSLKPTITKKTSTFDYLSAKTKAKEEKVTIEKSDKTINSEERKTEPIQQ
SEQLLTDKKNKSEPNSEVNLKDNNDSDKATAGCALGPDKNITGKNDSDKSETTQPKLARSESFADT
SLLSPVNESDITDFNFNELAEIPEAKDGSVVAANVSENIDENENISEAETVIADDLPRLEDEGKLLR
EQTADVVRHKLKTKLNTIFSSDEEEIEIPEDFKLOEPEKLPEDDQHPDFQNSKATTEISNDKTE
VNKPEVKEVGEKERNHQLDRLPIKKEKMRSENAKTSSENGVSSKSESKISKSKLPIYKVRDSSGR
SLLQRACKKGNFADVQDYIERGASANEDFCGFTCLHEAALEGHTQIVKYLIENGANVNAKADEAG
DSETPLIDAAENKHLDCVKVLLENDADPTIFNIDGFTALTKIYNEHEGEEGYDEIIQVLEEATANY
NSRLPREVQFVSDAPIGSGPIMEDPNDNYFAELIKGKGIYKYAAENSKEKTAEFVAGHNLEGKPD
ILILAARNGHTELVDIILGLNPTPFNIDTESSCGVTALLASIGRGHFEVVDLSLSKGADPFKTRKK
DGLNALEIAQHS PHFDSREVSVMKFMEKKS GTKILSGIPSRVVS RATSRAPSVPVSSDEDDVVEE
KEITAHTENKSAEKKSEDKITKTVNEHVSNRKPHESTGRKLEKTHSNEERKRKREWSDDPEKPHL
LKKS KSDLKLKSLHREFTSDDHHTSESHSDSFAEKRKHLSATPPAPPPPPPPPSQAVIKAQEEQK
IKDAEEARLWQEKVEAKKRARREMF LKSEKEKEQKRKEEEEELRAQEEKRIAKAKQEEQERLAREAE
EKSKELEEKVGLRQQLTLDHY PVGLRYCKFDGNPNISAVDKFLPFYVVFVIDDKKYAVDLQVSLIT
STVSVKINTVQPHQKREINATEKSKLWKLFKFIGIDPRNPNCQORSSITNGQKQFQNLHLHFE
VDLAEFLKEFPEVHSAKDNQIDVSLESLSGFSDCVKDDIIVDGNLEIDIDSKKIEKFI PPHLNT
RKDIIRT VSTLAHPLW

YIL148W_YKR094C_homolog 659bp PathoSeq: 1..659; CDS: 501..656 (SEQ ID NO 371)

TAGTTTCTTTTGGCGGTATATCCTCACTCATGATTGATGATTTTGGCCACTAAAAAGAAAACCAAT
GAAACAATAAGATTGATTGATAGATTGTTGTTGTAATTAATCTGATGCTTTCAACATTTGTTTTGT
TCGTGTCTCGGTCAATTGAGGTTGGGTAAATGTTTCTTTTGAAGAATTGTGAGCATGCAATGTCG
CATGCAAATATGATGTCGCTCAATTGCGACATACTACTTAGGGCTATAGACCTATTGCACGTGCGT

127/161

TAGTTTTAAACCTAAAAAACAATTTTGTGCAGTCGTGCACCATTTCGTTCTATTTTTTCTACTGTGA
TTGACGTACAAACCTTCACAGTTCACGCACACTTTTGTGCGATTCTCAAACCTCTCTCACAGGCTTG
GTAGGAATGAAAAAATTTTGGTAAAGGCGAAAAAATAAACTTGAATATTTTGAATC
CCCTTTTTGATTACTACAATAGATTAAAGTAACTAAAGATGATTGAACCATCCTTGAAAGCTTTAG
CTTCAAATACAACCTGTGAAAAATCCATTTGTCTGTAATGTTACGCTAGATTGCCACCAAGAGCCA
CCAACCTGTCGTAAGAGAAAGTGTGGTCACACCAATCAATTGAGACCAAAGAAGAAATTGAAGTAG

YIL148W_YKR094C_homolog 52aa (SEQ ID NO 372)
MIEPSLKALASKYNCEKSICRKYARLPPRATNCRKRKCGHTNQLRPKKKLK

YIL150C_homolog 2297bp PathoSeq: 1..1162, public: 1163..2297; CDS:
501..2294 (SEQ ID NO 373)

ACTCAGCCTTTTGAAATTCACTTTTGGTAAAGGATATGTAATTGAATCCGCATAATGGACTTTCT
CTAACTCCATATTGTTGTTCTACCCTCTTGCATAGAGACTTTGATCGTGACATTTTGTAAGTGG
TAGAGGTATGGGTAAGATTATTTTACCACCGTTTCTTTAGCAAATAGTCTAAAGCATTCTTG
AATTGTTGAGTTTCGGTACATCATTAGCTATCTTTTGTACAATTGATTGCTTCTACCTCTAGTCA
TGGAATAACAAGTTAAACAGCGTGTGTTGTTGGTTGTTGGAACAAATAAATTTGTGGTGTGTAAT
GTGTGTGTTTGTGTTTTTTTTTTTACCAGCATTTGTCTTGTCTAAAAATGAAACAGCGCAATGAT
TCTTTTCATAGTTTTTTTTTTTCCATACATAACTTCTGACGCGTGCACATATATCTGCTAACATCTC
GGCAACAACAAGAAAGAGAATTTGAACTAATCCGAAGATGAACGACCCAGAGATGAACAAATTG
ACTCCGATGATGTATTAACAGAAGATTCATCTGATGAATTGAAGGACTTGGTGCAGGAGTTTGAAT
TGAAATATGCAGAATTAAAGAAGAACAAAGCCTTGAAAAAACGTCGTTACAGTCCACTGGAAG
ACATGCTGAATAAACAGAAACCCATCAACCGAGGTCCCCAGAACCCAGAAAAAGCTAAAGTCC
ATTTGGATAAGGTAGTAGAAGAACCAGCAAGAAAGAAATTTTACCAAGAAGGAGCCTCGGGATTCCA
AGATAAAAGAATCAAACCTTCTTAAACAACTCTACGAGACAAGTAATAAGCATGATAAAGAAGATG
CCCATAAATAGATTTTCACTAAAGAGTTTGAAGTTTCAATTGGATAAGTATACTTTTACGCCAA
AAGACGTTGTTGATGATTTAGAACCAGATATCCAAGCTTTACTTGCAGCAGAAGATACCTTGCCCAAC
TGCAAATTGCCGACATTATTGCCGAACTGATAGCAACATGAAATTCCTTAAATTGACAAGTTTTT
TAGCGAAAACCCATAAAATCAAACAACCTATGCTGAACCCAAAGTATTGTAATTGGTGTCTTGTGCTT
TTGTGGTGGCGAAGGACCCAGTGCAGGTTGCTGCCAACAACTCTAAATACATCAAGTTGAAGGTTG
GAAATTTTATGAATTCTGTAGACTTGATGCTTTTTGATAAGGCTTTTCAGAAAAACGGGAAAAATCC
AACCAGGTGATTTATTATTCATTTGAAATCCATTGATCAACAAGTATGAAATACAAGTTGGCAAGG
GCCAGTTTCACTGCTGGGTTCAATTTGAAAGTAGAAAAACACCAATGTGTCAAGTATTTTAGAGATAG
GATCGTTAAGAGATTTTGGGTTTGGCAAGTTTACTAGAAAGCTAGATAATAGCAGATGCAAAAGGG
CCATCAACACAAGGACGCAAGAATTCTCGGATATACATTTGGATATGAAGTTTAAAGTTAGTACAA
GAATGGAATTAAATGGAAGTGTTCGATTAGATCCCCGCAAAAAACAAGAAAAAGATGTACATGA
ATAAAATGGGTCTGGCTTTTATTAAGCAATATAACGAGGAGAGTACTGTTATAGGAACAAGCTACG
GTTCTCTCTTGATCCAAAAAGGTACCAAGACCCGAAAGTACTCCAGAACCAATCAAGCGGCGCA
AACTAATAGACGACAAGGCAAGGAGATGCTTGAACAAAAGCTATCGAAACTAGGTTTCGGCTTCAT
TATTGAACAATTTACAATTATCTAAGAAAGAAGCAACAGATAAACTTGCAGTGATCGTCTGAAGA
GCAAGGATTACCAACACAATGATTTACATATTTGGGTTTGGATCCAAACAGGTACATCTTTGAACC
AAAATAGTACCCTGCTTGGCAGCAAGCTGATGAAAAATCTCGAGCACGGGAATTGCATGATTTGA
GTGTTGAAACATCTGGTCATAAGTCGTTGTCTTCGTCTAAACAAGATCGCCAGTCGAAAGTTGCAA
AATGGAACACGAATATCAGAATTTTACAAAATTACGATCGACGAGTTGCCAGCCACTCCTTGAGTA
CCTCTCGTCGGTTACAGAATCTTGTAGGAAAGCAACACACGCTACACTAGTAGATAAAAGGAAAA
GAGTGGTTGTCTCAGATGATGAACAACCGGGGATGGAAGAAGATGAAGAAGACATTGAAATCCAGT
TTGACGACGAAAAGTCTAAGATGCTCTACATGAAATGACTGGAGCCAGGTAA

YIL150C_homolog 598aa (SEQ ID NO 374)

MNDPRDEQIDSDVLTEDSSDELKDLVQEFELKYAELKKNKALKKRRSQSPSEDMSNKKQKPHQPEV
PRTPEKAKVHLKDVVEEPKQRIFTKKEPRDSKIKESNFKLNKLYETSNKHKDEDAHKIDFSKRRFEF
QLDKYTFTPKDVVDDLEPISKLYLRRRYLAQSQIADI IAETDSNMKFLKIDKFLAKTHKSNNYAEP
KYCNWCLVAFVVRKDPVQVAANNSKYIKLVGNFMNSVDLMLFDKAFQKNGKIQPGDLLFILNPLI
NKYEIQVGKGQFQSGFNLKVENTNVSSILEIGSLRDFGFKFTRKLDNSRCKRAINTRTQEFCDIH

LDMKFKSSTRMELNGSVSIRSPOKNNKKMYMKNKNGSGFIKQYNEESTVIGTSYGSPLDPKRYQDPK
VLQNIKRRKLIDDKAKEMLEQKLSKLGSASLLNNLQLSKKEATDKLASDRSKSKGFTNTMISHIG
FDPTGTSLNQNSTSLGSKSMEKSRARELHDLVETSGHKSLSSSKQDRQSKVAKWNTNIRTLQNYD
RRVASHSLSTRRLQNLVGKQTHATLVDRKRKRVVSDDEQPGMEEDEEDIEIQFDDEKSKMSYMKM
TGAR

YIL167W_YIL168W_homolog 1499bp public: 1..1499; CDS: 501..1496
(SEQ ID NO 375)

TTTCTTCATCAACTTGCTCAAATGTCCTTTGAAAGTGAAAGCTTACTTTTTTGGTTTCGTTTAGGTG
GCATCAAGGTAAAGGAGGGAGTTTTTGGTATAGTTAGGTTTTTGACTTATTTCCTTTTTGGAGTAGA
TATAACAGAACTACCAAAAGTGAGCCACATCTGTTAATCTTGAAAAGCAAAATTGAGAAAACCAT
TTATGCAAGTCGTGTACTGGTGATATTCTTGGTCAATTGCTACACTTTTGTAATGAATACTGTAAT
GTAGCCGACGTGGGTGAANAATATATATTTAAGTATATAGAATCAGGTCAATATAAAATGTTTGA
AATATAACAAAATGTTTCAATGTAACTGATGGTTAAGGGATTATAAATCAAACAGTAGTGTCTT
TTGTTCTTAAAAAACCATCGTGGTGGTAACGTCAGGAGACCGGACATCAAATGGAATTCACACA
ATCAGTCTCCGAATTTATTAACCTTTGAAACTTAACCTTAATGAAAGAGCCTTCCATCACTACTACCT
TTGTTGAGGTTACAGACAACTTCTTACAAAGCCTCCGTGCAGGGTGTTTTTCAAGAATGAGTATG
AGCAGCCCTCCGGCAGTGTCAAATTAAGAGGCATGGGACACTTGGTTGGCCAGTCTATAGATGTGG
CCAGAAAACCTGGCAAATCGAACGTAGCAGTTTTTTCTCATCTGGTGGTAATGCAGGATTAGCAG
CTGCTTATGCCAGCCAGTTTTTTGGAGTATCGTGCACCTGTTGCTGAAAGTTTGAAGCCAA
CTGTTATAGAAAAGTTGAAATCCTTGGGTGCAGATGTCATTATTCATGGGAAACATTGGGGAGAGG
CCGATAACTATTTAACGATTTTTGTTATTAATAATCTTGACAAAACAGTCTATCCGGTCTATTGTC
ACCCTTTTGATGACCCATTGTTGTGGGAGGGTCATAGTAAGATCATCACGGAATCATCGATCAAA
AGCAATTACCCAACCTTGATAAAGTTAAGGGGTTCATTGTTCCGGTAGGAGGGGGTGGCTTATACA
ACGGAATAGTTGAAGTTTGGAAAATCATAAGGAGATACCAAGTGTGGCAATTGAACTAAACAAG
CGGCCACGTTTTCAGAGGCGGTCAAAGAAGGTAAAGTTGTTTACAAAAGTGCAAACTTTGG
CCACTTCTTTGGCTTCGCCGTACCTTTCTTCCAAGGCATTAGCAAACTATATTGAGCGTCTACAG
TTCTTGTCTGAAATTGATGACTTGGACGCTGTTAAAGGTGTTGTTGATGTATACGACCATTTCCGAT
ATATGGTTGAGCCTGCATGTGGTGCATCCGTTGCATCAGTGATGCACAGGCAAGATTTATTGAATA
AATTTGGTACATTAAGTCCAGATGATATTATCATTTGTTGTCATATGTGGTGGATCGGCTATCAACA
AGTATATTATAGACGAATATAGAAGTTTATTAGAAAAGACTCTTGA

YIL167W_YIL168W_homolog 332aa (SEQ ID NO 376)

MKEPSITTTFVEVTDKLPKPPCRVFFKNEYEQPSGSVKLRGMGHLVGQSIDVARKLGKSNVAVFS
SSGGNAGLAAAYASQFFGVSVTVVLPESKPTVIEKLKSLGADVIIHGKHWEADNYLTFVIKNL
DKTVYPVYCHPDDPLLWEHSGKIIITEIIDQQLPNFDKVKGVICSVGGGGLYNGIVEGLENHKEI
PVLAIETKQAATFHEAVKEGKVHLQKVQTLATSLASPYLSSKALANYIERPTVLAEIDDLDAVKG
VVDVYDHFGYMEVPACGASVASVMHRQDLLNKFGLTSPDDIIIVVICGGSAINKYIIDEYRSLLEK
DS

YJL034W_homolog 2564bp PathoSeq: 1..806/1401/2504, public:
807..1400/1402..2503/2505..2564; CDS: 501..2561 (SEQ ID NO 377)

TTTTTGAAAACAGAGAATGAATGAACAATTGATGACCATAGAAAATGAAGTGAGAACACATAAATCT
GCGACACTTCAGTGATAACAACAAAGTGACATGAACAACAAATGTCGTTGTATAATTTGCGACA
TTTGTGTTTCAAGCCAAAAAAGAAAAGACAGAAAACAGAAAAAAGAAAAATCTCAAAGTTGCCACGT
AAGCACAATTAATCTTTTTATGGTTGTAACATTTTCTAGTATATTCTACGTAATAGGTGAGGTCTT
ATATGCAGTACACACAGGTTTTTTTTCACAGATGTTGACACAGTGTGAAAATTATTACGTTGATT
TATAAATATACAACCTTACCCTCCACGGTTTTTTTTTTGATTTTTTGATTTTTTGAATTCTTCTTCT
TTTTTTTTGTCATTTATTTATTAACATTTCTTGTAACTTTATTTGATAAATTTTACAAGATT
TAATTAGATCAATTAGATTATAGAATCATTTTCAATATAATGAGATCATCACAATCTCTTGGTTAC
CACGTATTGGTTTATTATATGTGGCGTTAGTTATACTTATACCATTTTTGGTTTACCGGAAGCAGC
CATTTGCGGTTGCTGCAGTGAGCGATGATGAATCCTCGACAGATAATTATGGTACAGTCATTGGTA
TAGATTTGGGTACCATTATTCTGTGTTGGTGTATGAAAAACGGTAAGGTTGAAATTTTGGCCA
ACGATCAAGGTAATAGAATCACTCCATCATACGTGTCGTTCAATGGCGATGAAAGATTGGTTGGAG

ACGCTGCCAAGAATCAAGCTTCCTCTAATGTCAACAACACTGTTTTTCGATATTAAAAGATTGATTG
GTTTGAAATATAATGATGACACTGTGCAAAAGGAACCTAAACATTTGCCTTACAAAATTGAAAATA
AGGGTAACAAACCAGTTGTTAAAGTTGAATACCAAGGTGAAGAAAAAACTTTCTCCCCTGAAGAAA
TTTCATCTATGGTTTTGGGTAAAAATGAAGAGTATTGCTGAAGATTACCTTGGCAAAAAAGTTACTC
ATGCCGTTGTCACTGTTCACGCTTATTTCAACGATGCTCAAAGACAAGCTACTAAAGATGCCGGTA
CTATTGCTGGTTTTGAACGTTTTGAGAATTGTCAATGAACCTACTGCTGCCGCTATTGCCTATGGAT
TAGACAAAAGGCGACCAAGAAAAACAAATTTATGTTTACGATTTGGGTGGTGGTACTTTTGATGTTT
CTTTATTGTCCATTGAAGGTGGTGTTCGAACTCTGGCTACTGCTGGTGATACTCACTTGGGTG
GTGAAGATTTTGATTTCAAGATTGTCAGATACTTGGCCAAACAATTCAAGAAGAAGCACAAATATTG
ATATCACTGCCAATTCATAAGCCATTTCCAAATTGAAGAGAGAAGCCGAAAAGGCCAAGAGAACCTT
TATCTTCTCAAATGAGTACTAGAGTTGAAATCGACTCCTTTGTTGATGGTATTGACTTTTCTGAAA
CTCTTTCAAGAGCCAAGTTTGAAGAATTGAACATTGCTGCTTTTCAAGAAAGACTTTGAAACCAAGTTG
AACAAGTGTGTAAGGATGGTGGTGTCAAGAAATCCGATATTGATGATATTGTTTGGTTGGTGGTT
CCACCAGAATTCACAAAGTTCAAGAATTATTGGAAGGATTCTTTGATGGTAAAAAGGCTTCTAAAG
GTATTAACCCAGATGAAGCTGTTGCTTATGGTGCCGCTGTTCAAGCAGGTGTTTTGAGTGGTGAAG
AAGGTGTTGATGACATTGTTTGTGTTGGATGTTAACCATTGACTTTAGGTATTGAACTTCTGGTG
GGGTTATGACCATTGATCAAGAGAAACACTGCCATCCCAACCAAGAAATCTCAAATCTTCTCAA
CTGCTGCTGATAACCAACCAACTGTTTTGATCCAAGTCTATGAAGGTGAAAGAACCATTGGCTAAAG
ACAACAACAGATTGGGCAAATTCGAATTGACTGGTATTCCACCAGCTCCAAGAGGTGTCCACAAA
TTGAAGTCACTTTCTCATTTGGATGCCAATGGTATCTTGAAAGTTGAAGCTGCTGATAAGGGAAGCTG
GTAAATCTGAATCCATTACTATCACCAACGAAAAGGGTAGATTATCCAAGGATGAAATTGATAGAA
TGGTTGAAGAAGCTGAAAAATACGCTCAACAAGATCAAGAATTGAAAGAAAAGATTGAAGCTAGAA
ACTCATTAGAAAACTATGCTCATGCTTGGAGGTCATTTGAGAGGTCAATTGAGTGATACTTCTGAAACCGTTT
GTTCTAAATTGGATGACGATGACAAGGAACTTTGGATGACGCTATCAAGGAAACTTTGAATTTA
TTGAAGATAACTTTGATACTGCTACTGCTGAAGAATTTGAAGAACAAAAACAAAAATTAATTGACG
TTGCTAACCCAAATCACAGCAAAATTTATACGCTGGAGCTGCTGGTGAAGGTGCTGGTGGCGCTGGGG
ATGCCAAATTCGGTGATGATGATTGATGATGAATTGATCAGATGAATTGATCAGGATGAATTGTAG

YJL034W_homolog 687aa (SEQ ID NO 378)

MRSSQSSWLPRIGLLYVALVILIPFLVSPKHAFVAVAVSDDESSTDNYGTVIGIDLGTTYSVGVGM
KNGKVEILANDQGNRITPSYVSFNGDERLVGDAAKNQASSNVNNTVFDIKRLIGLKYNDTIVQKEL
KHLPYKIEKGNKPVVVEYQGEKTFSPPEIISSMVLGKMKSI AEDYL GKKVTHAVVTPAYFNDA
QRQATKDAGTIAGLNLVLRIVNEPTAAAIAYGLDKGDQEKQIIIVYDLGGGTFDVSLLSIEGGVFEVL
ATAGDTHLGGEDFDFKIVRYLAKQFKKKHNIDITANSKAI SKLKREAEKAKRTLSSQMSTRVEIDS
FVDGIDFSETLSRAKFEELNIAAFRKTLPVEQVLKDGGVKSDIDDIVLVGGSTRI PKVQELLEG
FFDGKKASKGINPDEAVAYGA AVQAGVLSGEEGVDDIVLLDVNPLTLGIETSGGVMTTLIKRNTAI
PTKKSQIFSTAADNQPTVLIQVYEGERTMAKDNRLGKFELTGIPAPRGVPQIEVTFSLDANGIL
KVEAADKGTGKSESITITNEKGRLSKDEIDRMVEEA EKYAQQDQELKEKIEARNSLENYAHVLRGQ
LSDTSETGLGSKLDDDDKETLDDAIKETLEFI EDNFDTATAEEFEEQKQKLIDVANPITAKLYGGA
AGEGAGGAGDAKFGDDSDDEFDHDEL

YJL035C_homolog 1346bp PathoSeq: 1..125, public: 126..1346; CDS:
501..1343 (SEQ ID NO 379)

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TCTGGTATGTCATCTTCTACTAAGCCGACAAATCCCAAAGCCGCTCTTGTCTTTTATTCTT
CTAAGGAATGCTTTATGTAGTTCTGACATTTCTGCGTAAAAGGAAGTACAGTATTAAAGCTCGAAA
CTCAATTGCAACAAAAGCTCTTAATTTTCTTCTATAAGTAATTGATCTTGGTCCCCCAACAAAA
AGATACAGAGGAGAAAGGAGGGCCTTAGGCTGCAGAAAAAAAATTTAGTACCTGCCACACCAG
TAGCTCCAAACCCATATATGATTTGATAGAGTTGAAGTATGCTGCAGATCTTACTTCACACTTTC
AGTACATGGCTATAAGCTTGTTCGCTTACAAAGCCTTACTAAATAATGAGACACCAGTGTCTAT
GTATAGTCGTGGATTCAAAATCAGATAAAATCATTAGCATAGGCTACAATTATACCAACCACTCTC
TAAATGGTACACAACACGCAGAATTTATTGCTTTACAACGATTTGGGGAACAAAACTGAGTATTG

ACTATAATGATTTAATTTTGTATGTGACAGTGGAGCCTTGTATTATGTGTGCATCTTATTTACGTC
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TATCAATACATAGTGACATCACCTTGCCTAACGCAGCTTATTCAGTATCGGGGGTATATGTAGGA
CAGAAGGAATCCAACATTTACGAAATTTTTATATCAACAAAATGAGTCGGCACCAGAAATCCAAAAA
TCAAAAAGAACACAGATATTGAGAGTAAGGAATACCCAGAGAATCAGTTTTGTAGCATTTCAAAGG
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CTCCATTACAAAACAAGGGTTATGATATATAAAGAATTGATATCGTTGGATATGATGCAAAAAGTTC
CATTTCTAGAGGATGAGTTGGGACAAATTACAGATGAGCAATAATTGAATTTACAACTTATTTT
TCAACATAAATGATGATGGAACGGTTAATTATAAAAAACCAATAGGCAATATAACAGTAAAAAGA
GACACTTTGCAAACGATGAAGAATAG

YJL035C_homolog 281aa (SEQ ID NO 380)

MSTDLTSHFQYMAISLFVGYKALLNNEPVSICVVDSDKIISIGYNYTNHSLNGTQHAEFIALQ
RFGEQKSSIDYNDLILYVTVPCIMCASYLRLQGIKKVIFGCGNDRFGNGTILSIHSDITLPNAA
YSSIGGICRTEGIQLLRNFYIQQNESAPNPKIKKNTDIESKEYPENQFCSISKDEFIEFYGNERNVH
IYDGKIFEITPLQNKGYDIKELISLDMQKVPFLEDELQITDEQIIIEFHNLFNINDDGTVNYKK
PIGKYNKKRHFANDEE

YJL180C_homolog 1504bp public: 1..938/940..1504, PathoSeq: 939;
CDS: 501..>1502 (SEQ ID NO 381)

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GTGTGTGTATGGGCGATGAAGCTGAAGGTTTTGCAGATGTGGTGTCTATAAGAGTAATTTGATGTG
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GGAAATTAAGATCTATTCCAATTGCCACTATTCAATATAGACAATTTACTTATTCCTACTATATGTT
ATCAATTAATAAACCTTACTCCATCTTTAGGAATAAATAATACCATTGAATCCAATATACCTTCAG
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AATTACCAATCAATAAAAAACAATTGGCATATTTAATTGCTCATGAATGGACTCATTTACCTGATA
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GTGGAATTACTTTTATTAAGATCAATGTTAATGATATTGAACTTTAAAGAATTATATCAATTTA
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YJL180C_homolog 334aa (SEQ ID NO 382)

MLRFTRTTAWKLRSIPIATIYRQFTYSTICYQLKLTLPISLGINNTIESNIPSETNRLAKTGTRFW
KKGEVKFNNETQKYEIQLDGKTLRTPPLGFPLELPINKKQLAYLIAHEWTHLPDIKVKSSSTLPLTAL
ATRAIDLQQHLSDMKTEKAEEMLALEDIKQLMLRYLDTDCLIFATNKECDGKLRKRQEEIYRPL
INEFNEFFTIIYAHNKNLI PRQKSIELKYLDCE TDGLRGNKQDETTQLVVLVDWLNQLPIYDLIALEK
TILTTKSFCLGITLLRSNVNDIETLKELYQFNKNSIDEDYHKTLEELVELGNLETIYQTEEWGEV
EDTH

YJL187C_homolog 3689bp public: 1..452/3414..3689, PathoSeq:
453..3413; CDS: 501..3686 (SEQ ID NO 383)

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AACTCAAGGGTGAGCTAGATGACTGAGCGTGCGAGAAAAAATCATCATCCAAAGTTTAAA
CAAAGTATTCTTTTTTTTTTTCAATTTTACAACCAAAGATAAATAACTACACAACACCCAACATTA
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CGGGTGATACCAGTAGCACACCAATGGCCAACAATAATCCCACTAATGACAGCACAACTCTCTCTC
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CAACAGACGACGATCAGGATTTTGATGATGAAGATATTGAAGATCCTGAAGCAGTGCAGTACACCC
CAACTTTGAATATCTTGAAATCCAAAAAGTCGATAGCTTCAATATTATATCTAGCAAGCATAGAA
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CGATGGCTACAATAAGGTTATCTAACAACCTCACAAAGTTCAATTAAGAGATCGTCAAAGTATTTGA
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MDSNPCQDVSGDTSSTPMANNNPNTNDSTISSQNHSKTGLRKHQQQHYHQHSHSQMHSHSQSPYIN
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KPSEEDTSSSMATIRLSNNSQSSIKRSSKYLNLSDSNLKTVDGGKIPDEIDDISLNEIDVAVAPN
DFSSPLSARKPDIFAATAANGNSNNQFKRPHKLVSQSPSPSSKNKFRISSTTSSPQSNLHSPSK
LGSKGFKMFKNANRDAIMSSSRVMTPEKPKMVSKIFGKSAKIRRAYTPHTSTPMAVSSSLNPPSSS
TSNSTTAAITSTSPAADDEHYDIDNDCDSPSKNRKSSNISASSIIYQDENHIKSNHARKSSNPIPY
PPTEPLPTNISASVAETGKGSTTTKSNLSKGCPLFDDKENKASYQFVKPLQTAFNSSGLVKKNSIS
GSSDRKLPPETPIKRNPLMILNTNKVVPYSSGFAEGKDVMGDQHDYSHIPQONQRFPGSVNPNT
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IELDDNIIPETPTKKSLLPNQHHQHLLPLYTQSKSPLLKFDTEKDGRNLSIVLDKSNATKREISE
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NIKYIGSGAFSIAFECLFNNKFAIKRTKKPLIGKLEKQTIKREIEALRVLTSIKEDATNMQE
EGKEYLVYFIEAWDFNNYYIMTEFCEGGTLDFLEENKHYKIDEFRIWKILIEILNGLKFIHKN
YLHLDLKPANIFITFEGSLKIGDFGLATKLPILKDFDLEGDRNYIAPELINDKIYTPFADIFSLG
LIILEIAANIILPDNGTPWRKLRSGDLSAGRLSSDNISMFLQHNPNNTNSNISGSGSRSGSGSTGG
NGSAGD

YJL189W_homolog 887bp public: 1..666, PathoSeq: 667..887; exon 1:
501..506, intron 1: 507..737, exon 2: 738..884 (SEQ ID NO 385)
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AGCATTTGTTGATGGCGTTTAAAGCATCAGCTAAGACGGAGGTTCTAGTCATGGTTGAATTGTCTGT
TGATAAAAAGAAACCGTGAAAAGGAAGTATTGTGAAAAATCGATTGATATTTTTTTTTTCCCTCCT
TCCTCAGTGTAAACAGTAGTAAACACACTAGTTACAACCTGATGACCTGCATATTATAAATCTTTCTG
AAAAAATTTTTTCCCTGTATTTTTGTAAATCTTTTCGCTCTTTCTCACTCACTCACACTTATTAAT
GAATGAAAGGTTTGGTGTCTACAACTCCACTAACAAAATCTCACTCCTGTGCCTAAACACACACA
GACCCACACGCAAACTTTCTCTCAGAAACAGAAAAAAAATTTCAAGCAAAAATTTTTTCCATC
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AATGATGTCTTTTCACTCTTTTATTTGGGTGATTATTATAATAAATGGCAGATGAGAAATATATTGGA
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TGCTGGAACAAAGACGAGAGAACTAGACAACTCAGATATAATAGAACATCCATACTAATCTCACTC
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GACCATTGCCCAATGGATCAGATTGAGAAGTACAACAAAATCAGATACAATGCTAAAAGAAGAC
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YJL189W_homolog 51aa (SEQ ID NO 386)
MPSQKSFRTKQKLAKAQKQNRPLPQWIRLRTDNKIRYNARRHWRRTKLG

YJL190C_YLR367W_homolog 893bp public: 1..893; CDS: 501..890 (SEQ
ID NO 387)
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AGAGAAAGGTTTGGTGTGGGTCTGTGTGTGTTAGGCACAGGAGTGAGATTTTGTAGTGGAGTT
TGTAAGACACCAACCTTTTCATTCATTAATAAGTGTGAGTGAGTGAGAAAGAGCGAAAGAATTACAA
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CTTTAAACGCCATCAACAATGCTGAAAAAACTGGTAAAAGACAAGTCTTAATCAGACCATCCTCCA
AAGTCATCATAAAAATCTTGACTGTCATGCAAAAACACGGTTACATTGGTGAATTGGAATACATTG
ATGATCACAGATCCGGTAAAAATGTTGTTCAATTAATGGTAGATTAAACAAATGTGGGTGTCATT
AACCAAGATTCAACGTCAAAATCAACGACATTGAAAGATGGACTGACAACCTTGTGGCAGCTAGAC
AATTCGGTTACGTTATCTTAACCACTTCTGCTGGTATCATGGACCACGAAGAAGCTAGAAGAAAGC
ACGTTTCTGTGTAATCTTAGGTTTCGTTTACTAG

YJL190C_YLR367W_homolog 130aa (SEQ ID NO 388)

MTRTSVLADALNAINNAEKTGKRQVLIRPSSKVIKFLTVMQKHGYIGFEFYIDHRSGKIVVQLN
GRLNKCQVIQPRFNVKINDIERWTDNLLPARQFGYVILTTSAGIMDHEEARRKHVSGKILGFVY

YJL197W_homolog 4619bp PathoSeq: 1..3041/3260..4619, public:
3042..3259; CDS: 501..4616 (SEQ ID NO 389)

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CTTATCCTTTCTGTAAATTTCTTGATCTCTGTTTGAATCAACAACGCCTTTGTTTTCTCTTTCTGCC
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MPDNIEDRSEIPSDAKEIVTTNEI EATDSEHTTNVDNELPQGESNEQTGDDSDNDNLASKRQLINDL
LHNDHFEEGTERYIIPQNFLHEFLNLPIDNFSDLKDLGLPIDFHSLLNEQGNLYPENEEPVTFCHV
SPEVFOHLGEWFGILGQPIIRAI IINPDTKKQIERFPPLFWVHQLGKKTQPTYLRHRHNGSNHNH
HHHGHDSPIPVLLSKTSTFHRLMDVIRYNVLKAPRKSTKDFRIWFIVPQDKGLQYLI SIQTFMFI
ISKKTIVSPNMLEDALKDHGIVASSYIMVEAKEKHQTEFPIDQFILSHSNAYEEVSQGGGHLGLS
NMGNTCYMNSALQCLLHVPEINYYFFNIYKKELNFNPLGNYHGDVANAFCEGSLLKQAFDHVKNSS
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KLANTCWNQHKARNDSVIIDLFTGLYQSTLICPCDGKKSITFDPFNDLTPLPI SKKWHYFTTIVD
LSNQGVIPERIMKLEVLNKTSNFDDLLSYLSNFINLVPSTELFAYEIFQNAIYSDFQLDYTKNKFL
PISDIIRDTDVIVYIVPHNPAVDIIVPVFNAVEDADSSYQMVNFPGIPLFVVMNKEVDVNSFGFI
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NLPNPELEKNRAHFERQRKAKITLSDCLKSFSTPEILGEHDLWYCPRCTEHKRATKTIQLWSTGDI
LTHLKRPHSARAFSDKIDVLVDFFPIEGLDISSYVANTDLTPEDCLYDLIAVDNHYGGLGGGHYTA
SVKNFRDDKWYFYFNDSRVTEINNPQEVVANSAYLLFYRRRSSKGAGILGGENFIDLLQKGREEYSE
SLQKKRLDVLQNVGQIVNTYAKIEQDIIDKETEKQKEQEQEQEQEQEQEQEPEVQEPDQEQEP
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YJL198W_homolog 896aa (SEQ ID NO 392)

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QNIINIDVFKFTQAYNYSDEPNIIINTDDHHQYHLKSTLSRTVTNASVFD TINHIDNDYDNNNNNQKN
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SNKLTQSTTKEDLDNIKFELRSYLRDHIVFERNTVWKDLSLEKKSYNIDLDNSVVQNNKMGEDE
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CLAVLVAAAMLWASEALPLYTTALLIPLLVVTCVKCTPGTDDPMDATKASQYIFGTMWNSTIMIL
IGGFTLAAALSKYNLAKILSSYILALAGTNPRNVLLAIMCVSLFLSMWISNVAAPVLCFSLIQPV
RSIPTDSPVAKALVLGIALASDVAGMASPIASPQNVIALESMPNPNPGWKWFAVALPVAIISLILI
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YJR049C_homolog 2279bp PathoSeq: 1..839, public: 840..2279; CDS:
501..2276 (SEQ ID NO 393)

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YJR049C_homolog 592aa (SEQ ID NO 394)

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SAFRTVLSKCFDSGVKANLRMRFTCRVHTDEGKLICEQQVLNELVVDGRGPSYVTHLELYGDGSL
TVAQADGLIIATPTGSTAYSLSAGGSLVHPGVSAISVTPICPHTLSFRPILLPDGMFLKVVPSSS
RATAWCSFDGKVRTELKKGYVTIQASPFPLPTVMSSKTEYIDSVSRNLHWNIREQQKPFSSYLKP
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YLR048W_homolog EMBL_entry 1042bp public: 1..1042; CDS: 28..786
(SEQ ID NO 395)

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YLR048W_homolog SWISS-PROT_entry 253aa (SEQ ID NO 396)
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IKESSYVNIPVIALTDMQSPSEYVDVAIPCNNKGKHCIGLIWLLAREVLRRLRGIIPDRTTTEWSVM
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YLR088W_homolog 1335bp public: 1..80/494..776/821..1335, PathoSeq:
81..493/777..820; CDS: <1..1332 (SEQ ID NO 397)
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YLR088W_homolog 444aa (SEQ ID NO 398)
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LSSVSAVVVAGFDRLKLYFVVVVEIACAIIAFVVPVQVMLVAISAVVLLPRQAIFSKQAFLISI
ALLAVALLLITALLIVHFALAFSIGILALPLTFVPTLMKNKSRLTAFCLAVSNPFFVIFVAGKVLGH
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YLR167W_homolog 1190bp public: 1..1190; CDS: 501..1187 (SEQ ID NO
399)
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YLR167W_homolog 229aa (SEQ ID NO 400)

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YLR234W_homolog 2390bp public: 1..2390; CDS: 501..2387 (SEQ ID NO 401)

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YLR234W_homolog 629aa (SEQ ID NO 402)

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YLR241W_homolog 3098bp public: 1..827/2190..3098, PathoSeq:
828..2189; CDS: 501..3095 (SEQ ID NO 403)

ATATATAGAAATTATGGCTTAGTGCCCTTTATTAACTAAATTAGAGGTTACATTAATACAACCTTAAC
AAACAAGGAACTAACATCCACGTATAGGGCTTCTTATATTAATATACCTAATTCAACCTGATTAT
ATTGCCCTTATATACAGCTTGTAACAAAAACACATAAGAAAGTTTACATCTCAAGATGAATTATCCCC
CTATTGTAAAAAGTACATCGCCTAATGATAGACATCATAGAGTACTGGCGACTCCTTACATGATGG
TAACGACAACAACACTACAACAAAAAACAATTATCTTGACGGTATAATTAGTAGTGTGCGAGAGG
CACACGATAAGATTATCAGTTTCTCTTTCTCGGTTGACCTTAATCTGTTTTTGTATAGACTTTTAT
TTTTTTTGTTTTTGACCACACCCACTTTTTAATATCACAAGATATTTAACTGATTATAGAAAACAA
CAACAATAACCCAAATACGTTAACCCTTTTATTACATATGATAGACAATATAATCAATAATTTGC
AAATCATACTACAGCAAAATGATGATAATTTTACATCCCTCAGCAGCATGTGATATATCGACCAC
ATTCTGCTCGTGTAGCAGCATCAAGTAATAATTGCATCTACATTGGGACTCACTGCCCTATTAC
TATTTTCTATCTTACGATTAAATATCCCAAAATATATGTGGCAAACCTTTAATCATTTGAATTTCA
GTCTACATTTCGACCTCAAGAAAGGAATTTTACCTGAATTGCCCTTCAAATTCATTATTTGGTTGGATT
CTACAGTTTACAAAATTACTGAGCAAGAAATTTTGGAAACATGCTGGATTAGATGCAGTTGTGTTTT
TGGAAATTTTTTAAATGTGCATTCTGAATAATAAGCATATGTTTAGTATTTGCCATTATTATCATAT
CTCCTATCAGATACAAGTTTACAGGGAGAGTAGATGAAGATTATCCCGACGATGATAGTGACAACG
ATGACGATGATGGAAGTAATAATAATGGTACCACAATAATTAAGCATATAGTGTGAGCTGGAATTC
TGGTGCAAGTAAAAATAACGATGGAGAACAGTATCAACAATTTCTTTGGTTATACACTATTTTCA
CCTATGTATTTACATTTGTTACTGTTTACTTTCTATTCAAACAAACCAATAGGATTATTTCTATGC
GTCAGAAGTATCTTGGATCGCAAAATTCAGTCACCGATAGAACGGTAAAAATATCTGGGATACCAG
GATCATTTACGAGATGAAGTGGCACTCGCACGGCACATTGACCGTTTGAATATTGGTGAAGTGGATT
CTGTGTTGATTGTCAAGGAGTGGCAAAATCTAAACAAACTATTCAAAGAAGGAGAAGAATAGTTC
GAAAATTAGAGGAAAGTTGGGTTGAATATTTTGAAAAAATGGGATAACCAATAAGAGCGATTGGA
TATCGTTGCATCCCCAAGTTGGCGAACTGTATCGTTTTTCCAATAGGTATACTGATGATGCAGAAG
AATCACCAGACTGGGGATCTCAAAATTCGAACCTCTGCACAAGCTTCAATAATAGATCAAGACTCAG
AATCTGTTGAAGGAGATTCTTCTGACACTTTGAATCGCTTGTGTAATGATGAACGAGAACAAGAC
CAAGTCTTCGGAAAGGTTGGTTCGGATTGTTTGGACCTAAAGTGGATTCAATAAACTACTACACCG
ATAAATTGGAGGTCATAGATAAAGAGATTACCAGGGCCAGAACTAGAGAATATCCCGCCACTTCGA
CTGCATTTCTCACTATGAAAACCGTGGCTGAAGCAAAATGTTGGCACAGGCAGTCTTGGATCCAA
AAGTCAATCATCTTATCACCAACTTGGCCCTGCTCCTCATGATATCCGATGGGATAATTTGTGAT
TAACTAGACAAGACAGAAATACAAAGATCCTTGCTGTACGATATTTATTGGTATAATGAGTTTGT
TGTTGGTTTATCCAGTCAGATTTATGGCTAGTTTTTTAAACACTAAAAGCATTTCTAAAATATGGC
CATCATTTGGGGAAAGCTATTGAATCGCATAAATGGGCCGAAACTTTGATTACTGGATTATTGCCAA
CTTATTTATTTACAATTTTAAATATTGTGATTCCGTTTTTTTTATGTATGGATTTCTGAAAAGCAAG
GTTATTTATCTCATAGTGATGAAGAGTTGTGATCGGTATCCAAGAACTTTTTCTATATATTTGTGA
ACTTATTTTTGGTTTTTCAAACTTTTGGTACCGCCTCTTTTGTGATACGACCAAAATTCATTTG
ATTTAGCAAGATCACTCAGAGATTTGTCAATGTTCTATGTTGACTTAATAATTCTACAAGGATTGG
GTATATTTCCCATTCAAATTATTATTGGTGGGGAACCTTACTTCGCTTTTTTAGTGAATTCATTATTA
GGTGCAAGACCCCAAGAGATTACTTGAATTTGTACAAACCGCCAGTTTTCAATTTTGGTCTACAAT
TACCACAACCAATATTGATATTTATTATTACGTTGGTATACCTCGGTAATGTCTTCGAAGATATTAA
CTGCAGGGTTACTATATTTTTATTATTGGTTATTTGTGAGCAAATACCAATTGCTTTATGCTTGTG
TTCACTCTCCACACTCAACGGGCAAGTTTGGCCAATAATTTCCGAAGAATCATATTAGGGTTAT
TTCTTTTTCAAATCACAATGGTTGGCACATTAGCATTACAAGATGCAATCACATGTGCTACTTTCT
TGGCACCATTGCCGTTTTTGTACACTTTACTTTTGGTGGAGTTTCCATAAACAATATATTTCCCTTGT

CAACATTCATTGCCCTTGAGAGCAATTGAAAGCAATGAAAATATCAACCCTACTGATTTGGAGCAAA
TCATTGAAAACAACAATAATAAACTCTTGACGAAAGAAGGAATTGAACACTAAATACGAATACC
CCAATCTAGTTAATGATTTAGACGGGCAATGATTGCATTGGATGGTGAAGATGTATTGATAGTTA
ATCGAGATGGTACAACGTGTACGGAACCACCTCAATATTTAGTTTCAAGATGGGACTATTAA

YLR241W_homolog 865aa (SEQ ID NO 404)

MIDNIINNLIQIILQQNDNFTSPHDDVIYRPHSARVARYQVIIASTLGLTALLLFSILRLKYPKIY
VANFNHLNLSLHSTSRRLPELPSNSLFGWIPVYKITEQEILEHAGLDAVVFLEFFKMCIRIISI
CLVFAIIIIISPIRYKFTGRVDEDEDYDDSDNDDDGSDNNNGTTIIKHIVSAGISVASKNNDGEQYQ
QFLWLYTIFTYVTFVTVYFLFKQTNRIISMRQKYLGSQNSVTDRTVKISGIPGSLRDEVALARHI
DRLNIGEVDVSLIVKEWQNLNKLFRRRRIVRKLEESWVEYFEKNGITNKSDLI SLHPQVGESYRF
SNRYTDDAESPDWGSQNSNSAQASI IDQDSESVEGDSSDTLNRLNDESRTRPSLRKGWFLFGP
KVDSINYTDKLEVIDKEITRARTREYPATSTAFITMKTVAEAQMLAQAVLDPKVNHLITNLAPM
HDIRWDNLSLTRQDRNTKILAVTIFIGIMSLLLVYPVRFMASFLNNTKSISKIWPSSLGKAIESHKWA
ETLITGLLPTYLFTILNIVIPFFYVWISEKQGYLSHSDEELSSVSKNFFYIFVNLFVFTTFTGTAS
FVDTTKIAFDLARSRLDSMFYVDLIILQGLGIFPFKLLLVGNLLRFLVNSLFRCKTPRDYLNLYK
PPVFNFLQLPQPILIFITLVYSVMSSKILTAGLLYFIIGYFVSKYQLLYACVHPHSTGKVPWI
IFRRIILGLFLFQITMVGTLALQDAITCATFLAPLPFLTLYFWSFHKQYIPLSTFIALRAIESNE
NINPTDLEQIIENNNNKTLDERRELNTKYEPNLVNDLDGPMIALDGEDVLIVNRDGTTVRKPPQY
FSSEWDY

YLR321C_homolog 1559bp public: 1..947/1189..1559, PathoSeq:
948..1188; CDS: 501..1556 (SEQ ID NO 405)

TTCCAGAATTAGTAGATATTTCTGATATCAAGTFTGGAGATAGGGATATCGAACTGGGATTCTATAT
TTTGT'TTTATCTTGGAGAACC'TGTGTGTGTGTGGCGTTCTATCTCTTTATATATTTTCTCTATTA
ATTCAATTGAAACATTTGAAGGAAATCTTTCTTAAAGCATCTAGTGACACATGATCTCTAATCT
CCAGTCTTTTGATTAAATATCTTTTAGAATATCAGGTGAAGAAGTGTGGTAGTCATAGCTAGTA
GATACTGTGTGGTGTCTGGGATAATAATTAATGTAAACAAAACAAAGTCGTGTCAAGTGTATATT
TTTCTTTTGTCAATTCATCTTTTCTCTTGGAGAAATGTATAACAGAGGATCCATCCATT
TGCTTGACAGAGAAATACAGAACACTAAACAAACATTTTTCATTCTCTTTCTTGT'TTGTCTGT
ATACCCCAAAAGTTTGAATAAGTCTTCAGATATCTAGCATGGCAACTTCTCAAGAATTGACAGCAG
ACATACAAGCTCTTGCAACTAGTTTCCCAAGCGATTAGCTAATGATAGTGACAATTCATTACTTA
TTAATGTTGCACCAACTGGTTCGACAGCCAAAAGACATATTCAACAGATTAATTAATCTCCGAAGAGT
TTGGAGATGACCTTGATTTTGATGAATTCCTCTTCGACACCCGGTACTAGAAGCTTAAATGAAA
ATAAAGCTCAAATAGAAGCACAAAGATATTCTTGGGAAAAACACACCAACGCCCAAGAGAATCT
TAGAAAAACCGGTGTATCTGAGTTGGTTGAAAAACAGTGGTGTATTCTCTATCAAAATAATGA
TTGAGAATTTGAACACAAACCAAAAGTTGATTGATTCTTTATGTGGAACCTGAATGAAAGCTTGA
TTACACCAACTGAGTTTGCAGGAAATGTTTGCAGTGATTAGATTACCATTAGTATGGCTGCAC
AAATAGCAGACTCCATTAATCAACAGATTGAAGAGTATTCCTATGCATCTAATTTACAACCTACCAA
ATAAGGGCCCTTACAATGTTACCATTGATTTATCAGTAACTTAAATAAACAATTATACCAAGATA
GATTTGAATGGGATATGAATCAAAATGAAGTTACACCAGAAATTTTGTCTGAAATAGTTGTTGCTG
ATTTGGGGTTATCGTTAGAATTTAAGAAATGCCATATCACATGCATTGCACGAAATAATTATCAGAG
TGAAAAAAGAAGTAATAGATGGTACTTTTGACAATGAAATGCACAACCTGCATCTAGTAAAAGGTA
TAATGTTTGAACAAGGAATTAGAATTTTCACTGAAAAACAGTGTTCAAAATGGAATGACCGTTGGG
AACCTTTGGTCGAAGTATTGACTTCTAGTGAAATCGAAAGAAGAGAAAATGAAAGGGTTAGAACT
TGAGAAGATTAAAGAGAGAGAATATGAGAAGAGATTACGATGATAGTAGGAGAAGGCAAGCAG
GAAAAAGAAGGTATGATGAGTTAGAAGGAGCCTGGGTATAG

YLR321C_homolog 352aa (SEQ ID NO 406)

MATSQELTADIQALATSFPRKLANDSDNSLLINVAPTGRQAKRHIQQINYSEEFGDDLDLDFDEFPSS
TPGTRSLNENKAQIEAQRYSLAKNTPPKRILEKPVLSLVEKPVVLIPIKIMINIENLNTNQKLIDS
FMWNLNESLITPTEFAEIVCSLDLFPMSMAAQIADSINQIEEYSYASNLQLPNKGPYNVTIDLSV
NLNKQLYQDRFEWDMNQNEVTPEIFAIVVADLGLSLEFKNAISHALHEIIIRVKKEVIDGTFDNE
MHNHLHLVKIMFEQGI RIFTENS VQNGNDRWEPLVEVLTSSIEIRRENERVRNLRRLKRENMRDY
DDHSRRRQAGKRRYDELEGAWV

YLR325C_homolog 737bp PathoSeq: 1..737; CDS: 501..734 (SEQ ID NO 407)

AAGAAAAGTATAGTCAAATTGTTATACAAGCTAAGGAGCCATAAACTTTCTTTGGACATGCTAATA
TCGCTCCTGACCATTGTTTACTATATTCAACAAAACGAATTCAACAAGGCAAACGAAAGCTACATG
AAACTAAGTATCGGCAACGCTCTGTGGCCAATTGGGGTGGTCAATGTAGGTATTCATGCAAGAAGT
GCAGCACTGAAAATAACCGGTGCCTCTAACGTCAGTAACATAATGCTAAGCGAGTCTACACGAAGA
TGGATTATAAGTATAAAGAGGTTGATTAGTTTTAAAGAGAGAGTATATAATAATGCACGTGATTAG
TTTAGTAATTTTTTTCGAGTTAGGGCTATAGCCCTAAGACATTCACACAACCTAACAAAAAGGAAGT
TCTCACGCACATAACGTGTAACCCACATAAAGAAAAGAAAAAAATTTCTTTGAAAAAATTCACA
TCACGCTTTAACCCTTCAACCTATAACAACCTCAACCATGGCTAGAGAAATCAAGGATATCAAAG
AATTCGTCGAATTGGCTAGAAGATCAGACATCAAATCTGCTATTGTCAAAGTTAACGCCAAGGTCA
ATGCTAACGGTAAAAAATTCAAACAAACCAATTCAGGTCAGAGGTTCAAGATACCAATACACTT
TAGTTGTCAACGATGCTTCTAAAGCTAAAAAATTACAACAATCTTTACCACCAACCTTAAAAATCA
CCAACCTGTAA

YLR325C_homolog 78aa (SEQ ID NO 408)

MAREIKDIKEFVELARRSDIKSAIVKVNANGKKFKQTKFKVGRSRYQYTLVVNDASKAKKLQ
QSLPPTLKITNL

YLR344W_homolog 1348bp PathoSeq: 1..1348, exon 1: 501..515, intron
1: 516..979, exon 2: 980..1345 (SEQ ID NO 409)

ATACCATGACAAGCAAGCTCAGGGTCGCGGGTTCGAGTCCCGCGGGGAGCTAATTATACCCTCATT
TTTGAACCCACCAAATTTCTTTCACATTATAATGAAATAAGAGTATCCCTGGCTTCTTTTTTTTT
TTTTTTTTTGGCAATATAGAGAAGACTGTAATAAGTATAGCTCACTAAAGTCTTTTTTTTTTCTATT
CGTTTTATATTTTTTAAGAAATTTGATGTTGATTGGTAAATGCCAAATTTTAAATGTGTGTAG
GGCTATAGCCCTAATGTACTGTATATGCAGTATCAGAAATACTTTTGTACGCACAGTTTGTCTTA
CCAAATACATTATATATATATATTTTTTTTTTTTGAGTAGAGGAGCTACACTAGACCACAGTGC
AAAAATTCATCTCTCTATACACTTACTCAATTTGAAGATATTCAAATTTTTTCAAAAAAAATTC
CTTTTGGATCGATACTAGATAGCATATAATCATCAAAAATGGCCAAGATCAGTCAAGGTATGAAAT
AGATATTCAATTAGATATGGAGAAAGGAAGATAAAAAGGAAAAGAAAAAAGAAAGAAATAA
AGGAATATATACATTGAAAAGGAGATAGAACATCAAAACAACCATTAAGAATTAAGTTTAATAC
AGTTTCAATAAAGAGGGTTTTTTTCTCAGAACAACCATTTGACTGAAGTACTACACCAAGAGGTA
TAATGATTTACCGATTACCTGAATATAAAGAACATCCTTAATATTGAATTTCAATATTAAAAATA
CAATTTGGGGATATTGATGAAATTATGTATAGGAGATTCCATTTTTCAAACCTGTTGAATGGAAAA
CTTGAAAAATCAAATCAAATCAAATCATAACCCTTCAATATATTCCTTCTTATCTTACTTTTCTC
ATTAAAAACAAGACTAAGAAACATTCAGTAAAATACTAACAATAATTCATTTATATAGACGTTTC
TTCATCTCGTTCTAAAGCTAGAAAAGCTTATTTCACTGCTTCATCAGTTGAAAGAAGAGTTCTTTT
ATCTGCTCCATTATCCAAAGAATTAAAGACAACAATACAATGTCAAATCTTTGCCAATTAGACAAAA
TGATGAAGTTTTAGTTGTTAGAGGTTCTAAAAAGGTTCTGAAGGTAAAGTTAATCTGTTTATAG
ATTGAAATTTGCTATTCAAGTTGATAAATTACAAAAAGAAAAATCAAATGGTGCTTCTGTTCCAA
CAACATTCATCCATCTAAAGTTGTCATTACTAAATTACATTTGGACAAGATAGAAAAGCTTTGAT
TCAAGAAAAGGTGGTAAAGCTGAATAA

YLR344W_homolog 127aa (SEQ ID NO 410)

MAKISIDVSSSRKARKAYFTASSVERRVLLSAPLSKELRQQYNVKSPLIRQNDVLLVVRGSKKGS
EGKVNSVYRLKFAIQVDKLQKEKSNGASVPINIHPSKVIVITKLHLDKDRKALIQRKGGKAE

YLR393W_homolog 1631bp public: 1..1207/1209..1631, PathoSeq: 1208;
CDS: 501..1628 (SEQ ID NO 411)

TTCATCTTTTCGAAATCTTCCCTCTTGGAAACGACCAAGAGTTGGATTCCGGTGCCTTGGCTAGCAC
AACTTTGTTCAAATCTTTATTGAATAATGCAACACCACGAACCGGTATGGTCGATTTATATTTTCC
GAATTTAGATAATGCTTCCCTGTGGGTCACCCCATTTCAAATAAGCGGGCATTTCTCTAAAAATCTT
TGTAAGTGAACGTTTCATCTTCATGCTTTGCAATCGGGATTCAACTGACGAACAAAGTCAGCATA
AAACCAATTGTGCTTCCCTCAATCTGAAACATTATTCTTTCAATGGAAGATAAATCCTCTTCGGGAAC
ATTCACCACAAATCTAACTAACAAATCTTCCAACACCCGATCTAGAGTTTGATTAGCTAAACCATT
CGGTAATTGGATCGACATATCTTGTATTCTTCTATGATTAAATCTTTCTTTTTTCTTTCTTTTTCAC

TGAATATTCGTAATTAAAAATTGATTCAAATTTGATTGATGTTTGTATACTGGATAAACAACTTGT
GTGAGATCATTCATGTATTTGCTGGCGGAGAAGGAGGCAAGGACGAACTTTTTTCTTCATACT
TTTTTTTTTCTCTCTCTCTCTTTTCTTTTCAGTCACATTGTCTGAGTGTTAAAGGCTGGCTTTTCTGTG
CTGAACCTTGTGGACTGGTAAACGCACGACATAGAGTAATATTTGGAGAAACCAAAGAATTTTGA
AAAACCGTGGTTTGAATTCGACCACAGATTGGTTGGACGACAAAATGCAAAGTGATTTCATCCGGA
CTTTTGCTACCTCAAGAATAGAGTTCCAGCGGTACCAGCCGCGTTTGTTAATACCATTAAAGAAA
CGGTCAAATCGGCACAAGAAAAGTCGTACAGTATTACTAGACCATTGGGGTTGTCAAACACAGTTT
TGTTAAATCATAAATTGTTCAGACACATCTCATTTGTCCAATATATACGAGGAGTTGTTTGGTCAA
AATCCAAAGAAAGAAGACAGAAACAACCTAGACTACGATTTGAAACACTCGCCAATTTATGAAGTCA
AGTCATTTGAGAATACAAAGGGGAAAAATTTACTCCTCCTGTTTTCGTACTTTTCGACAAGACAAAT
CTTTGTATTTCCCGGATTTTATAGCGAAACATTGGCAGGTAATCAGAGAAGTTTGTACGACTCAT
TAGACAATAGATTAAGCATAGTCAAATTTGTTTCTTCTGTTGCTGGTGAGCAGTGATCCCGTTTCGT
ACTTTAAGGTTGAAAACAAGATTACTATTTCCAGGATTATGATACCTTTGTGGAGGAATATCCCC
ATACCCAGATACCTTGATGTGAATATGCCGAAAGTTGGATCAAGGGGTTTGTGACAAACTTGAGCA
CAGGAAATTTAAGAAAGACTTTGAAGCCAGCTCTGAGATACGAGAATTATTTTCATCTTGCCTGGCC
ACATAATGTGACGGGAAATTTAGAGAACAGTTGTACTGTGATAATCAATGTTCCGGGTATATTTATA
TTGTTGATTCGATGGGGAAGATAAGATGGGCGACAAGTGGGTATGCAACTCCTGAGGATTTGAAAT
TGATGTGGAAGGTTGTGAAAGGGGTGCAAAGAGAAATGACCAAGTAA

YLR393W_homolog 376aa (SEQ ID NO 412)

MFVYWINNLCEIIQCICWRRRRQGRFFPSYFFFLSLFFQSHCSSVKGWLFC AEPCGSVNARHRV
IFGETKRILKNRGLNSTTDWLDDKMVSFIRTFATSRIEFQRYQPRFVNTIKETVKSAQEKSYST
RPLGLSKPVLNHLKLSDTYSLSNIEELFGQKSKERRQKQLDYDLKHSPIYEVKSFENTKGKIFTP
PVSYFRQDKSLYFPDFIAKTLAGNQRLSYDSLNRSLIVKLFSSVAGEQCTRSYFKVENKDYYSQD
YDTFVEEYPHTQILDVNMPQSWIKGFVTNLSTGNLRKTLKPASRYENYFILPGHIMS AEIREQLYC
DNQCSGYIYIVDSMGKIRWATSGYATPEDLKLMMWKVVKGVQREMTK

YML063W_homolog 1271bp PathoSeq: 1..773, public: 774..1271; CDS:
501..1268 (SEQ ID NO 413)

CCAGTGCCTTTTGTGTTTCCACATCATACACTTCACTGAAACTAAATAAGTTTGTTTACATTTT
GAGACTTCAGGTACGACCCAGGGTTGCGACAAAGTTTAGGTAGTTTGTCTGCTGAATGTCGCAACA
AAATAGGGCTGTAGCCCTAGTCATGTGATGTGAATTAACATAACAAGAAGATTGCTGGTGCAGCA
AAAGATTATGTGTATTTTATGTGCGTTGTTATCCTGCACACTAAAATTGAGCAGTGACACACACA
CATATTGGGCTGTATTTTATTCTTTGTTTTCTGCTGTTCTCTCACTGTTAAGCTCTAAGTGAATT
TGTTGTGCTGTAAATAGTGTGTGTGTTCCAGTCCCAGCTCTCACAGATACTCAGCAGCAGCCCAT
CTACTGAAAATTTCTTGACTTTCTGTATCTAAAAATTTTTTACTAGGAATTTTTTTCTTTTACGTT
TTTCACTTGTTTTCATATAATCACCAACTCAAGTACAACATGGCTGTGCGTAAAAACAAGAGATTGT
CCAAAGGAAAGAAAGGATTAAGAAAGAGGTGCTTGACCCATTACCCAGAAAAGATTGGTTTGACA
TCAAAGCTCCAACCACTTTTGAAGACAGAAATGTTGGTAAACTTTGATCAACAGATCTACCGGTT
TAAAGAATGCCGCTGATGGCTTGAAAGGTAGAGTTTTCGAAGTTTGTGTTGGCCGACTTACAAGGT
CCGAAGACCACTCTTACAGAAAAATCAAATTGAGAGTTGATGAAGTTCAAGGTAAAAACTTGTGTA
CCAATTCCATGGTTTGGATTTCACTTCTGACAAATTAAGATCATTGGTCAGAAAATGGCAATCAT
TAGTTGAAGCTAATGTCACTGTTAAACTTCCGACGATTACGTTTTGAGAGTTTTTGCCATTGCTT
TCACCAAAAGACAACCAAAACCAATCAAGAAAACCTACTACGCTCAATCCTCTAAATTGAGAGAAG
TCAGAAAAGAAGATGATTGAAATTATGCAAGAGAAGTTTCCAAGTGTACTTTAGCTCAATTAACCT
CCAAATTGATTCCAGAAAGTCATTGGCCGTGAAATTGAAAAATCCACCCAAACCACTTTTCCCATAC
AAAATGTCCACATCAGAAAAGTCAAATTGTTGAAACAACCAAAATTCGACTTGGGTTTCAATATGG
CTTTGACCGGTGAAGGTTCAACCGAAGAAAAAGGTAAGAAAGTTTCTTCTGGTTTCAAAGATGTTG
TTTTAGAAATCTGTTTAA

YML063W_homolog 256aa (SEQ ID NO 414)

MAVGKNKRLSKGKKGLKKVVDPFTRKDWFDIKAPTTTFENRNVGKTLINRSTGLKNAADGLKGRVF
EVCLADLQGSSEHSYRKIKLRVDEVQGNLLTNFHGLDFTSDKLRLSVRKWQSLVEANVTVKTSDD
YVLRVFAIAFTKRQPNQIKKTTYAQSSKLREVRKKMIEIMQREVSNTLAQLTSKLIPEVIGREIE
KSTQTIFPLQNVHIRKVKLLKQPKFDLGSLLALHGEESTEEKGKKVSSGFKDVVLESV

YML128C_homolog 1517bp public: 1..1499, PathoSeq: 1500..1517; CDS: 501..1514 (SEQ ID NO 415)

TGATATGGATTTTTTCAAACTAAGAAACAATACCAACTACAACAACAAGAAACATAAGTGTGCT
TAATTC AATGACCTCGAGTCATATCCCACGTTTTAAGTATGAGTGTGTTTACGAAGTTGTGGATCC
TATTTTAAATAAAACAATAAGTAATAAAAAAAAAAACCTTCTTTGCTTTTCGAGAATTTGTAAC
ACATTTGTTCTTTCTTTCCACAGCAACCAAAATTTTATTTTATTTTCTTTTGGGACTTACCCACA
GTTGCTCAATTATGTATAACAAGGGTAGAAACTCTGTGGGATTCCTCCTTAAAAATATAGCAATC
CTTTTCTTCAACGATTGCTATATGACCCCCCCTAAGCATTTCATTGCTTTTATATATATTTA
ATAATGTATTTCTCTTTGTTTCAGGATAATTATCACTATTTGTGACGTTTAATTTTACATTTCTTCT
TCTTCTTCTTCTTATTTCAACATTAAAGAACATTTAATATGTATTTCCCAATCATTTGTATGGTTAT
ATGTATCTATCACTTTTGTGGTTGCCAATTATGGTTTGTATCAATGGACAAATGATGATTTAAAC
AATTTTAAAGAAGCTAAAGTTGCATTCAATGATGCCTTGGAGAATCCAAATTAATTAGTTTGG
CTAATGAAGAAGCTAAGAAATTAGAAAAAGGTTACAAGAAAGTTACTGAAGAATTAATAACAATT
TGAATCCTCCAGATGATTCAATTAATGATTATTTGAATTTTGATTACTTATTTGGGAAAAGAAAAG
AAAATTATTC AATTAAAGAATGGATTTTGAAGTTGGCCAGTAACCAAGTTTGC AAAC TTTTAA
CTCAAAATAATATCCAATATAGTGCAAAGGATACCAAGATGATTTAATCAATAAGGTTAAAGATC
AATTTGATTCATTTCTAAGAAAAATCATGGGTCTAGTTTTATCCTGGCAATTGGTTATATGAAT
CTTGGTCAGAAAAATGATTGAAAGATTGGTTGAAATCTTATGGCATTGAATTTAATCCTAGTTCAA
CAAAGGATCAATTGGTTGAAAAATTAAAGAATTAGTTATCAAGCCACTCATTCAATTAGAGATT
CCAAAGAATCTTTATTTGATTTCATTGGATTTATTTGATAAAACCATTTTGTATAAAAAAGGTCAA
TTGAAGATGAATTTTCCAACTTGGTCATATCTCAATTACGTGAATGGCTTTATTTACATGGAT
TTATTTGACACTAAACCAGGAATTTACGTTGAAGATTTGGATAAGGAAAAATTAGTCAAGATTGCC
AAAGTTATAAGAAATGTTTGTGAGTGACATTCATACTTGGTTGGCAAACACTGAAAGAAGTCTC
AACCTTGGATCACAAAGGGAGAACAAAAGTCTCAGAAAAAGAAGGGTAGTAATTTGATTAAATGATA
CATTTCTTTGTTGGTATTAATAATTGGTCCAAGGATAAATTGCGTGAATTGGGCAATCTTGACTAA

YML128C_homolog 338aa (SEQ ID NO 416)

MYFPIIVWLYVSITFVVANYGFDQWNTDDLKQFLKERKVAFNDALENPKLISLANEEAKKLEKGYK
KVTEELNNLNPPDDSLNDYLNFDYLFGRKENYSIKEWIFESWPVTSLQTLTQNNIQYSKDTK
DDLINKVKDQFDSISKNHGSSFYPGNWLYESWSENDLKDWLKSYGIEFNPSSTKDQLVEKLKEFS
YQATHSIRDSKESLFDLDFDKTIFDKKGQIEDEFFQTSYSQLEWLYLHGFIDTKPGIYVEDL
DKEKLVKIAQSYKKCLLSDIHTWLANTEKKSQPWITKGEQKSQKKKGSNLINDTFFVGINNWSKDK
LRELGNLD

YML130C_homolog 2243bp public: 1..829, PathoSeq: 830..2243; CDS: 501..2240 (SEQ ID NO 417)

ATGAGTTCATAGATGATCTGTTTCACTTCAAATAACGTGTCAACAAAAATAAAGTTAGAGCATAG
ATTTTGCCGCCACTTGTACAGATGGATAGAATTGAATGCAAAATCTGCATAAAGATTAAAGTGAAA
ACAATTTCCGAAAAAGAAGAAATCGAACACATTAGAAAAAGAAACGAACAAAAGAAAAAAAT
TTCAAATTGTAGTTGCATGTATATAAAATAATATAAAAGATATATCACCAGCACAACTGATTACTT
TTATTTATATACCTGTCAACACAAATTTCCAAATAAATACAACTCAGAAAAACACTTACTAT
CTTTTCTTAGTTTGGTTTCTATAATCTTATTAACATTCCTTGCTTTCATCCTTGATTATCATATT
AGATCTTATCTTTAATTTGTTTGA AAAATAATACCAATAATCTTCCCATTAGAACTTACAACACA
ACAACAAAAAACCCATTCTAAATCACTATTCTCCATTATGAAAATTTTCAGATTATTTTCACTAC
TAATCGTACAATTTATCATAAATACCACTGTGTCAGTATCACCTGTGTCAGCAGTTTACCAAAAC
TGAGTTTCAGTCCATTGATTCAACGAAATTTGTTTCACAGATCATAACTCCCCTTGTAATACAA
CTTTCACCTACATTGATGAATTGAATAAAGATATTCGTCCCTACTTGTGCGGAATTAGTCAAGACCC
TGTATTTCCGTTATTTTAAAGTCAATTTAGATAAACAATGTCGTTTTTGAAGTCTCAACATTTTT
GTGCTAGTGA AAAC TGTGCTGTTGAAATATTGGAAGATTTCAATTGGAGTCAAGTCACCAATGAAA
GTTTGAACCTTCAGGATTAGGTAAAGATTTCAATTACCTGACAAATCATCAATTGATAATTCCATTG
AAACCGAAGAAGTTCAAAC TGTGAAGATTTAGATTATAGTGAAATAGATGATGACCATTTGTG
TTTATGTCAACTTGGTAAATAACCCAGAAAGATTTACTGGGTATGGTGGTAATCAAAGTTTGTATG
TTTGAAGGCTATTTACCTGGA AAAAT TGTTCCTAATACTAATCCAATGTCAGTGACAAATGATG
CCGACAATGGTGGTGAACAATGTATCGAAAAGAACTTGTTTATCGTGTGTTAGTGGTATGCATG
CTTCAATTGCAGTACATTTATCAAGAGAATATTTGAATTCTGAAACTGGTGAATTTTATCCTAATT
TAAAGGTGTTTATGGAAGAGTAGGTATGCATAATGACAGATTATCTAATATTTATTTCAATTATG

CCTTAGTGTCCCAAGCTATAGTTAAATTGAGTGAAATTTTACCATTGAGAGAGTTTCATTCAACTGG
GGTATGATGACATTACTCCAGCTCAAAGCAACATTTATTGGCTAATAATGATGTGCAATCAGTCG
AAGTTTATGATCGTTTGTGTTAGATGACATTATTCCTAGTTTGGGAAGCAAATGTTGTGTTTAATA
CTTCCAACTTGTTTGATAATAGCAATTTGAGGGATGAATTTAGATCAAGATTTAGAAACATTTCTG
CCATTATGGATTGTGTTGGTTGTGATAGATGCAGAATGTGGGGGAAAATCCAAACCATTGGTTATG
GTACCGCTCTCAAGATTTTATTTGAAGATGACAACCTATGATAATCACAATTTGAAATTTAGAAGAA
TTGAAATTTGTTGCCTTGATTAATACTTTTGATCGTTTATCTAAATCTATTGAAAGTATTAATATGT
TTAAAGAAATGTATTTGCAACACCTTAAAGATATTGCTGAAGGATTAACCCAACCTGGTGTTCACG
ACAAAATACAAAACAACAAACCAGGTAACGGATTGTCCTTCCCATTTGTTAGTCCATTACCTCAGA
AAAAACCTGACCAACCAACACCCCCAAAAATCAACAACAAAAACAACCTCAAGAACTGACAAAA
AAAGACTTACATTAGAAGAAATGCCCCACAAAAACCTGAAGATCGAATTTTTATTGAAGACTTCA
GATTATCCTTTGATGAAGTTTGGCAAGCATTAAGATTTGTTTTAACTAGTTATCAAAGATTCCCAG
CCGTATTGATGATTACATTTGTTCAATTGAATGAATGGTGAATAAATTGCTTGGTAAACCAA
CAGTTTATGATTACCAAAGTTCCTTTGATGTTGATGCCCTACAATACAGTCAAGTCCTTGGATAA

YML130C_homolog 580aa (SEQ ID NO 418)

MKIFRLFSLLIVQFIINTTVAVSPVSAVLKSSFSFSPFDSPEFCSQIITPTCNTTFTYIDELNKDIR
PYLSELVKTSYFRYFKVNLDKQCRFNAQHFCASENCAVEILEDNWSQVTNESLKPSGLGKISLP
DKSSIDNSIETEEVQTCEDLDYSEIDDDHHCVFYVNLVNNPERFTGYGGNQSFVDVWKAIYSENCFPN
TNPMSVTNDADNGGEQCIEKNLFYRVVSGMHASIAVHLSREYLNSETGEFYPNLKVFMERVGMHND
RLSNIYFNALVSQAIVKLSEILPLREFIQSGYDDITPAQKQHLLANNDVESVEVYDRLLDDIIP
SLEANVVFNTSNLFDNSNLRDEFRRFRNISAIMDCVGCDCRMRWGIQTIGYGTALKILFEDDNY
DNHNLKFRRIEIVALINTFDRLSKSIESINMFKEYLQHLKDIAEGLTQPGVYDKIQNNKPGNGFA
FPFVSPLPQKKPDQTNTPKNQQKQPQETDKKRLTLEEIAHTKPEDRTFIEDFRLSFDVWQALRF
VLTSYQRFPAVLSRFTLVQLNEWNNKLLGKPTVYDYQSSFDVDALQYSQVLG

YMR022W_homolog 1004bp public: 1..507/668..1004, PathoSeq:

508..667; CDS: 501..1001 (SEQ ID NO 419)

TGTGAAAAAAATTTGTGGTGTGGATGTTGTTGTGCGTTGTTGCCGTGTCACAACAAAAACAAGT
AACAATTTCAAAGTTTGGGCTTGGAGATCGATTTTTTTTCCCGCGTCTGTGTGGCAGGACAATTTG
AGTCGACCAGTACGTTTTAATTGAATACGAGAGTCGACGCAATTACATCAATCCAACATTTCCACTT
ATTCATATATCAATGTAAAGTCATTTTTTGATAATATCGTAATTTACACATTTCTGTATATCTCGGCA
ATAGGGGGGATAAAAAATAGTATTGACTAATTAATATATCTTGTATTATCAAATCAGGAGTATAGAA
TTCCACCAACAACCTAGATTTTCCGAATGCGAAACGACGAGGACGACACAACAACGACTAAAGAAG
AAGAAGAAAAAAATATAAATAAATTGATCACGCACACATTAGAAAACACAATATTGGATCACTTTT
TTCGATAATACTACCACCACACAGCTCATTCAACCACTCATGCCCCGAAGTTCTACTGCTCAAAAGC
GTTTACTAACAGAGTATCAACAATTATCGAGGGACCCACCACCTGGGATAATCGCAGGACCAGTGA
GTGAAGATAATTTATACAAATGGGAATGTTTATTAGAAGGACCATCCGATACTCCATATGCAATG
GAGTATCCCCAGCAGTATTGACTTTCCCTAAAGATTACCCATTATCACCACCTACATTAAAGTTTG
ATCCACCATTTGTATCCAAATATTTATGCTGATGGAACCGTTTGTATTTCGATTTTACATCCCTC
CTGGTGAAGATCCAAATCAATATGAACGACCAGAGGAAAGATGGTCACCTGTGCAAAGTATTGAAA
AGATCTTGTGAGTGTCTATGCTTGCAGAACCTAATCCTGAAAGTGGGGCTAATATCGATG
CTTGTAATTTATGGAGAGATAATCGTGCTGAATATGACCGACAAATTAGACAACATGTCAAGGAGT
CATTAGGATTATGA

YMR022W_homolog 167aa (SEQ ID NO 420)

MPRSSTAQKRLLEYQQLSRDPPPGIAGPVSEDNLYKWECLLEGPSDTPYANGVSPAVLTFPKDY
PLSPPTLKFDPLLPNIYADGTVCISILHPPGEDPNQYERPEERWSPVQSIEKILLSVMSMLAEP
NPESGANIDACKLWRDNRAEYDRQIRQHVKESLGL

YMR118C_homolog 1031bp PathoSeq: 1..1031; CDS: 501..1028 (SEQ ID NO 421)

CTACACAAAGCTTCGAGAGTTTTTTTTTTCGTTGCAGGGGTGGGACAGGTGAGTAACGAATAAAACGT
CGATTGTCCTTCCCTTTATGATTGTTCTTTAACGGAATTGTGTTCTTAAACAAAAATCAGTTCTGC
ACGTGATATAATCTCCTATCGCTAGTAGTAAGTTTAAATTTTTTTGATCAAAAGTACACTCATCAG
TCTATTGTCGTAGATTTTCGCATACTTGTGATAATATCTGGTGTGTACACTACTTTTTTGGTTTGTG

TTGTAAATTACAATTTTTCTATTGGTTAAAATGATAATTGTTAACAAGTCTTTTTTTTCCCGGGA
TTGAATCCGGAACTACCATTAATTCACCTACTTACTCACTCACCTTACACCCTCACTCACTCAA
ACAATTATATCAACCCAAAAAATCTTCACTACACCAATAACAAAGAACCAATAGTTCAAT
CTAATAAACCATCCTTCCCCCTAGCCTGCCACAACAACATGATTTCTCGTATTGGATTATTGAAAA
GACCTACCGTGTCCACTTTAAACAACATATGTCAAATTACAATCGACATTAGCCCTTAAAAGATACA
CATCAACCGTACCAGCAACTTCAAATCAAGAACAAGAAATATTGGTTGCCCAACGTAAAAATAGAC
CTACATCACCTCATTTACAAAATTTATGAACCACAATTAACCTGGATCATGTCATCATTCATAGAA
TCACTGGTGTGTGCTATGGCCGGTGCCCTTTATGCTTTAACTTGTGGATTGTGCTACTTCAATTT
TAAATATTCCATTTGATACTACTACTTTAGTATCTGCATTACCACATTACCAACATTTGCTCAAT
ATGGTATCAAAGCTATTTGTGCTTATCCATTTGTTTATCATATTGGTAATGGGATTAGACATTTGG
TTTGGGATTTTGGTAAAGAATTAACCATCCCTGGTGTTTATAGAAGTGGGTATGCTGTTTTGGCTG
CTACTGCTGTCATTGGAAGTTATTTAGCTTTCTTATGGTAA

YMR118C_homolog 176aa (SEQ ID NO 422)

MISRIGLLKRPTVSTLNNYVKLQSTLALKRYTSTVPATSNQEQEILVAQRKNRPTSPHLQIYEPQL
TWIMSSFHRTGVAMAGAFYALTCGFAATSILNIPFDTTTLVSAFTTLPTFAQYGIKAICAYPFVY
HIGNGIRHLVWDFGKELTIPGVYRTGYAVLAATAVIGSYLAFLW

YMR230W_homolog 1176bp public: 1..1176; exon 1: 501..551, intron
1: 552..870, exon 2: 871..1173 (SEQ ID NO 423)

AAAAGCAAGAAGAGAAGGACTCGTTGGCCAATTTCTTCGGCAATTTCAAGAAGAAAAGAGTAGCTG
TTTAGAACTATATATATATGTAAGTCTCGCGCTTTAATGTTTATAGCAATAATGAAATGTTTAAAT
TATTTAATCAAACCTGGTTGTAACTTATGATTATGGTAGTATCTAAGAACACAACCTTGCAAAGCA
ATGGTAGTTTCTTTGATTTTGTGTTTCTATTAGATTCTGTTTCTATTAGATTCCCGCTTTTTTTT
TTTTTGCAGACATTAAACCTCAGGGCTATAGCCCTAATGGCAAAACATGCACGTGTATGTTTCTTG
ATTTTTCTACACTACTAGTAAAAAATTTCTTTCCGCTCACTATTACACATACACTCTTTTTTCG
CACAATTACAGTCTACCAACAGGAAAAAGAAAAAAGGAATCTGGTAATTGAAAAATTGAAGTT
TGGTTCCTTTAATACATCAATCAACTAGAGTCACAGCATGTTAATTCCAAAAGAAGACAGAAAGA
AGATCCACCAATACCTCTTCCAAGGTATGTAAATATGAATTATAAACTGGAACAGAATATGGCATT
TCAAGGGATGCACGATAAGTCAAGAGTTCATGAAAAAGCACAGATTATAACAGTCGTAAAGAAAA
TTTCACCTACCAACAACAATAAGAAGATATCAAAGAGATTCAAGTAATCACTACTTACAAGAAACATA
TAACATCATGGAGAGTTTAAATTTGAAATACGAATGAATATACAAATGAACATATACCTTTTTATGG
CCATATCACGTTTCAAGAAATATTTAAACAAAAATAAAATGAAGAATAAACTTGGATATACTAAC
ACATGATTTATAGAGGGTGTGCTTGTGCTAAGAAAGACTTCAACCAACCAAGCAGATGAAATT
GATACTAGAAACTTGTTCGTCTCAAGCTTTACAATCTTTGACTTCTAAAGGTTACGTCAAGACT
CAATTCCTCATGGCAATACTACTACTACACCTTGACTGATGAAGGTGTTGAATTCTTGAGAACCGAA
TTGAACATTCCAGAAGGTATCTTGCCATTGACCAGATTGAAGAATGCTCCAGCTGAAAGACCAAGA
CCATCAAGAGGCGGTCCAAGAAGAGGTGGTTACAGAGGTAGAGCTAGAGACTAA

YMR230W_homolog 118aa (SEQ ID NO 424)

MLIPKEDRKKIHQYLFQEGVVAKKDFNQPKHDEIDTRNLFVIKALQSLTSKGYVKTQFSWQYYYY
TLTDEGVEFLRTELNIPEGILPLTRLKNAPAERPRPSRGGPRRGYRGRARD

YNL054W_homolog 2840bp public: 1..2197/2199..2840, PathoSeq: 2198;
CDS: 501..2197 (SEQ ID NO 425)

TGTTGGGAGTATTCTGGCACAACAAATACTTACTTTTAGGTTACTAACATTATTTTTCTTCAGCTA
ACTAATTATCTAGTTTATATCTATATCCATTATTGTTGAAATCACTATCGTGAGGTAAATAACAAC
TACAGAGTTGTCACAGTATCCAAAAAACTTTGTACCTATCAATACATTTTAAGCAATAGGTCAAT
TTATTGCTGTAATCAAGTGTACCAGTATCTCTAGTTAATGTTGAGTTTATACCTAAAACATGAAC
TATATCAACTTTAAATGCCCTAATCACGTGATACAGCATGGGAATTTGCTGATCTTGCTTCCT
TGCACGTACACGGCACATGTACACGACTTTTTTTCTAAATATTTTTTTTTTTGTTGTTGTTA
TTAAACAATATTATTTTCATATATATAATTGCTTAGTTTACTTGCTTCTTACACCCTTTGCATATT
TTTTTTTTTTCTTTTCTGCCAACTTGATCAAATTCGATGCTACATCCTAATAATTCAAGTAGTCG
ATATGCTTAGCACTGGAAACATGAATGAAAATACAGATGCTCCACCGAAACAGCAGACGAAAAAGA
AAATATCAAAACAGAATTCAACCAAAACCGATTTTTTTGCTGCACGATTGGCTAGTGCGGTTGACG
ATATAGAAAGCAGTGATAGTGATGAAACGTTTATATATGAGAATAATGATACTGAACTTGATGATA

ATGCTAGTAATATTAACAATAACAACAATAACAGCACCAATAACATTATCAATTTAGATAATGCTA
GTGTAAACGGAAGTATGATTGCTTCATCCAATGCAATGGTGAAGTGGTCTCCCGGAACATCGATAG
CGTTAGGATCGGGCCCTCGATCGCCATCCATACTAGAGGGGGAACAGCTTCAATATTTTCATGACC
CAGTGAGGCAACAACAGTTCAAACCTTCTTCTACCAAGGCTCCGTCAATTTCCAACCTCCATCAGCA
GTTCAAATAATATAGATTCAATACCTTAAACGACCTGTACATCTACGTGAGGCATCAACGTATTTCAG
TGAATGATAATGACCACCGAAATCTTGTGCTACCAAACCTCAACTGAAAGGTTTACTGCTTCACCTT
CGAACAATATTGGTAATGAAAATATACCTCAATACCAAGAACTAGTAGTGTGGCCCACTCAATCA
ATGAAGGATACAATGATGATACATTTTCATATAATGAAGTTGAGGATAATTTAATTGATGAAGATT
CCACGGACGATGGGGATTGACAAAAAATACCATTACTAATAACAACAATCCACCAACCACGTCGA
GCCAACAGCAACCACAACCGCAACCACAGCCGCAACCACAGCAACCACAACCTACATACTCTGTCTC
CTCTAAATCAGATACAAGCAGCGACATCAGCAACACCTTCTGTGTCCACTAAAAACGCGTCTAAAA
GAAATTACAAAACCTCATCCACTTCTCAAATTAAGATCAACTACATCAAACTTTTCGATAAAA
AAGGGTCACAACCAAGAAGATACAGTACCATTCTGATGATATTGACATTGAAGATTTTCGATGATG
AGCTTATATACTATGACAACACAGCTAGGTTCCAGCGAACGAATCAACTTCATTACTAAATCAAA
ACCAAAGAATCCCCCATTATAGATCACTTAATTTGAATTTCCCTCAGGTGAAGCGCCAAAGCAAGC
GTTATTTGTCAACTGGCCAACCTTTAGAGAGTTCTGATCGTGGCTCTAACAAGATGGTACTGATA
ATGGAAACAACAGTGATCACAATATTAATTTCTCTTTGACTGCTAATAATAATAATAACGTCAT
ATCACAACGATCATGGTGATAACAAAAAGAGTAATACCAACAACAACAACATTGCTAATAATAGAG
CATTTCCATTTCTTATCAAGATCAACAACATCATTATTACTACGACTACGATGATTTTGACCAAG
AATCACAATCAATGGACCAATTTTGATTTGCCAGACCTCCCTATAAACAGATCAGCTTCACGGA
ATTTTAACAACAACAATAACCCCCAAAAGATTTGGCGACAGTCATTTTCTACCAAGAAAGACAG
ATCAGTATAGTCAAAGAACAAGCTTTCTAAAGTCATGCATTTATACCTTTGTTTGTATATTAATTG
TGCTTACCATAGGGTTTGTATTGGGGTTGTPTTTGGCCACAACAAGATTTAAGTATGATAGGTA
TCACATCCATTGAGAACCCCATTTGTTAGTAAAGATGAGTTAGTTTCAATGTTGTTATTGAAGCAT
TTAATCCAGGGTGGTTTTCCGTTGACATCAATGAAGTAGAGTTGGATTTATTTGCAAGAAGTGGCT
ATCTACCTGATACAGATAATCTGAAAAATATCTAACATGGGAGGGTCACAAAAAGTAGAGACGGTTA
AATTAGGAACGATTTTGAATTTTGAATCGGTTCTCAATTTCAAAGGTGGGTTTCTCTCTCGAGAAC
CGACAATTTCAAAGGGAGGAATCCGATTATATATCTTGGCAAAAATGTTACTGCCGAGGCTAAAT
TGGTTGTAAATATGGCTGATATTAAAAATAGCTGCTTCCAATAGCATTGCTAAAGAAAGCACTACTA
GTAATGACACCAACGATAATGACAACCTCAAGAAGTGGGAAATCATATCAAGCAATCCATTTGATT
TGATTATAACTGGAGTATTGAAGTATGATTTACCATTTTCAAGAACCTCAAGATCAGTCGTGGTTA
GAAAACTGGGTATATTGATCCTACCTTATTCGTAATACCACAAGGAGAGAATAATATTTCAATTT
AG

YNL054W_homolog 779aa (SEQ ID NO 426)

MLHPNNSVVDMSSTGNMNTDAPPKQQTQKKISKQNSTKTDFFAARLASAVDDIESSDSDETFIY
ENNDTELDNANINNNNNNNSTNNIINLDNASVNGSMIASSNAMVTGPPGTSIALGSLRSPSILE
GEQLQYFHDVPVRQQQFKLPSTKAPSISSNSSNNIDSILKRPVHLREASTYSVNDNDHRNLVLPN
STERFTASPSNNIGNENIPQYQKTSSVAHSINEGYNDDTFSYNEVEDNLIDEDSTDDGDLTKNTIT
NNNNPPTTSSQQQPQPQPQPQPQPQLHTSSPLNQIQAATSATPSVSTKNASKRNYKTSSTSSKL
STTSKLFDDKGSQPRYSTIPDDIDIEDFDELIYYDNTARFPANESTSLLNQNRIPHYRSLNLN
FPQVKRQSKRYLSTGQPLESSDRGSNKDGTDNNGNSDHNINSPLTANNNNNNVNHNHDGDNKKSNT
NNNNIANNRAFPFPYQDQQHYYDYDDFDQESQINGPNFDLPDLPINRSASRNFNNNNNPKRFGD
SHFFLPRKTDQYSQRTSFLKSCIYTFVCILIVLTIGFVLGFVLATTKDLTDVGITSIENPIVSKDE
LVFNVIIEAFNPGWFSVDINEVELDLFARSGYLPDNDNSKISNMGGSQKVETVKLGTLILNFESVLN
FKGGFLSREPTIQKGGIRLLYPGKNVTAEAKLVNMADIKIAASNSIAKESTTSNDTNDNDNSKKW
EIISNPFDLIITGVLYDLFSPRTSRSVVVRKTYIDPTLFVIPQGENNISI

YNL075W_homolog 1352bp public: 1..136/138..1352, PathoSeq: 137;
CDS: 501..1349 (SEQ ID NO 427)

CCCACAGACCAATAACGTTTACCAACCAAAACCTCTGATATCAATGATTGCAAAAGATTCAATTCA
ACCCCGGTTAGCTGTTTGAGTATTGGATAGCAACACTTTCAATTAGTGCAACACAATCAAATTACC
AATACTTGTTTACCTTTCATCTGATTCTAATGGTTCATAGCAATATAGTCTCTTCTGTTGTTTGA
TATTAATATAAATAAACTTATTTATCACGTTGTTTAGTAGTCTCGCAAAATTTGAAACCATGGATG
AGTAAACTTGTTGTGTTAGATGAGCTCAAAATATCTGGTGGAACAATTGTGTAGTAGCTCTTTGATA
AATATCCAAGAACAGTCGTGCAAGTTTCAAAATACCATCGCAAAAATCCTAACAAAAA

TAATAAAGAAAAGAAATAATTCATATAATAGCTCATCACAACAATTCGTCTACACTTCCCACCTGAT
TTGTTGGTTTTAAATATAATAAGACAAACCTCAGAAGCTATGATAAGAAAACAGGCTAGAGAAAGAA
GAGAGTATCTTTATAGAAAGGCTTTACAGCTTCAGGAATCTTCCTTAACAGAAAAAAGACAACAAT
TGAAAGCAGCTCTAGCAAGTGGAATAATCATTAATCAAGGAGCTTGCCGAAGATGAAAAATTACAAC
GTGATTTTATTTACGATGAAAGTGAACAAATAGAAATTGATGACGAATACAGTCGGTTGTCTGGGAA
TATCTGATCCAAAAGTTGTTATTACCACATCCCGTGATCCATCTGTCAAGTTGCTACAATTCCTGA
AAGAAATCAAGTTAATGTTTCCAAATAGCTTTGAAGTTGAATCGAGGAACTATATAATCTCAGATT
TGGTAAGTACCTGTAATAGAGTGCAAGTTTCCGATATGATTTTATTGCACGAGCATCGTGGTGTCC
CATCAAGTTTAACTGTAAGCCACTTTCCTCATGGCCCACTGCGATTTTCACGTTACATAATGTCA
AACTAAGACACGATTTGCCAACTTGGGAAACGCTTCAGAGTCCTATCCTCACTTAATATTTGAGA
ATTTCCAATCCGACTTGGGTAAGCGTGTGGTTAAATATTGCAACATTTGTTTCTCCAGGTGTCA
AGAAAGATAGTCCAGAGTAATAACATTTGTCAATACGATGACTACATATCGGTGAGACACCATG
TTTACGTCAAAACTAAGGATTCAGTGGAGTTGAGTGAGATTGGCCACGTTTCGAAATGAGATTGT
ATGAAATCAGACTAGGATTACCTGACAACAAAGATGCTGATGTGAGTGGCAGATGAGAAGATTCA
TAAGAACAGCTAATAGAAAGAATTACTTGTAA

YNL075W_homolog 283aa (SEQ ID NO 428)

MIRKQARERREYLYRKALQLQESSLTEKRQQLKAALASGKSLSKELAEDKLRDFIYDESEQIEI
DDEYSRLSGISDPKVITTSRDPVKLLQFSKEIKLMFPNSLKLNRGNIIISDLVSTCNRVQVSDM
ILLHEHRGVPSSLTVSHFPHGPTAIFTLHNVKLRLDLPNLGNVSESYPHLIFENFQSDLGKRVVKI
LQHLFPFGVKKDSSRVITFVNNDYISVRHHVYVKTKDSVELSEIGPRFEMRLYEIRLGLPDNKDA
DVEWQMRRFIRTANRKNYL

YNL096C_YOR096W_homolog 1061bp public: 1..1061; CDS: 501..1058
(SEQ ID NO 429)

TCCTTTTGTTTTTATTTTTTGTCTGTGTTACTCCAGAAATGTGCATAATAATGATAATAGTAATTTGT
GACTAATATGAGATGATCGTATGTGGGTGGGTGGGGAGGAAGGGACCCGGAATTCAGGAACAGGA
AAAATAAAAACGAATAAACAAAAACCCCAATCGGCATGCATCGGAATTCCTTCAGCCCAATTAC
TTTATTTTGGCCACTTCTTTTGGATTAGGGCAATAGCCCTAAAGCTCGTGTTTTAGCCCTTTATA
TGCAGTCTATTTTTATTTTTCTCTTTTTTTTTTTGGCTGTGGTAAACTTTTTTTTTTTTCGCAGGTG
TTGAAAAAAAATCATTTTTTACAGTTTACATTTCTCTAACCTGCAAAAAGCTCTCGTTTTTTTGTA
GTGAGAGTTACTCGTTTCAATAGTATACCTTTACAGGGGAGTTCTTTTCTTTTGGGAATAGTCAACC
AACAGCAAATAGCCAAGGATCAAGCTTCATCATTAATCATGTCTCTAAGATCTTATCAGAAAACC
CAACTGAATTAGAAATTAAAAGTTGCTCAAGCTTTTCGTTGATTGGAATCTCAAGCTGATTTAAAAG
CTGAATTGAGACCATTACAATTCAAATCTATCAAAGAAATTGATGTTAATGGAGGTAAAAAGCTT
TAGCTGTTTTTCTGTTCCACCACCAAGTTTACAAGCTTACAGAAAAGTTCAAACCTAGATTAACTAGAG
AATTAGAAAAAAATTCAGATAGACATGTTGCTTTTGTAGCTGAAAGAAGAATCTTACCAAAAC
CAGCTAGAAAAGCTAGAAAACAACAAAAAGACCAAGATCAAGAACTTTGACTGCTGTTTCATGATA
AAATTTTGGGAAGATTAGTTTTCCTCAACTGAAATCATTTGGTAAAAGAGTTAGATACCTGGTTGGTG
GTAACAAAATCCAAAAGTCTTGTGTTGGATTCTAAAGATTCAACTGCTGTTGATTACAAATTGGATT
CTTTCCAACAATTGTACTCAAATTTGACTGGTAAACAAGTTGTTTTTGAATCCCAGGTGAATCTC
ATTAG

YNL096C_YOR096W_homolog 186aa (SEQ ID NO 430)

MSSKILSENPTLELKVAFVDLESQADLKAE LRPLQFKSIKEIDVNGGKKALAVFVPPPSLQAY
RKVQTRLTRELEKKFPDRHVFLAERRILPKPARKARKQKRPRSRTLAVHDKILEDLVFPTEII
GKRVRYLVGGNKIQKVLDSKSTAVDYKLD SFQQLYSKLTGKQVVF EIPGESH

YNL178W_homolog 1256bp public: 1..1024, PathoSeq: 1025..1256; CDS:
501..1253 (SEQ ID NO 431)

TGTTTTGTTTTTGCAATCAACATAATAGAAGACCAAAACAAATAATTTCTATTTTTTTTGA CTCTCC
CGTAGTTTTTACACTTCTAGCCTCTCTGTAAATATACCTAATTGACAGTACCATTAGGACCCCA
TCTTATTGTTAAGGATAATACCTTCTTCTTCTTCTTCTTGTTTAATCAAATTTGCAATAAATA
AAAAA AAAAAAAAAACAAAGCCGCACAAGTTTTCCTAAAATGACTTATTTTGTGTAACGCATTAC
GTGATCATATAATTTTTTTTAAATTCAAAAACCTGAACCAATTCCTGCATATTGAGGTTGAAAAA
AGAAAAAGAAAATTTTTTCAATCTTGTTTGAGGAGAGAGAGGTGAAAAATTTTTCTCTCTCTCTTT

CTTCTTTTCATTCTCATATACCATAAACCTTAAACAACCTTCTTTTACTTTTTCCTTTCTTTTCTTTT
CAAACCTCTACAACAGATCCAATTAATTAACAAAAAATGGTTAACGCTATCTTATCTAAGAAAA
AGAAATTAGTAGCTGACGGTGTCTTCTACGCTGAATTGAACGAATCTTCCACCAGAGAATTAGCTG
AACAAGGTTATGCTGGTGTGAAGTTAGAAAACTCCATCTAAATTGGAAGTTATTGTTAAAGCTT
CTAACACTCAAGGTGTTTTAGGTGAACAAGGTAGAAGAAATCCATGAATTAACCTTCATTGATTGTTA
AAAGATTCAAATTATCTCCAGAAGGTATTGCCATTTATGCTGAAAGAGTTGAAGAAAGAGGTTTAT
CTGCTGCTGTTCAAGCTGAAGCTTTGAAAGCCAAATTAATGCTGCTGTTTACCAATTAGAAGAGCTG
CTTATGGTGTTTTAAAGATTGCTATGGGTGCCGGTGTCTAAAGGTGTTGAAGTTGTTATCTCTGGTA
AATTAAGAGCTGCTAGAGCTAAATCTCAAAAATATGCTGATGGTTTATGATTCACTCTGGTCAAC
CAACTAGAGATTTTATTGATATTGCCATTAGACATGTTTAAATGAGACAAGGTGTTTGGGTATCA
AAGTTAAAATTATGAAAGATCCAGCTGCTAATAGATTGGTCCAAGAGCTTTACCAGATGCTGTTA
AAATTGCTGAAGCTAAAGATGAAGATGAAGTTATTCCAGCTCCAAGTGTAAATCTTATAAACAAA
CTGCTGAAGATGAACTGAACTGATGCTCCAGTTGAAGCTGAAGCTGAAGTTGAAGCTACTGCTT
AA

YNL178W_homolog 251aa (SEQ ID NO 432)

MVNAILSKKKLVADGVFYAELNEFFTRELAEQGYAGVEVRKTPSKLEVIVKASNTQGVLEQGRR
IHELTSILVVRFKLSPEGIAIYAERVEERGLSAAVQAEALKAKLLSGLPIRRAAYGVLRPFAMGAGA
KGVEVVISGKLRAARAKSQKYADGFMHSGQPTRDFIDIAIRHVLMRQGVLGKIKVKIMKDPANRF
GPRALPDVAVKIAEAKDEDEVIPAPTVKSYKQTAEDETETDAPVEAEAEVEATA

YNL182C_homolog 2105bp public: 1..728, PathoSeq: 729..2105; CDS:
501..2102 (SEQ ID NO 433)

AAACTTTCTGATTGAATAAAGTGAACCTCAAATCACATTCCTTCGGCATATATCAAACCATTATTAGT
TTTATCACGTAAATCTTCAATATACTCAGCCACCCATTGATCATTGGTCTTCTAGTAAGTAATAT
TAGTTGTGCTCCTCGTTGTCCCAATTCATATGCTATTTGAGCTCCAATACCAGTGGTCCCACCAGT
AATCATAAACACTTTCCCATGCATGTCTCGCTCCCACGTATTGGTGGCACCATGGAAATAATACTT
GGTCCAGCAAGAGTTAATAGAATGGGAAGAACGGTAGGTCCATATCTTTAATTTGGTCCCAATA
TGGAATCACCTCTGGCCCATCAAACACAACACTAGTTAAAAAATTCAGTGGCATAATTGGTATATC
AAGAGTGAAGAAAAATGCTGTATTGGAGGTTGGAATTTGTTTCAAAATTTGGTTGCCCTTTTATTCT
TCTTGTCTCTTTTTTTTTTTCAGTGCTAACATAATTTGGGATGTATGTATTGAAAAAATTTTG
TACAATTTCTTGTCTTGTCTCTCCCACTCATCTCATCGCTCTCTTATAAATTCACAAACATGGATG
AAGTAGTATTTTACATAGCTCAAGGTGATCCAGCTGATAAACACAGTCAAGAATCATATGGATATG
TTATATCAATCCATTCCTTCCAAACAATATGCATCTTATCGACAAGCAGACTCGCATATAAACGGTA
CTGCCATAACTGGTATTGGCCAGGAGAAAGAATTTTCACTGCTGTTCTTAACAAGGCATTAATCA
ATGTATATTCATGGGAAAAGAAAGTGTGATCAACGTATACCGATACCAGAAGCATTGACTTGTA
TCACGTTGATAAACCATCCAAATGGCAGTAACAACAACAGCGACAATGATGACAACCAGTTATACA
AATTACCAAATTACCGAGTTCCTTGGTGTGTTAGCAGGTGGATCAAAGAGTGGGAAATTTGACATTT
GGGAATTAAGTTCAGGCAATTTATTATGTGTGTCAGAGACGCCATTATCAGGGGATCACTACCATCA
AGGGTTCAAGCTGTGGAACATTTTAAATTAAGTGGAGAGAGGATGCCAGATGCTTGTATGGAATTT
TAGCAGAATTAATTAGTATTTATGACAAATCAGACCATCAAGTGAACCATATTGGCAAATCACTG
ATAACACATTACCACTCACTGATCTTTGTTTAAATGATACTCATAACATTAATGATCTAAAATTAT
ATACAACCTTCAGAAGACAGCACGGTCAGGATTTATGATATAGTCACAAAGAGTTTGTAAACCACAT
TTATTTTACCCAGTTCGGCTGAATGTATCACAAGGATCCAGCTAATAGAGCGTTATATGTCGGGT
TGAATAACGGTCTTGTAAAGATCAATTCCTTTATATTCTATAAATAGCCATACATCAGTGTGGAAA
GTATTGGCGGCATGAATAAGATAATCACGGTTGATGCTGATCAAAATTTAAAAGAGACATTTGTTG
CACATCAACAAAAGACGAAAACAGGAGACGATAAGCCTGTTGTTGTTACGAAATTTGACAATTTCTT
TTGATGGTACAAGTATAATATCTGGTGAATCTGAAGGCAGAGTGTGTTGTCTGACATTTGTAACGA
AACAAGTTGTGAATCATTACACCTTGTAACTCTCCAATAGCTTATATTGCTGTTGAACTATCC
CTGATGACTTTGTCAATAACTTAGTACTAGTACTACCCTAATAAAGCTGACAAAGAAACATAGAA
TGATACCTCAATTTAAACAGTACTAGCAAGCACCAATCTGAAGAACATCAGATATTCTTGGACA
TTCTGGTAAAACACCGCAACCACCAACGCAACCGGCAATATTGACTTTGCAACTTGGTTACAAG
GCAACAATCTGAAGAATTACAATTCAAAAACCTTTCTGGAATAAATCTATTGTCAAACAAGTTG
GCAACGAGAATGTATCGGATCTCGAAGAGAGATTACAAAGAGTTTCTCAAGCATACACTGAATTA
GAAACAAACATGAAGAATTAATTAAAGAACATGCCAAATTATTAGATAAATTAGAATAG

YNL182C_homolog 534aa (SEQ ID NO 434)

MYVLKKKNFVQFLVLVPLISSLSYKFTNMDEVVFYIAQGD PADKHSQESYGYVTSIHSSKQYASY
RQADSHINGTAITGIGPGERIFTAVPNKALINVYSWGKESVDQRIPIPEALTCITLINHPNGSMNN
SDNDDNQLYKLPNYRVPWLLAGGSKSGKLYIWELSSGNLLCVRDAHYQGITTIGKSSCGTFLITGG
EDARCLVWNLAELISYDKSDHQVKPYWQITDNTLPLTDLCLNDTHNINDLKLYTTSSTVRIYD
IVTKSLLTFFILPSSAECITKDPANRALYVGLNGLVRSIPLYINSHTSVLESIGGMNKIITVDA
DQNLKETFFVAHQKTKTGDDKPVVVTKLITISFDGTSIIISGDSEGRVFSVDIVTKQVVKSFPCNSP
IAYIAVETIPDDFVNNLATSTTTNKADKKHRMIPQFKRVLASTNSEEHQIFLDIPGKTTATTNATG
NIDFATWLQGKQSEELQFKNLSGINSIVKQVGNENVSDLEERLQRVSQAYTELNRNKHEELIKEHAK
LLDKLE

YNL190W_homolog 896bp public: 1..896; CDS: 501..893 (SEQ ID NO 435)

TTTCTGCAAGTATTGCGTGTGCTGCACAACTTTTTATATCCGAAAATTTTGGCCGGGAACGAAA
CGGCAAGAAAAACAGAAACAATACCACCAGCACGGACAAAAAGATTATAAGCTTTGTGTAATAAG
GTTATGTCATCGGGTATTACAGATTGCAGGGCCATCTTGTCTTCATCAGTTATAGCATTTCATATA
AAATAAGCCACATATGTGTACAGCGCTGAGTCTACTCAACATGTGTAAATAGAAATAAATCAATTGA
CACAGTCTTTTGAGATCTGTTATTCTGGCCTATAGCGTTTTAGGAAATTGCGGTATTTCTTGCTCT
GTTTTCTTTTATCTATTTTCGCACGACTTGGGGTGGTTTGTGTGACTTTTTTAGCAAATTAATTT
TGTCGGTCTTTCGCAGTAAAAATAAAAAATTCAAAAAAACAATAATGACTTTTTTTTTTACTTTT
CTTCTTTTCTATCAACAATACTAATCACAAGCCAACCATGAAATTCACTACTGTTGCCACTGTTT
TTGCTATTTCTCTATTAGCTGCCGCTAAAGGTGGTGAAAAAGATCACGGTAAAGCTTCTACTGTCA
CCAAATATGTCACTGAAACTACCCACAGATACGGTCGTTTTTGACAAAACCACTAGATCTAAAAAGC
CAAAGGAACTGGTACTCACAGATACGGTAAATTCACAAGACTCCACGTCCAGTTACCACAACCTG
TCTTGGTCAAAGAAAGCGACCTTCCAAAGAAAAGAGATGCTGTTGTTGCTAGAGATTCTAAAAACG
CTTCTTCCAACCTTACCACCTCTAGTGGTAACAATGGTGTGCCACTGGTGTACGCTTGGGTCTTG
CTGGTGTCTTAGCTGTTGGTGTGCTTTGGTCATCTAA

YNL190W_homolog 131aa (SEQ ID NO 436)

MKFTTVATVFAISSLAAGGKEDHGKASTVTKYVTE THRYGRFDKTSRSKKPKETGTHRYGKFN
KTRPRVTTTVLVKESDLPKKRDAVVARD SKNASSNSTSSGNNGVATGVSLGLAGVLAAGALVI

YNL208W_homolog 1076bp PathoSeq: 1..1076; CDS: 501..1073 (SEQ ID NO 437)

TTTTTGATCAGGCCTTTTGTTTTTTTTTTTGGGTGGTGTGTTGCTGTTGGGTAGTTGGCTCTTG
TTTCGGTTCTACTTGTTCCTTTTTTTTATTCTCCTCGTTAATCCTAATTTTGTGTAACAAATTAAT
TATAGGGAGTTGGAATAATAAGCTTGAAAAGAAAGAAAGAAAGAAATACCAACGTGGAATTTCT
ATTACGTAAGTCACTATAACTTGCATAGAAATTTCAAGTTTTCAATTTAAGAAAGTATTAATCAAC
TGAATTAAGCAATTGAAACGAATTGAACAGCTCAGCATTTATTTTTTCGTTTTCTTTTTTTTCAA
GGGGGTGGGTGAAAGAAAAATCTAAAAATATATAAATACTCCACTTATCTCCTCTCTCTCTCTCT
TCTCTCTCTAATTTCAATTTTCCCAAACCAAAATTTCTTTCTTTCTTTCTTTCTTTTATT
TTTACTCAATTGAATCAATATTAACAATAAAAGCCATGTCAGCTAACGATTTTATTCATCTG
GTGATCAATCCAATTATGATCCAAAAAGATCCTCGAATCAAGGATCATCATCAAAATGATGAAC
AACAAGACAGAGGGTTATTATCTACTGTCCCGGTGGTGTGCTGGTGGTTATGGTGGTCACAAAT
TAGGTGAAAAGGCACAACATGGTACTTTGGGTACTGTATTAGGTGCCATTGGGGGTGCCATTGGTG
CCAATAAACTAGAAGATGCTTATGAAGACCGTAAAGAACATAAAAAACACGAGCAACAATATGGTG
GTAGTGGTAAACACGAAGGCGGAAGACATGAAGGTGGTTTTGGTGGTGGTAGACCAGATGATCGTT
ATGAAGGCGATAGAAGAAATGATAATTACGGTGGTGGTTACAATGATAGAAGAGATGACGGTTATG
GTGGTGGTTACGGTGGTGCCAGACCAGACGATAGAAGACACGAAGGTGGTTTCGGCGGTGGCAGAC
CAGATGACCGTTTGGTGGCGGTAGACCAGATGACCGTTTTGGAGGTGACAGAAGAGATGATAGAA
GAGATGACCGTAGATGGTAA

YNL208W_homolog 191aa (SEQ ID NO 438)

MSANDFYSSGDQSNYDPKRSSNQSSSSNDEQQDRGLLSTVAGGVAGGYGGHKLGEKAQHGTGLGTV
LGAIGGAIGANKLEDAYEDRKEHKKHEQQYGGSGKGHEGGRHEGGFGGGRPD DRYEGDRRNDNYGGG
YNDRRDDGYGGGYGGGRPD DRRHEGGRPD DRRFGGGRPD DRRFGGDRRDRRDRRDRR

YOL031C_homolog 1745bp public: 1..1342, PathoSeq: 1343..1745; CDS: 501..1742 (SEQ ID NO 439)

TTGGTATTGAAGACACCGAAGACTTGTGAAAGATATTGAACAAGCTTTACAAAAGGCTGCTTCTG
TTTGAGGGGATGTTTCATTAGCAATGTATATAATTATTGTATATTATGACAAAGAAAGAAAAAGAA
AACCAGAAAAGTGGTTTATACAGGAATATTTTAATAGAAATATCGCTTATATTGTGATAAAAAATT
TGAAAGACAATCCGAATGTAGTGCTTGTCTTATTCTGCTTGGGAATACTGTAGTATTAGCATCAAT
TGAGGAAATTCAGATAGCTAACGGTTTTGCGATTACGAATTTTCGCAACCAAATAAATATGTGACA
AGGAATACACTACTGATCAAGGTTATTCTTAGTACAATGGAAAAAAGAAAGCAACAAAA
AAACGAGAAATTAATGAACACGACTTCACCTTCTACAACCTACTGGGAAAAAAGGCAGAGAGTTA
TTGAAAAAGGATCATATCAAGTTCTTATTGTATATTATATGAAGTTTTCTGTTTTAGTATTACTTG
CCAGTTACTTTAGTTGGTGTGAATTTCTCTGATTGTTGATACTTCAGAGGAATTAATTTGTCCAGATC
CAGAAAACCCCTTTAGATTGTTATCCAAAATTGTTTGTTCACAAACGAGTGGCAACCAATTAAAC
CAGGTCAAGATATACCACCTGGGTTACACGTTAGATTAAATATAGATACGTTGGAAAAAGAGGCCA
AGCTAATGAGTGCTGACGAAAAAGACGAGCCAGTTCAAGAAGTAGTTGTTGGTGGCGAATTGCAGG
ATCATTCGAGGGAAGCCATCACTGAGAATCTACAAAAGTTGCATGAGCTGAAACATCCTGAAGTAA
AACAGGAGCACGCTCATCGTACAAAGGTTAGCCAGGGAGATTTGAGTAATTTTGACGCAGCTTGTC
TGGAAATTGAGAGTTTCAAGCCACATGAGAGTGATGTGGAAGGTTGCATTTGGCACTAGATACTT
TAGAGGAATTAAGTCATGATATCGAATTTGGGGTGAAATTGACCTCAGACAAAGCCATATTTCAGA
GTTTTGTCAACATTGCCAATGGTGCTTCTGATCCAAAAATAACCGAAAAGGTATATCGTGAATGG
GGTCTAGTTTGAAGAAATAATCCTGAAGCGATTAGTAATATCTTGACCAACTTCGACAAGAGCTATG
TGGATAATTTGTTTGAAGCAATTAGCGAATGAAAATGATGTTCTACAAAAGAGGATTTTGGGTATAA
TTCAAGCTTTAGTCCAAAATAGCCATTTTGAAGACAATATTTTTTCATTTGACCACAGTTCCGGGT
TAAATGATTTAATAGCGATTTTTCCTCCAACTTGGTCCAACTCAAAGTCCAGGGCAAGTAACATTT
TAGAGGATTTACAATTGTTCCAGTAACAAACGATAGAAGATCACTTGAAGATCAAGATCCTGAAT
CACAGGTTTCAAAATTTATTCAGAATTCCTTTGTTGGAAATAAACTTGACGAGAAGAAATTTCAAGT
CTTATTTTGTATCAACTAGTAAATTTGCATCAGCTGAATAAGAGTTTGCGACCAAGTGGTGACTTTTC
TCAATTGGTTAGCTGAAGAAGTGGAGTCGCGTAAAGAGAATAAAAAAGAGACGATTATTCACAAG
AAGACAAAGACTTTGATGAGTACATGTTGCGAGCACGTCATGAAGTATTTGGCAATCCAATGGGAT
TAAGAAAAGGCAATTGCCGACGAGTTGTAG

YOL031C_homolog 414aa (SEQ ID NO 440)

MKFSVLVLLASYLGVNSSIVDTSEELICPDPENPLDCYPKLFVPTNEWQTIKPGQDIPPLHVR
NIDTLEKEAKLMSADEKDEPVQEVVGGELQDHSREAITENLQKLHESKHPEVKQEHARTKVSQ
DLSNFDAACTSEIESFKPHESDVERLHLALDTLEELSHDIEFGVKLTSKAIHQSFVNIANGSDPK
ITEKVYRVMGSSLRNPEAISNLTNFDKSYVDNLFELANENDVLQKRILGIIQALVQNSHFARQ
YFSFDHSSGLNDLIAIFPKLGPNSKSRASNILEDLQLFPVTNDRSLEDQDPESQVSKFIQNSFVG
NKLDEKNFKSYFDQLVNLHQSNKSLRPSGDFLNWLAEVEVESRKENKKRDDYSQEDKDFDEYMLRAR
HEVFGNPMGLRKAIADDEL

YOL048C_homolog 1244bp PathoSeq: 1..27/985..993, public:

28..984/994..1244; CDS: 501..1241 (SEQ ID NO 441)

ATGATTTTTTCTTGTATTAGAGCTGTTAATTATACCTTTTTTGTTCCTCCAAATAAGCGCTAAAAA
TGATTGAAATTAATAATACTAATATCCAGGTCAAAGTAAACACTATAAAACAATATATTCAAT
AACAGGAGCAGTAATTAGCTTCAACATCAAGGTACTCTTTTATTTTCTACCAAAAACACATCTGA
AGTAGCTCTTATCCATAGATCCAAATATTTTAACCTTTTTTTTTTCTACTCTCATCTACTTTTTT
TTGCAACACTTACTGCTCACAACGCCAATGACCATAACATTAATTTCAATAATCAATCAAGAGCT
TATTTGTATCCTCTCAAGGTATGTTAATGTATTAACAACACCGATTCTATTTACCAACTAACACG
ACAGAAAGGGGTTGTAATTTTGTAAACACATCCCACCGTTTGGCCCTTTTACATAACCATATTGA
TACCTCAATTGGTCTTACACTAGTCATTTACCTGATTATGTTTTTATTGTTCTTCCACCTCAAG
CTATTGTATATACATTTGTTAATGGGACCATTAGGGGTGATTGGTGCCTGGTATAGTTTGTATCTGC
AAGCGAGCACATTGTCTATATTTGTTGTACAATATCCTTAATGCCTCACATACAACGAGTGGCAT
ATGATGCAATATTGAGTAGAGAGTGTGCAATGATGTGGTACTAATGGGAAACTTAGGAGGTATA
GAAACTACCCATTAGAGTAAGGCCAGAGAATACCTTAAGGCCATTCCAGATTTTTTCATCTTTTC
CCTTCTCTTTGCTCAAGCTACTTTGTGTTTTTCCGTATTTACTTCATACCCTTTGTAGGTCCAATCA

TTGTATTGTTTTTCCAATCTTCCAAGCGTGGACTAAAGGCACATGCAAGATACTTTAAGTTGAAAG
GGTTTCGCGTAGTGACATAAGAACAATCCACAAGCTAAACAGACCAGCATATATGGGGTACGGAG
TGGTTGCGCTTTGGCTCGAGCTGTTTCCATTTATCAATATGTTTTTTATGTTCCACCAATACTTTGG
GAGCTGCTTTGTGGGCAGTTGATATTGAACAACAAGAGAAGGCCGTACAGAGAATGTGGCCGCAG
CTACTACCACCGCCACAGATACGAATAGCGTCAATCAACAAGGTCTAGTTATACCCGTACACAATG
AACCAGCAACTAATATACCTGAGGCTACCCCAAAAACCTGCTACAAATACCATCTAA

YOL048C_homolog 247aa (SEQ ID NO 442)

MFSLFPPQAIIVYTLMLGVLGAWYSLISQASTLSIFVVTISLMPHIQRVAYDAILSRECANDV
VLMGKLRRYRKLPIRVRAREYLKAI PDFSIFPFSLLKLLVFFGIYFIPFVGPIIVLFFQSSKRGLK
AHARYFKLKGFSRSDIRTIHKLNRPAYMGYGVVALWLESFPFINMFMFTNTLGAALWAVDIEQQE
KAVTENVAATTTATDTNSVNOQGLVIPVHNEPATNIPEATPKTATNTI

YOR027W_homolog 2270bp PathoSeq: 1..947/1781..1828, public:

948..1780/1829..2270; CDS: 501..2267 (SEQ ID NO 443)

GCATTTTACTTATTTAGATATTACTTCATATTGCTTTTATTTAGATTGATTTTGTAAACAGTGAA
AGTTTTTATTTTTTTTTTTGTTTAAAGTTTTTATTTTTTTTTTTGTTTAAAGTTTTTGTATTATACAA
TATTTAAATTATAGTAATCATCTATAAAATTTCAAAGTCAAAAGACAGATCTTAAGGCTAAATTAA
TAACCTCTATGGCCTTCTGTGTCAAATTGTTGTCTGTTTGATAACAAGTTTGGAACGGTAATGGTT
GAAATTAGAAAAGAAAAAATTACACATGGTAGCAGCTGATGTATAGAACTTTCTAGCAAAAAAAA
AAAGAAAGAATTTTTTTTCTTCCATTTTCAAATTTGAGAGATCGAAATAATTTTCTTGAATTTA
TTAAAAGGGAACCCCTTCCCGAAAAATCCAAAACCAAACTTCCACCCAAATATCAAATAACTAAC
TTATCATTTCCAACAGATAATATCCCACTTCAATAACAATGACAACAGCTGACGAATACAAAGCAG
AAGGTAACAATAATTTTTGCTGCTAAAGATTTTGAAAAGGCGATTGAAGCATTCACTAAAGCAATTG
AAGCATCACCTGAACCAACCATGTTCTTTATTCAAATCGTTCTGGATCTTATGCCTCTTTAAAAG
ATTTTAAACAACGCATTAAAAGATGCTCAAGAATGTGTCAAGATCAATCCTAGTTGGGCCAAAGGGT
ATAATAGAATTGCTGGGGCTGAATTTGGTTTAGGTAATTTTGATCAAGCCAAATCCAATTATGAAA
AATGTTTGGAGTTGGATCCAAATAATGCCATGGCTAAAGAAGGTTTAAAATCAGTTGAATCTGCTT
TATCATCTGGTGGTGGTGAATGACAAGGATTTAGGATTTGGTAAATTTTAAATGATCCCTAATCTTT
ATACTAAATTGAAAAATAATCCTAAAAACAAGTGAATTTATGAATGATCCTCAATTTGTTGCTAAAC
TTGAACGTCTTAAACTAATCCACAATTGGGTAATCCTGATATGTTTAGTGATCCAAGATTATTGA
CGGCTTTTGTGCTTTAATGGGTATTGACATGGATTACCAAATATGGGATTCAGTCTCCAAACG
AATCACAATCCAATGCATCAGAACCAAACTGGAACCAAAATCAGTACCAGAATCTAAACCAGAAC
CAAAAGCAGAACAAGGAAGAAGAAATCAACCTCAGCCAAAGATGAAGACACTCCAATGATGATG
CCCAAGACGACACTAATGATAATGATGCCAAAACCAAGCTGACAATGCTAAAGCTGAAGGTAATG
CCTTATACAAGAAACGTCAATTTGATGAAGCAATTGCCGCTATAATAAGGCTTGGGAATTACATA
AGGATATCACTTATTTAAACAATCGTGTGCTGCCGAATATGAAAAAGGTGATTATGATGCTGCTA
TTGCTACATGTGAAAAGGCCATTGATGAAGGTAGAGACATGAGAGCTGATTATAAATTGATTGCTA
AATCATTTGCTAGATTAGGTAATATTTATTTGAAAAAAGATGAATTACCCGAAGCAGTGAAAAATT
TTGAAAAATCTTTAACTGAACATCGTACCCCTGATGTTTAAATAAATTAAGATCAACTCAACGTG
AAATTTAAACTAGAGAATTAAATGCTTATATAGATCCAGAAAAGGCTGAAGAAGCAAGATTACAAG
GTAAAGAATATTTACCAAAGGAGATTGGCCAAATGCCGTTAAGGCTTATACTGAAATGATTAAAA
GAGCACCAGAAGATGCTAGAGGATATTCATCGTGTGCTGCTGATTTGGCAAAATTTGTTATCATTTT
CTGATGCTATACAAGATTGTAATAAGCCATTGAAAAAGATCCAAATTTTATTAGAGCTTATATTA
GAAAAGCTAATGCTCAATTGGCAATGAAAGAATATAGTCATGTCATGGATACTTTAACCGAGGCAA
GAACTAAAGATGTTGAATTGGGTGGTAAATCAATTCATGAAATTGATGAATTAATGAATAAGCTA
CTTATCAAAGATTTCAAGCCATTGAAGGTGAACTCCTGAACAACTATGGAAGAGTTTCTAAAG
ATCCAGAAATTGTTCAAATTTTACAAGATCCAGTAATGCAAGGAATTTTAGCTCAAGCTAGAGAAA
ATCCTGCTGCTTTACAAGATCATATGAAAAATCCTGAAGTTTATAAAAAAATTAATATGTTGATTG
CTGCTGGTGTATTTCGTACCAGATAA

YOR027W_homolog 589aa (SEQ ID NO 444)

MTTAD EYKAEGNKYFAAKDFEKAIEAFTKAIEASPEPNHVLYSNRSGSYASLKDFNNALKDAQECV
KINPSWAKGYNRIAGAEFGLGNFDQAKSNYEKCLELDPNNAMAKEGLKSVESALSSGGGDDKDLGF
GKILNDPNLYTKLKNPKTSEFMNDPQFVAKLERLKTNPQLGNPDMFSDPRLLTAFALMGIDMDL
PNMGFTAPNESQSNASEPKSEKSPESKPEPKAEQKEESTSAKDEDTTPMTDAQDDTNDNDAKTQ

ADNAKAEKNALYKKRQFDEIAAYNKAWELHKDITYLNNRAAAEYKGDYDAAIATCEKAIDEGRD
MRADYKLIASFARLGNLYLKKDELPEAVKNFEKSLTEHRTPDVLNKLKLRSTQREIKTRELNAYIDP
EKAEEARLQKEYFTKGDWPNVAVKAYTEMIKRAPEDARGYSNRAALAKLLSFPDAIQDCNKAIEK
DPNFIRAYIRKANAQLAMKEYSHVMDTLTEARTKDVELGGKSIHEIDELMNKATYQRFQAIETETP
EQTMERVSXKDPKPEIVQILQDPMQGILAQARENPAALQDHMKNPVYKKINMLIAAGVIRTR

YOR312C_homolog 1019bp public: 1..1019; CDS: 501..1016 (SEQ ID NO 445)

CCACTAACAAACTTTTTTTTGGCTATACACCCTGAAAAAATTTTTTGTAAAAATCT
TAAGAAATTCAGTTTAGAAGGTATTCACAACAACCGAAGAGTATGTTCAACATCGTTATAATAGA
ATAGAATAAGAGCATGACAACAAGGGATACAAGCTTGAAAAAGAAAAAGGGTGGGATATCTTAA
AATTATTAAAGAGTTTTTTTTATAACATGTCATTGAGATTGAGATTGGGAATACTGAATTCGATTT
TAAAGTCATTGGATGGGAGAGTTAATTATTCGTTTTATTATTAGGATTACCAATGAATAGTAATGA
AGTGATGGAGAGATAGAATGAAAGTATTCAGAAGAGCATCAAGTCCCTTATAAGTTTGTGAGACAT
AATATGTCCTACCCCTTGTCAACTTGTCAATAATTTATTGCTCGTCTTTTAAAGAAATGAATAA
AAAGATTTACTAATTAATTTCAATTTATATAGAAAGATGTCTAGATTAAACGAATATCAAGTTA
TTGGTCGTAATTTACCAACTGAATCCGTTCCAGAACCAAGTTGTTTCAAGTGAATTTTGTCTC
CAACACCGTTGTTGCCAAATCAAGATATTGGTATTTCTTGCAAAAATTGCATAAAGTTAAAAAAG
CTTCTGGTGAAATTTGTATCTGTCAACATTATTTCTGAAGCTAAACCAACTAAAGTTAAACTTTTG
GTATTTGGTTAAGATATGAATCCAGATCTGGTATTCATAACATGTACAAAGAATACAGAGATGTTA
CTAGAGTTGGTGTCTTTGAAACCATGTACCAAGATTTAGCTGCTAGACACAGAGCTAGATTTAGAA
GTATCCATATTTTGAAGTTGTTGAATTAGAAAAAACTGATGATGTTAAAGACAATACGTTAAAC
AATTTTGTGACTAAAGATTTGAAATTTCCCATTTACCACACAGAGTCCAAAAATCTAAGAAATTGTTCC
AAGCTACTGCTCCAACCACTTTCTACTAA

YOR312C_homolog 172aa (SEQ ID NO 446)

MSRLNEYQVIGRNLPTESEVPEPKLFMRIFAPNTVVAKSRYWYFLQKLHKVKKASGEIVSVNIISE
AKPTKVKTFGIWLRYESRSGIHMYKEYRDVTRVGAVETMYQDLAARHRARFRSIHILKVVELEKT
DDVKRQYVKQFLTKDLKFLPLPHRVQKSKLFGATAPTTFY

YOR369C_homolog 932bp PathoSeq: 1..228, public: 229..932; CDS:
501..929 (SEQ ID NO 447)

TGTTTACTTTTTCTGTAGTTTTTAAAGTTTCCTAATTTAACTTCCAAAAGTTTCATTAAACAACAATA
TTAACATACCTTTTGTACAAGCAATTATATTGAAGTTTTTGTATACAAGTGTGTTGTTTTTTGTG
TACATGTGAGATATATAATTGTGTATATACAGTCACGTGAATAGAGCAGAAAAATTACGAAGTAGA
AATATTGGTAGCGCTTAGGGCTATAGCCCTATTTAGTTTGTGCACCACACGACTTACAATTTTTT
TTTTTTTCTTTCTTAGAATCCTTGAGGCACTGACACTGTACTCTCTCTCTCTCTCTCTCTCTCG
TAGGTAGTGAAAAATTTCCACTAGTCTTCCCATAAACCCACCTAGGTTCTTTCTTTTGGAAACCACT
GAGCAGTAAATCAATTTACTTTGACGAAGAAGTCTATACATAAATATAAACTTGTCCCTCCCCCCC
CTTTTTTTTTTAACTAACTAAGAAGAAAAAATTAATAAATGTCTGACGTTGAACAAGAACAATTTG
TTGAAGAAGTTGTTGTTGAAGAACAATCCGGTGCCATCACCATTGAAGATGCTTTAAAGTTGTTT
TAAGAAGTTCTTTAGTCCATGATGGTTTAGCTAGAGGTTTAAGAGAAGCTTCTAAAGCTTTATCTA
AAAGAGAAGCTCAATTTATGTGTTTGTGTGACTCTGTTACTGAAGAATCAATCATCAAATTTGGTTG
AAGCTTTATGTAATGAACAGAAGAAAAATCCCATTTGATTAAAGTTTCCGATGCTAAATTTATGG
GTGAATGGGCTGGTTTATGTCAATTAGATAGAGATGGTAATGCTAGAAAAGTTGTTGGTGCCCTCTT
GTGTTGTTGTCAAAAACCTGGGGTGCTGATTCTGATGAAAGAAACATCTTGTGGAACACTTTTCTC
ACAATAA

YOR369C_homolog 143aa (SEQ ID NO 448)

MSDVEQEIVVEEVVEEQSGAITIEDALKVVLRTSLVHDGLARGLREASKALSKREAQLCVLCDSV
TEESIIKLVEALCNEPEEKIPLIKVSDAKLGEWAGLCQLDRDGNARKVVGASCVVVKNWGADSDE
RNILLEHFSQQ

YPL047W_homolog 881bp public: 1..811, PathoSeq: 812..881; CDS:
501..878 (SEQ ID NO 449)

AAATTTTCCAATCTTGAATTTTCATCTTCAACGTCATAAACTTGTCTGTTTGAAATTTATCGTCCT
CATTATCGTTGTGTCATTTTCATTGTGTCATTGTCAATATTACGGTTACGATTTTGTTCCTTTGAAG
TCTTTGACTCTAGCTGTTCATCTGTGTCATTACCCTTGGCTTGGTTTGTCTTACTGTTGAGCGATGAG
ACAACTTTTTGATTGATTGCAACTGAACAAAAAATACGACAGACACACACACACACACACAC
ACACAAATTTTCAGTCTCTTCCAAGTCGTGTTTTTTTGGGAAGAAAAAACAACCTTGGCCCTAAA
AACTCTATGCTCTAACCGACAACATTAGATTACTTTGATAACTCACAACCTTTAATTAACACTATC
TACAAAAATATGACAAGTACACCAATAACGTACAAGACACTAGTATGAAAGGCAAGCACAACTTGC
AAACAAAAAACCCCTAACCTTTTATTATAGTTTGTGTTGATGTTATTTTGTTCCTTACTAACTAAAA
TCTGTTTTTTTTTTTTTTTCAAAGGCCGATTCTATATTTAATGATCTAATCAACAATATCATTAAC
AACATACATTAACCAATATTAAAGATCATTCTCATTATTAATTCATCTAATAGCA
ATACTAATAGCAATACCAACGGTACAATTGCCAGTAATGGTGGAAATGGGACTACAAGTGATGAAA
ATAATGAAATGAAAAATCAACAATTCAAGATAAATCAAAATTAACAATTAGAACTTCAAGGT
ATTTCCGATGCTTAAATGTGGTAGAAATATTGCCGGTGAAGATTTGCATCTCATATAAGTAAGT
GTTTAGAACGGAAACGGAAATGA

YPL047W_homolog 126aa (SEQ ID NO 450)

MLFCFILTKICFFFSKADSIFNDLINNIQHTLTSLTNIKDHSSLLNSSNSNTNSNTNGTIASN
GGNGTTSDENNEIENSTIQDKSKLKQLETSRYFRCLNCGRNIAGGRFASHISKCLERKRK

YPL137C_homolog 5344bp public: 1..3342, PathoSeq: 3343..5344; CDS:
1250..5341 (SEQ ID NO 451)

CTCTAGAAGTAGGACATCGTATAGTGATAAACTCAATAAGTAATGAAGAAACACGTTTTGTTG
TGCAATGTTAGCTGGCGAGCTCAATATTGGGTCTCTCCGCCGTCTGTCTGCCTTGCATTCTACTTTT
TTTTCTCCTTATGGGAAAACATTAGTACTAGTAGTGGTGGTAGTAGTTGCTGTTGTTGCACCTTTCG
ACGTAGTTGTTTTCCCTCATTTCTTTTCATCTGATTATTCTGTCTTTGTTAACTGCATACAAAGGGA
GGGGAAGAAGAAACAACAAAAGGGGAATTTGAATATACGTCAATCTTTTAATCCTACTACCACGGG
GGGGGGGGGGGTCATACTTCTTGGTGTAATAATGTATGGAGATTGAGGTTATTAGACTTTTAGAA
AGAGGTCTTGGTTGAGTAAGGCGGGATAGCACAAATAATGCGTGTCTAATTGGTCAGAGAATAATA
TGCTTTGGGGAACAATAGAAAGATGTAGCGAGAGAAATAGAATTNCAAGGGTAAGGATGATTAACT
TTTTTTTTTTTTTAATGCTTGGAGTACTTTGTTGTTGGAAAGAGTATTGCAGAAGTAATAGTTTAAAT
AAAAGAAAAGTATATAACTTTAGTAATCGGAGAACAATTGAAATCAATATTTTGAAATATAGTTT
TATAGAGTAACCTGGGTCGAGGTGAACCCGAATTCAATATTGGTTTTCCGGTGTATATGCTACAT
AACCATCCTCATCTTGAATGAAACAAGGATAATAGAAATGAGTATATTAAACAACAACATTATGT
TGTTACTGTTGTATCTGTTTTTGGTCATTGCCATGGTAATTTTCATATTTAGTAACAATTTAGTG
TTCTCGTAAGTCTCTCCTTCTCTGGGAGATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
TGTTAATTTGTTAATTTGTTGATTATTGATTGTTCCCAATTAATAATCCGATAAACTTGAACAATAA
ATTGTCATCATAAATTTTTTTTTTAGAAAATCACTCCATAAATTAAATTTATTTATATATTAAATTT
TAAATCGGAACCTCCGTCAATTGGATTCCGGTTTTTTTTTTTTTTTATTTGTTTCATTTATTTCTTGAT
TTTATTTTCTTTTTGCTTCTTCTCTTTTATTTTCTTAGTTTCATAATTTTGACAGATAATA
CTTGAACCTGGTTAATTTTAAATCAACTTCGTGATTTTTTCCGGAAATCTAATAATATCAATGAC
CAGTAATCTGCCACCCTTGGTCTACAACCAACGATCAGAGACTACCCCAAAGCGGAGTTTCATC
CATACCCACAAATAAATTGCCTTTACCTAATGCCAATGAAGATTTTGCCACGGGTGTGTCGAATGG
AGATGTTGACTGGCTATTTTCGAGGTAAATCAAAGAAATGGGGAAAAAGATGGCTAACAACAATGC
CAATAAGGATGAACGAAAGAATAGTCATGGTAACATCAAAAACCTCGGAAAAAATACCGCAAAACC
CAATGAAACTAAACATGAGTCTAATGGTGAGAAGTTAGAATTCAATGTTCCAAAATCTGTAATGCC
AACAAAGCATACATCGTCTGGGAACCCAAAAGCACCTACCAATGGACAAATCTCAAATGTAACACC
AAGTCAACCAAGTCCGAAACAGACCCTTCTGGGTCAACAAATGCAATGATATACCTCCAATTTT
TCCTAAACAACCAGAAAAGGCATCAAAGTTGAATAAACTAAAAATTTGGGCGTTCAAGATCGTCTTC
TGCATCAACAGTCTGTTCTATCTACAACAGCTTCAACTACTACTAATCCTGGAGATCCTAAAAG
TCAACCAAAAAGACGGAGCAGTAGTTTTAACTTGTACTCTCTCTCTGACGAGTGATTTGGCATA
TGACGATCCTGATTGGTATCTCAATTATCAAACAATTCAAATTTCTCTGAACATCCTCGCCTAA
TGTTTCTCGTTCAAATAGCAAAAAAGGTGGGTTATTTCAGTTCACTTTTCATCAAAATTTAGATCAAG
CTCGGCTTCATCTAAACAACCACAACCTGCATTCATCGTCTACACCATCAACCACAACGACAAATGG
TGGCGGTAACCTCGTCCGCTGCTCCAAATCATCCCATCACTCCCCCAAATTTAATCCTTCACTTGT
TGGTCCAGTATCAAAGCACAAATCGAGAAGCTGAAGATTTGGTGTCTCTTACCAATACCTTGCCTGC
TGGGAGTGAATACCAATTAAACGTAAACCATCAATATCGGGAATTCATTTTCAAAGATTTCATT

TCTCGATGATGCAAGTTCTTTCACCGTCATCTTCATTAAACTCTGATGGGGGGCTTAAGTTTTTTCAG
GAGACGTTCCCTCTGTGGCATCTACACCATCAACACACGCGTCAACACCTCGAGTGATTTTGAACAA
AAACCCCAATAGGAGAAAAGTACCCATTGAAGAAATATCTGAAGTTCGATTGCGTCGGGTACCTT
TTCTGTTGATAAACTCGAGCAGCATCCGCAACAGCAGATTCTTCAAGAAGACCTAAACGAGGTAA
TGTTTTAATPCCACAGGACATCAATGCACCACCTCCAAGACTATGTCTTGGGATTTTCAGTTAATGA
ACCAATAATAAAGATGACGGTAAATCACACAACCATTCCAAATATAGTGATCATGAAATTGCATT
AGCTGAAGATGCTCAACGCCGAGCAATTATTGAAGCAGAAAAACATGCTCAAGAAGCTCATCGACA
AGCCAAAAAGATTGCTCAAGAAGTTTCTGGGTATAGATCACATAGATTTCATATCCATTAAAGAAGG
TGGTAGTGTTGGTAATTCTAACACCAACGGCAACGACAATGACGAAGATGATGATGAGGTTGAAGA
AGCAGTTGATAAGAAATTTGGCAAATGATGTTTCTGTGGATGGACCGTTGCATGTCCACGAACAACA
TTTCGAAGAAGAAATTTGAAAGCAAAAACAGGTGAAAAGACCATTTCATTGGAAACAATCTATACAAG
ATGTTGTGCTATTACGAGAAATTTTACCAATCCCAGCAACATTGAAACAATTGAAAAATAAGACAGC
ACCGTTGGAAGTGTTAAAGATGCTCAACCCAAAAACCAACTTTAATTGATGTGTTATCTTTTTTCAGA
TTTTATTGCCATTACACCTATTAACACGGTCATTTTTGATAACGTGACTATGACAACAGAGATGTT
GAAAAACTTTCTTGGATCGTTGACATATAATAAACAATTGGAAAAGTTATCGTTGAGAAATGTTTC
CATTGATGAGTTGGGATGGAAGTATTTGTGTGAATTTTTGGCAACAATAAAACAGTTAAGAAATT
GGATATATCAACAACGATCAAGCCAGATACCCAGACACAAGCATTCTGTGGTAATATGAAGT
GGACTTTATTATTTCGATCATTAATTTTGGGTGGTGAATAGAAGAATTGGTTATCAATGGATGTAA
ACTATCCGATGCAATATTTGAAAAGTTCATCAATCAAGCGGTTAAGAAGTCAACCTATCGATTAGG
TATTGCTGGTATTGATTTGAATGTTAAAAAATCAGAAATGGTCACATCGTGGTTAACTGATGGTAA
TTCTCAATGTGTTGGTGTGATATTGCTTTTAAATGATTTGAGCAAGGGACAATTACGTCCATTTCAT
TAATGCGTTTAACTGGCAAAGTCAACAATTTAGTGTTTTTTTCATTGAATTCAACCAATTTACT
GAACATTGAAGAAACTTCTGACTTGATCAAGTCATTAATTAATGTTAAAACATTACGATTTTTAGA
TTTAAAGTTCCATACCTAATATCTTCCGAAAAATAATTACCCATTGGGACAAATACTTGGCCAGATA
TCCTAATCTTCGAAGAATACATTTTGATCTTAATGAATTAACCGCACAAAGCTATTGGGTGATTGGC
GGGGTGTTTACTGAAAATGCCCAATTAGTTTCATGTCTCGTTATTGGGTAATAGAAATTTGTCAAC
TACGTCAAGCAGCTACATTATACGGAGCAGTTAAACAATCCAAGACCTTGTTTGCTCTTGATTTGGA
CTACGATTTAATACCTGATCAATTATCACAACGATTTGCCTTTTATTGATGAGAACTTGGAAAT
CACTTTGAAGCCATCTCATGGCGGCAATATTGAAAGCAATCCAGAAAAACCAGAGGATTTGATGTA
TGATGGATCGTTATTAATGGAACAGCTGAAAAATTATTAGTTGAAATAGAAAAGGGTAAGAAAGA
GGATATCAAAATGCAAAGAATTATATCCGATTGAGTATTGGAAGAACAAGATCGATTTCGTAAGGA
TATTCACAAAACCATTTGATACATTATTCGAACAAAGAAATTTAGGTAAATTATCATTGGAAGGTAA
AGAGAAATTTAGTTTCGATTTTGTGTTATTAGATTTCGTCTTTAGAAAAATTGGTTGTTATGGTTGAGGA
ACATGCCAACCGATTATTATTAAACACCAACGACCTCCACGGACGATCTCAGAAGTAGAGCCATGTC
GCCATCGGTCACTGTTGATACAATCCATGAAAGTGCAAATGAGTTGATTACTGCTGGACCAATTTT
ATCACCACATGTCAATAGGAAAGCAGAACAAAGCTCGTATTTCCAGTGTTTGCCAATAATGATAA
TTTGACCCCTCATCAAGTTGTCTGTTGAGTCAAATGATGAAGGTAGAGATGTTCCAATAGATAAAAT
GACAGGACGACCAGTTTGTATTCGATCAATTAGTCAAACCTCTGTGCATGCAAAAGAGCAAGAAAT
TGAAGAAGGGGAGCTTCATAAATTTGGATTCTTTATTCAACAAAAAGAGAGACAAAAACAACA
ACAACAACAACAACAACAGAACTCACACCACCAGCACCAACCGGCCAGCTGATCCAACAAGAAAA
CCAGCTGCCGCTGCCACAACAAGGAAATATGAAGATTACCGATATTAAATACATTACCGTCAGG
ACCAGAGTTGAGAGATGCTATAATGGCAGCTAAGGGAGTAGCAAATGTTACTGAATTAATTGATCG
AATTAATAATCATCGTGTTAAAAATCGATGCACCATCGACAAAACACCATCATGAATTGAACAAACC
AAATTCGACAAAGTAGTTGAGGATGAAGTTGAAGTTTCTGATAATGCCTCTATTGATTCTACTAA
TGGTGACGATTTACATCAACTTGGTGACGGTAAACATAATGGTAATGGTACGGTTGATCCCATGGT
TAGTGAAGTTTATGACAAGTTGTTAAATGATGCTGAACGAGTCAGACTGAATAGAGATATATAA

YPL137C_homolog 1364aa (SEQ ID NO 452)

MTSNPPLGSTTNDQRLPQSGVSSIPTNKLPLPNANEDFATGVSNQDWDWLFGRKSKKLKMKMANN
NANKDERKNHGNINIKNSEKTAKPNETKHESNGEKLEFNVPKSVMPKHTSSGNPKAPTNGQISNV
TPSQPSPKQTTSGSTNANDIPPISPKQPEKASKLNKLKIGRSRSSASTVVPSSTTASTTTNPGDP
KSQPKRRSSSFNFVTPSLTSDLAYDDPALVSQLSNNSNSSNSSSPNVSRNSKKGGLFSSLSKFR
SSSASSKQPQSHSSSTPSTTTNNGGNSSAAPKSSHSPKFNPSLVGPVSKHNREAEDLVSLTNTL
PAGSGIPIKRKPSISGNSIFKDSFLDDASSPSSSLNSDGGLKFFRRRSSVASTPSTHASTPRVIL
NKNPNRRKVPIEIESEVRLRRVTFVVDKLEHDPQQQIPSRPKRGNVLIPODINAPPPRLCLGISV

NEPNNKDDGKSHNHSKYSDEHETALAEDAQRRAIEAEKHAQEAHRQAKKIAQEVSGYRSHRFISIK
EGGSSVGNSTNGNDNDEDDDEVEEAVDKKLANDVSDGPLHVHEQHFEIEIESKTGEKTISETIY
TRCCHLREILPIPATLKQLKNKTAPLEVLMNPKPTLIDVLSFSDFIAITPINTVIFDNTMTTE
MLKNFLGSLTYNKQLEKLSLRNVSIDEGLWKYLCEFLATNKTVKKLDISQRIKPDTPDTSIRGNM
NWDLFIRSLILRGGIEELVINGCKLSDAIFEKFINQAVKKSTYRLGIAGIDLNVKKSEMTSWLTD
GNSQCVRGVDIAFNDLSKGQLRPFINAFNTGKVMNLVFFSLNSTNLSNIEETSDLIKSLINVKTLRF
LDLSSIPNIFPKIITHLDKYLPRYPNLRRIHFDLNELTAQAIGSLAGCLSKMPQLVHVSLGNNRL
STTSAATLYGAVKQSKTLFALDLDYDLIPDQLSQRIAFYLMRNLEYTLKPSHGGNIESNPEKPEDL
MYDGSLLMETAEKLLVEIEKGKEDIKQRIISDSVLERTRSIRKDIHKTIDTLFEQRNLGKLSFE
GKENLVRFCLLDSSLEKLVMVEEHANGLLLTPTTSTDDLRSRAMSPSVTVDTIHESANELITAGP
ILSPHVNRAEQSSYFVFANNDNLTPHQVVESNDEGRDVPIDKMTGRPVLRISISQTSVHAKEQ
EIEEGELHKFGFFIQKKERQKQQQQQQQQNSHHQHQPAAQSIQQENQSPSPQQGKYEDLPILNTLP
SGPELRDAIMAAKGVANVTTELIDRINNHRVKIDAPSTKHHHELNKPNSDKVVEDEVEVSDNASIDS
TNGDDLHLQLDGDKHNGNGTVDPMVSEVYDKLLNDAERVRNSNRDI

YPL175W_homolog 1859bp public: 1..393/395..1859, PathoSeq:
394;CDS: 501..1856 (SEQ ID NO 453)

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CGGCTGCTTCTTTGCCTAGTGATGCATTTGTACAATAGAATTATAATTAAGAAAGGTAGAATAG
AATTCAATGTAGGTGATATCACTTTCTGAGAGTTCTTATTACGATATATAAAATACATAGCCAAAA
TTATAATGAAGTAAAAACATGTAACCTGTGTAATTTTATTCAAGTCCAAAGGTATTGATTAATATTG
TAGAGTGTGAGCATTAAAAATATGAAGGAAGACCGATAACCTAAAGTTTCTCAGGGTGTCGAA
GGCTAGGAGGAATAAAATCTGAGTAGAGAACCTTTCGTTTATATCAGTTTTTTTGCAGAAAAAAGG
AAAACAAAACAAAATAACACCACAAACGAATTACACAAGCACATCCTAAACACCACTCTGTTGGAG
CACCAATCAACCTGAGAAATGCAAACTTGTATAAAATATGGGATACAATATAGCAATGGTAACAG
ATTTTTTTTTACCCTCAACCTGGAGGAGTAGAGTTTCATGTGTATCATTTATCACAAAACTCATTG
AATAGGACACTCAGTGGTTATCATAACTCATAATTATTCATCAAGAAATGGTGTACGAGTATTAA
CGAATGGTTTGAAGGTGTATTATGTACCACTTTGGGTGATCTATAGAAGCTCAGTTTTCCCAACTG
TATTTCTGTGCTTCCCAATATTGAGGAATATCTTCATACGAGAAAAACATTGAGATTATTCACGGAC
ATGGTTCCTTCAGCACATTATGCCACGAAGCTATATTACATGGCCGAACAATGGGATTAAAAACAG
TCTTCACTGATCATTCACTTTTTGGATTTCGCGAGATTGGATCAATTATGGGGAATAAAGCATTAA
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TAAGAGGATCAATAGACCCCATAAAAGTGAGTGTGATACCGAATGCAGTTATTCTGAAAGATTTC
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TGTTTTCAAATAAAGGAGCCGATCTATTAACGGCTGTTATCCCCAAAATTTGCCAGTTGAAACCAA
AAGTGAAATTTCTAATTGCTGGTGACGGCCCCAAGTTTATTAGATTTAGAACAAATGAGAGAAAAAGT
ACTTTCTTCAGGAAAGGGTTACATTAGTAGGCGCTATAAAACACGAAGAAGTAAGAGATGTAATGG
TCCAAGGTGACATATACTTACATCCTTCATTAACAGAGGCGTTTGGTACAGTTATTGTGGAAGCTG
CATCATGTGGGTTATATGTTGTCACTACAAAAGTTGGGAGGCATACCCGAAGTCTTACCAAACGAAA
TGACAAGCTTTGCTGAACCGGAAGAAAACCTCACTTATTGATGCTGCTATAGATGCTATAAATAAAA
TTGAAAGTAATGAAATCGATACCTCAAAATTTACGATGCGGTTGCAAAGATGTACAGTTGGAATG
ATATTGCAAGAAGAACAGAAAATGTTTATAATTCACTTGATTTAGACAAACTAAACGAGTCTTTAC
TTCACCGATTACAAAGATACTATTGTTGTGGTATAATAGCAGGCAAACTTTATGCTTTATGTGTAA
TAGTGGATATTTTTATTTTCGTGATACTAGAATGGTTGTATCCCGCTGATCATATCGATAAAGCAA
CAAAATGGCCACTGGCTATCAAGGAAGAAGACGAGCTGGAAGAAGAAACATTTATTTTTCCGAACA
AAGTAAATTAG

YPL175W_homolog 452aa (SEQ ID NO 454)

MGYNIAMVTDFYPQPGGVEFHVYHLSQKLIELGHSVVIITHNYSSRNGVRVLTNGLKVYYYVPLWV
IYRSSVFTVFSFPIRLNIFIRENIEIIHGHSFSTLCHEAILHGRTMGLKTVFTDHSFLFGFAEI
GSIMGNKALKFTFSDVGHVICVSHTCKENTVLRGSIDPIKVSVIPNAVISKDFKPKSHCVNKNYTK
EITIVVITRLFPNKGADLLTAVIPKICQLKPKVKFLIAGDGPKFLDLEQMREKYFLQERVTLVGAI
KHEEVRDVMVQGDIIYLHPSLTEAFGTVIVEAASCLYVVTTKVGGIPEVLPNEMTSFAEPEENSLI
DAAIDAINKIESNEIDTSKFHDAVAKMYSWNDIARRTEENVYNSLDLDDKLNESLLHRLQRYCYCGII
AGKLYALCVIVDIFIFVILEWLYPADHIDKATKWPSAIKEEDESEETFFIFPNKVN

YPL218W_homolog 1231bp PathoSeq: 1..407, public: 408..1231; exon 1: 501..518, intron 1: 519..676, exon 2: 677-1228 (SEQ ID NO 455)
GATACAATTCACGACCTCTAATTTTCCTTAGTGATAGGTTAATCATGAAATATATAAAATGTCTAGA
AATAATTGAATAATGATATAAATATAATGTTGTGAAACTTGTGGAAAAATTTGACAGCCTAGTAAC
TCAAGTGTGTTACACTCTTGTATTATTATTATATATCGTTTACAAGTAGATTTCTCATTTTGA
ACAGCAAATACGTGTCGTTAATAGGAATCAGAGGCAGAAAGAAAGAGAGAGAAAAAAGGACA
CATTTACACGTACACCTTAACTTGAAGGAAAAAACAACAAGAGAGACAAAGAAAGAGACAAA
GAAAATACTTTCAACAACGAAAGATTGAGATATTGGTGATTTTCACAAACCAAAAAAAGAATAC
ACAACTTGTAGATTAAACAGAATTTGAACATTTCTAGAGTTTCTTATATTCCCCCAAGGTGGACAA
TTAATAATAACATTTGATTATACAAGAACATTTCAATCATGTGGATTTTGGTGGTGTATGTAAT
GATTTATCTTTTACCGAATCAATACTTTTATTATGAGTGATTGGTTGGTTGGTTATAATACCACCAC
TTTATTCTATTAAACCAAGTTTGTATCTAATTACTGATCTGTATATACTAACCAATATTTACCTTAT
CACTTAATTATTTACAGTTCAAGATATATTATCATCATTAGGATTATGGAATAAACATGCCAAATT
ATTATTTTTTAGGGTTAGATAATGCTGGTAAACTACTCTTTTACATATGTTAAAGAATGATAGATT
GGCCACTTTACAACCAACATTACATCCAACCTTCAGAGAATTGGCCATTGGATCAGTTAGATTTAC
TACTTTTGATTTAGGTGGACATCAACAAGCTAGAAGATTATGGAAAGATTATTTCCCTGAAGTCAA
TGGTATTGTCCTTTTGTAGTCGATGCTGTGATACCGAAAGATTGCTGAATCCAAAGCTGAATTGGA
AAGTTTATTTAGAATTGAAGAATTGAGTCAAGTTCCATTTGTTATTTTGGGTAATAAGATTGATGT
TCCTACTGCAGTAGGGGAAATGGAATTGAAAAATGCCCTTGGATTATATAATACTACTGGTAAAGA
TACTGGTAAATTGCCTGAAGGTACTAGACCAATTGAAGTGTTTATGGTTTCCGTTGTTATGAGATC
TGGATATGGTGAAGCCTTCAAATGGTTATCACAAATACATTTAA

YPL218W_homolog 190aa (SEQ ID NO 456)
MWIFDWVQDILSSLGLWNKHAKLLFLGLDNAGKTTLLHMLKNDRLATLQPTLHPTSEELAIGSVRF
TTFDLGGHQARRLWKDYFPEVNGIVFLVDAADTERFAESKAELESFRIEELSQVPFVILGNKID
VPTAVGEMELKNALGLYNTTGKDTGKLEPSTRPIEVFMVSVVMRSGYGEAFKWLSQLYI

YOL127W_homolog 429 bp, public: 1..429, CDS: <1..>429 (SEQ ID NO 475)
CTTATAGCAACTACTAAAGCTTCAGCTGCTAAAAAGCTGCTTTGAAAGGTGTTAACGGTAAAAAG
GCTTTAAAGTTAGAACTAGTACTACTTTTACAGATTACCAAAAAACCTTAAATTAACCAGATCTCCA
AAATACCAAAGAAAATCAGTCCCACACTACAACAGATTGGATGCCACAAAATCATTGTTGCTCCA
ATTGCCACTGAAACTGCTATGAAAAAGTCGAAGATGGTAACACTTTGGTTTTCCAAGTTGACATC
AAATCCAACAAACACCAATCAAATCTGCTGTATAAGAAATTATACGATGTTGATGCCTTATACGTT
AACACTTTGATCAGACCTAACGGTACCAAGAAAGCTTACATCAGATTAACCTCTGACTACGATGCT
TTGGATATTGCTAACAGAATCGGTTACATCTAA

YOL127W_homolog 142 aa (SEQ ID NO 476)
LIATTKASAAKKAALKGVNGKKALKVRTSTTFRLPKTLKLTRSPKYQRKSVPHYNRLDAHKIIIVAP
IATETAMKKVEDGNTLVFQVDIKSNKHQIKSAVKELYDVDALYVNTLIRPNGTKKAYIRLTSYDA
LDIANRIGYI

YJL188C_homolog 117 bp public: 1..117, CDS: <1..>117 (SEQ ID NO 477)
TTAGATACCCAACCTTAGTTCCTTCTCCAGTGCTTCTTTTAGCATTGTATCTGATTTTGTGTCAGT
TCTCAATCTGATCCATTGTGGCAATGGTCTGTTTTGCTTTTGAGCCTTAGC

YJL188C_homolog 39 aa (SEQ ID NO 478)
LDTQLSSSPVSSFSIVSDFVSSQSDPLWQWSVLLLLSLS

YGR183C_homolog 198 bp public: 1..198, CDS: 1..198 (SEQ ID NO 479)
ATGTTGACAGTCCTTGGTCGTTTACTTGAAGAAACTCAATCTACGTTGCCACTATCTTTGGCGGT
GCTTTTGTCTTTCCAAGGTTTTTTCGATGTTGCAGTGAACAAATGGTGGGAGGAACACAACAAAGCT
AAATTATGGAACCAAGTCAAAGGAAATTCCTTGAAGGTGAAGGTGAAGAAGAAGATGACGAATAA

YGR183C_homolog 65 aa (SEQ ID NO 480)

MLTVLGRLLERNISIYVATIFGGAFQGFDDVAVNKKWEEHNKAKLWKNVKGKFLEGEGEEDDE*

YDR529C_homolog 457 bp Pathoseq: 1..457, CDS: 1..457 (SEQ ID NO 481)

ATGGTTCAATCTATGACATCTGTCGTTAAGGCAGCTAATTTTCATTTTAGCAAGACCAACATTATCA
AAAATCATTACACCACTTGCTCAAAAATTCAGTCTTATGCAGGGTATAGAGAAATGGGATTAAAA
TTCAATGATTTACTTCTTGAAGAAACCCCAATTATGCAAACTGCTATTTAAAGATTACCTTCAGAA
TTAAATTAATCAAGAAATTTTAGAATTCTTACTGCTCATCAATTAGCTTTATCTCATCAATTATTA
CCAGCTGAAAAAGCTGTTAAACCTGAAGAAGATGATAATTATTTGATTCCCTTATATTTTAGAAGCT
GAAAAGGAAGCTTTTGAAAAAGCTGTATTGGGGAATATTGACGCTAGTGCGATTGTAATTAATACG
ACGAATAAGAAACCGACGAGGAAGAGGAAGAAGATGAGAAGGTCAAACATTGAAATATGAA

YDR529C_homolog 151 aa (SEQ ID NO 482)

MVQSMTSVVKAANFILARPTLSKIITPLAQKFTAYAGYREMGLKFNDLLLEETPIMQTAIKRLPSE
LNYSRNFRILTAHQALSHQLLPAEKAVKPEEDDNYLIPYILEAEKEAFEKAVLGNIDASAIIVINT
TNKKRTRKRKKMRRSNIEI

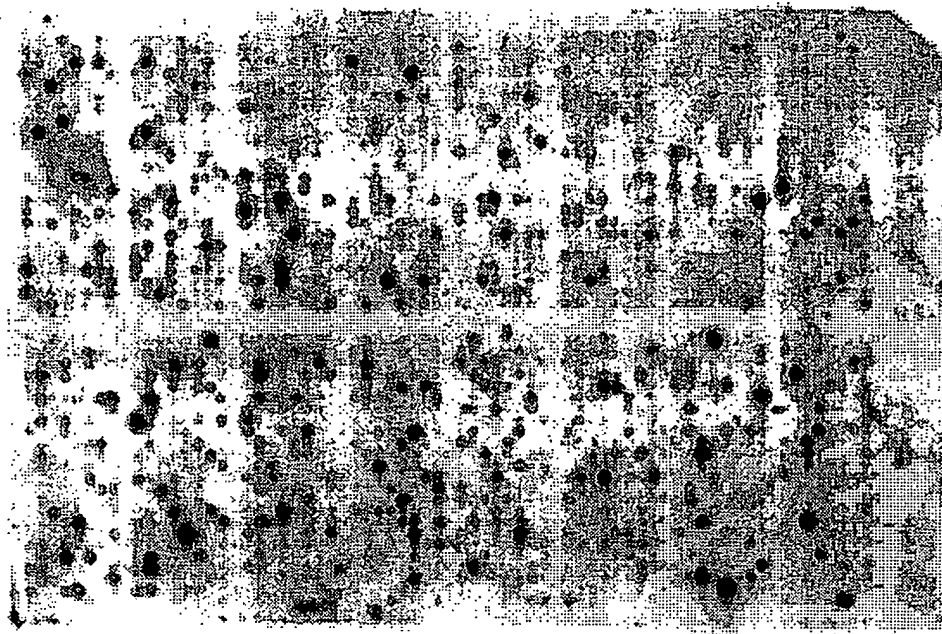
YBL003C_YDR225W_homolog 399 bp public: 1..399, CDS: 1..399 (SEQ ID NO 483)

CTACAATTCTTGAGAAGCCTTAACACCACCTTTACCTGATTTCTTTGGCAACAAGTTTGTATGGAT
GTTTGGTAACACACCACCTTGGGCGATGGTGACATCACCCAACAATTTGTTTAAATTCATCATT
TCTGATGGCCAATTGTAAGTGTCTTGGGATTATTCTGGATTTCTTGTTGTCTCTGGCAGCGTTACC
AGCTAATTCAAAATTTAGCAGCTAAATATTCCAAGACTGAAGTCAAGTACACTGGAGCACCAGA
ACCGATTCTCTGAGCGTAGTTACCTTTTCTTAACAATCTGTGGACTCTACCGACTGGGAAAGTCAA
ACCAGCTTTGGCTGATCTTGAAGTTGAAGCTTTTTCGGAAGTTCCTGCTTTACCTTTACCACCTGA
CAT

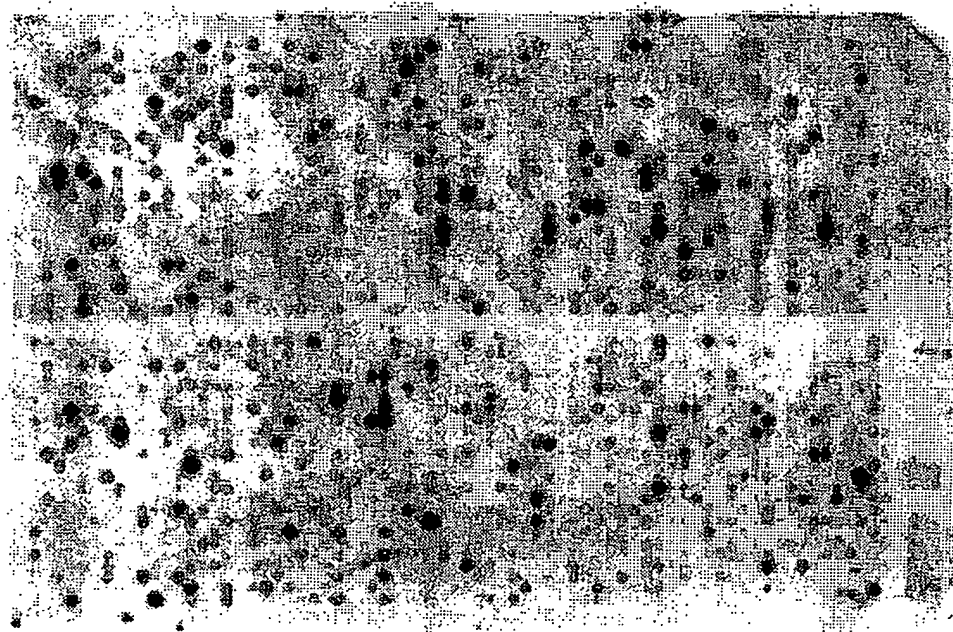
YBL003C_YDR225W_homolog 132 aa (SEQ ID NO 484)

MSGGKGKAGTSEKASTSRSAKAGLTFFVGRVHRLLRKGNYAQRIGSGAPVYLTSLVLEYLAEEILEL
AGNAARDNKKSRIPRHLQLAIRNDEELNKLGLDVTIAQGGVLPNIHQNLPPKSGKGGVKASQEL

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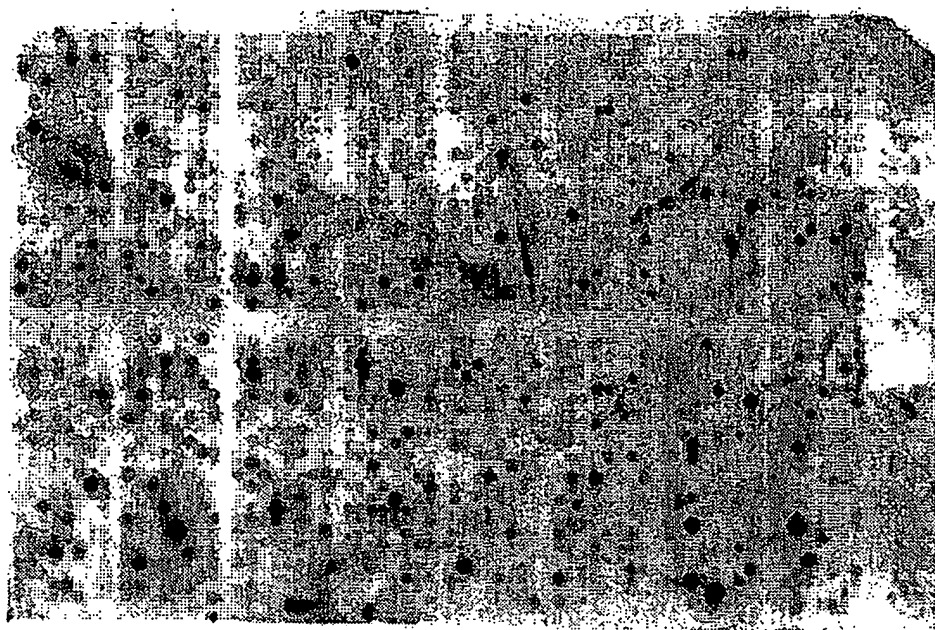
Filter I



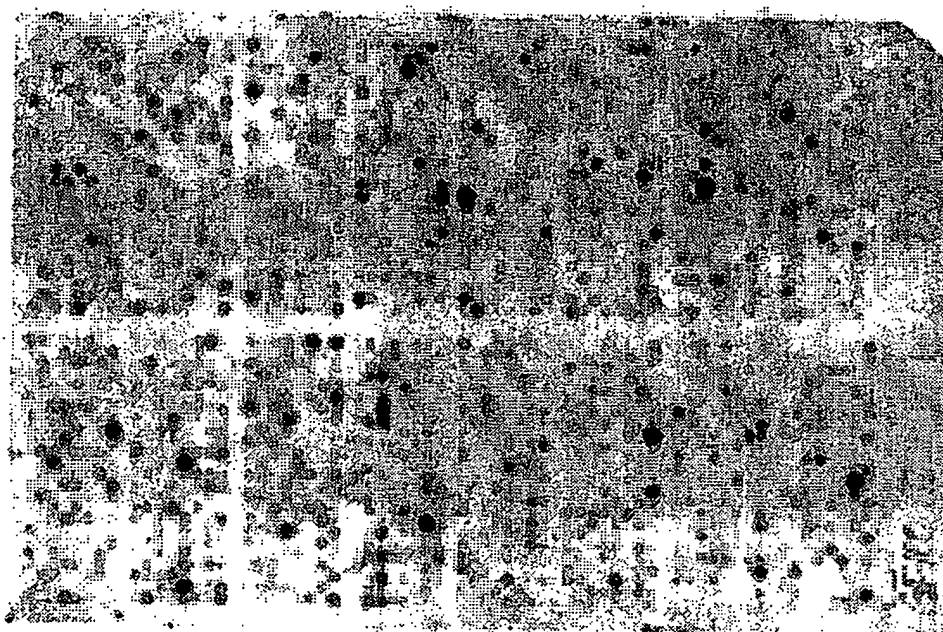
Filter II

FIG. 3A

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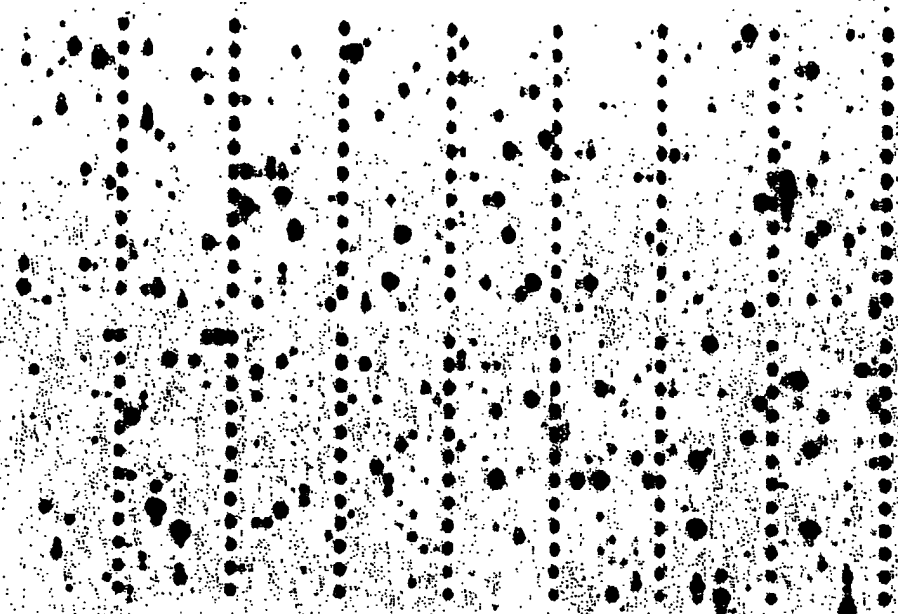
Filter I



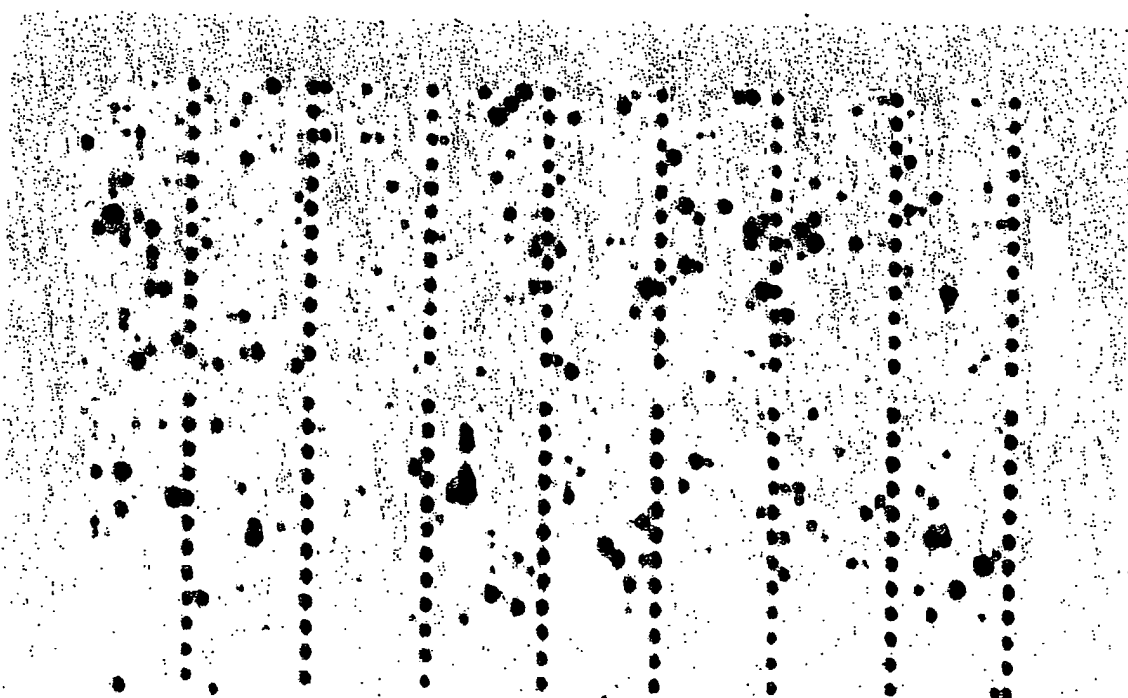
Filter II

FIG. 3B

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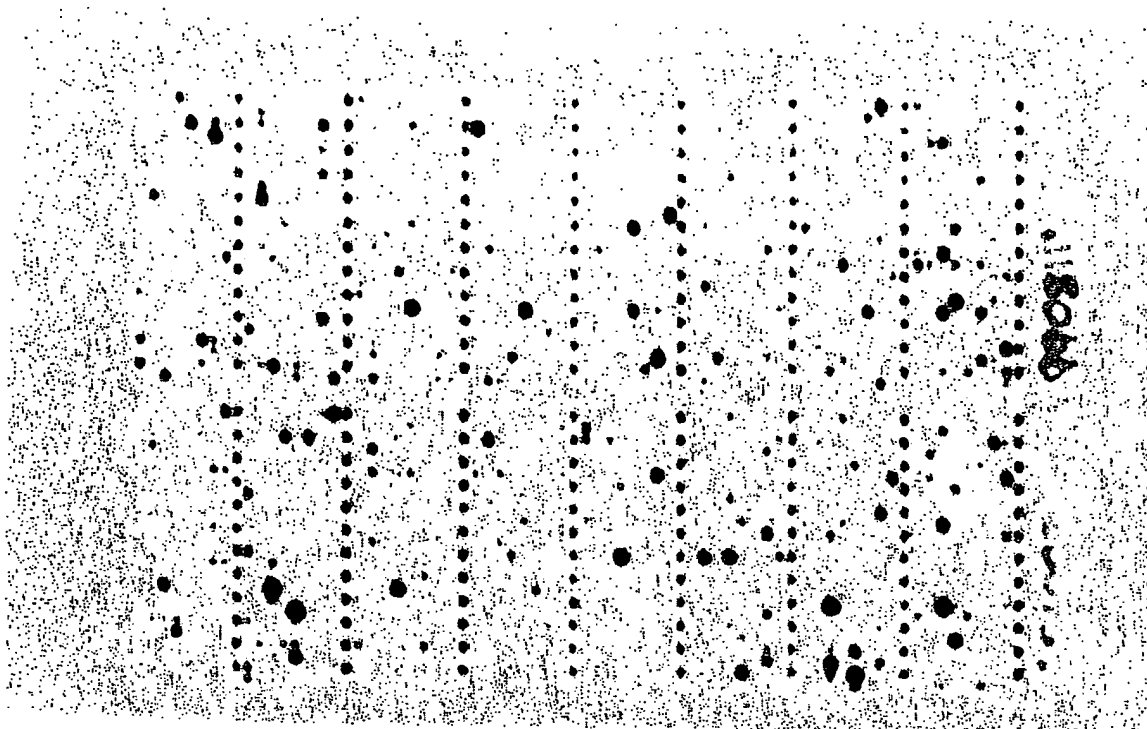
Filter I



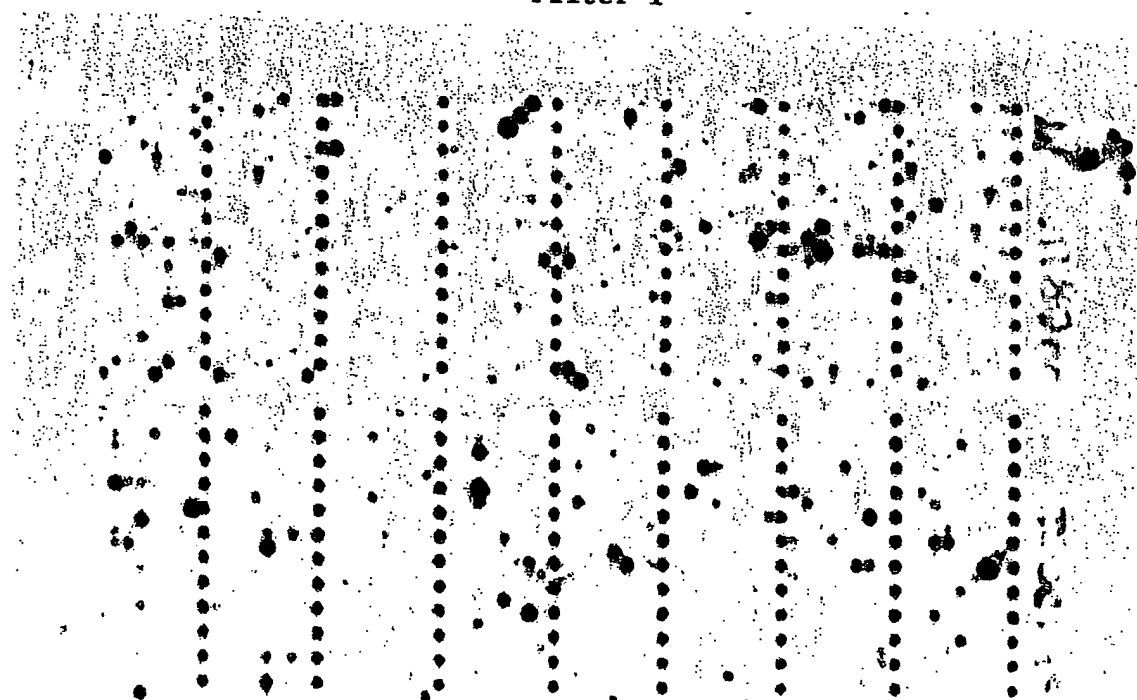
Filter II

FIG. 4A

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Filter I



Filter II

FIG. 4B

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